9th National IDeA Symposium of Biomedical Research Excellence

June 16-19, 2024

Washington Hilton, Washington DC

A Welcome Message from the Co-Chairs

We welcome you to the 9th Biennial National IDeA Symposium of Biomedical Research Excellence (NISBRE) at the Washington Hilton on June 16-19 in Washington, DC.

This year's conference will showcase the scientific and training accomplishments of the IDeA program of the National Institute of General Medical Sciences (NIGMS). The IDeA program supports scientific centers of excellence and trains biomedical scientists in the IDeA-eligible states. On behalf of the NISBRE Organizing Committee, we are so glad that you have joined us to highlight the activities and successes of the IDeA investigators.

The meeting program includes high-level scientific presentations in a variety of disciplines. The agenda includes plenary and keynote presentations in varied areas of scientific investigation, poster presentations of IDeA scientists, discussion forums, and workshops. The workshops are designed so that the attendees acquire new scientific and career skills. We expect over 1, 000 attendees ranging from undergraduate and graduate students to postdoctoral fellows, junior and senior faculty and staff from each COBRE, INBRE, CTR, I-RED programs including participation by programmatic and scientific staff from most NIH institutes.

A goal of NISBRE is to maximize opportunities for networking and collaboration. NISBRE will provide exciting opportunities to learn from and interact with colleagues and confer with NIH scientific and programmatic staff. This year's conference will use new technology, allowing communication among all attendees and opportunities to meet to discuss collaborations and individual presentations. We hope that your interactions will facilitate sharing and best practices within IDeA programs.

We are so glad that you have joined us for this important national conference highlighting NIH IDeA Programs. Thanks for joining us this year in DC!

Gus Kousoulas, PhD, Co-Chair

Rick Bevins, PhD, Co-Chair

The National Association of IDeA Principal Investigators (NAIPI) is the collective voice of all of us in the IDeA community. NAIPI aims to protect and promote the IDeA programs.

Louisiana State University and University of Nebraska-Lincoln have been awarded the NIH:NIGMS U13 grant (1U13GM143856 "National IDeA Symposium of Biomedical Research Excellence-NISBRE") to organize the 2024 and 2026 (In person) NISBRE Conferences.

Support for the NISBRE2024 conference was provided by the Louisiana Biomedical Research Network at Louisiana State University [PI: Konstantin (Gus) Kousoulas, P20GM103424] and the Rural Drug Addiction Research Center at the University of Nebraska-Lincoln [PI: Rick Bevins, P20GM130461].

ORGANIZING COMMITTEE

K. Gus Kousoulas, Ph.D., Chair
Hannelore and Hans Storz Distinguished Professor Head, Department of Pathobiological Sciences Principal Investigator, Louisiana Biomedical Research Network (LBRN) Director of the Division of Biotechnology & Molecular Medicine (BIOMMED) School of Veterinary Medicine Louisiana State University, Baton Rouge, LA 70803

Rick Bevins, Ph.D., Co-Chair
Rural Drug Addiction Research COBRE PI, Chancellor's Professor & Associate Vice Chancellor for Research, University of Nebraska - Lincoln

Carolyn Hovde Bohach, Ph.D.
PD/PI Idaho INBRE, University Distinguished Professor of Microbiology, University of Idaho

Lucy Liaw, Ph.D.
COBRE PI of Mesenchymal and Neural Regulation of Metabolic Networks,
Maine Senior Scientist and Director of Research Education and Training
MaineHealth Institute for Research

R. Scott Seville, Ph.D.
President, National Association of IDeA Principal Investigators (NAIPI)
Director, Wyoming INBRE
Professor, Zoology and Physiology
University of Wyoming

Sharon Rounds, M.D.
PD/PI Advance RI-CTR Associate Dean for Translational Science Professor of Medicine and of Pathology and Laboratory Medicine the Warren Alpert Medical School of Brown University

Krishan Arora, Ph.D.
Chief of the Networks and Development Programs Branch in the Division for Research Capacity Building, NIGMS, NIH

Michele McGuirl, Ph.D.
Acting Director of the Division for Research Capacity Building, NIGMS-NIH

ORGANIZING SUPPORT TEAM

Devan Crawford
Rural Drug Addiction Research COBRE, Director of Research Strategy, University of Nebraska - Lincoln

Ojasvi Dutta
Louisiana Biomedical Research Network (LBRN), Program Manager and Assistant Director, Louisiana State University

Alexis Noah
Rural Drug Addiction Research COBRE, Event and Program Associate, University of Nebraska – Lincoln

Bratie Leary
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Joey Caruso
Rural Drug Addiction Research COBRE, Administrative and Research Associate, University of Nebraska – Lincoln

Halley Horne
Rural Drug Addiction Research COBRE, Communications & Marketing Specialist, University of Nebraska – Lincoln

Harikrishnan Mohan
Louisiana Biomedical Research Network (LBRN), Postdoctoral Researcher, Louisiana State University

Md Hasan
Louisiana Biomedical Research Network (LBRN), Assistant Professor Research, Louisiana State University

Imran Hossain
Louisiana Biomedical Research Network (LBRN), Graduate Student, Louisiana State University

Christella Nelson
Louisiana Biomedical Research Network (LBRN), Master's Student, Louisiana State University

Emmanuelle Ruiz
Louisiana Biomedical Research Network (LBRN), Senior Postdoctoral Researcher, Louisiana State University

2024 AWARD WINNERS

Please join us in recognizing our award winners for the NISBRE2024 conference. Congratulations to all awardees for their exceptional work!

COBRE Rising Star Award

The COBRE Rising Star Award recognizes individuals who exemplify ideals of research excellence and commitment to mentoring, and who have established independence through a COBRE program.

> **James W. Checco, Ph.D.**, Assistant Professor Of Chemistry University Of Nebraska-Lincoln
>
> **Yun Li**, **Ph.D.**, Associate Professor (tenured), Neuroscience, Department of Zoology and Physiology, University of Wyoming
>
> **Osama F. Harraz, Ph.D.**, Bloomfield Professor In Cardiovascular Research Assistant Professor University Of Vermont, Larner College Of Medicine
>
> **Weishan Huang, Ph.D.**, Associate Professor in the Department of Pathobiological Sciences at Louisiana State University

INBRE Outstanding Mentorship and Teaching Award

The INBRE Outstanding Mentorship and Teaching Award recognizes individuals from INBRE programs who demonstrate excellence in mentoring and teaching.

> **Kenneth Cornell, Ph.D.**, Department of Chemistry and Biochemistry at Boise State University
>
> **Seetharama D. Jois**, **Ph.D.**, Professor of Cancer Immunology and Computation and Structural Biology at the Department of Pathobiological Sciences, Louisiana State University Baton Rouge

CTR Excellence in Service and Mentoring Award

The CTR Excellence in Service and Mentoring Award acknowledges a successful mentor who has generously given their time to guide and support junior clinical and/or translational investigators in an active CTR program. This award recognizes individuals who exemplify research excellence and service to facilitating the careers of junior investigators.

> **Daphne Koinis-Mitchell**, **Ph.D.**, Professor of Pediatrics and of Psychiatry and Human Behavior and Vice-Chair for Pediatrics Research at The Warren Alpert Medical School of Brown University

Entrepreneur Award

The Entrepreneur Award acknowledges the accomplishments of an investigator who has shown innovation in the areas of Entrepreneurship and/or Commercialization.

Brett Janis, Ph.D., Chief Executive Officer, DesiCorp Inc

Sreejayan Nair, Ph.D., Professor of Pharmacology, University of Wyoming School of Pharmacy

Scientific Presentation Awards

Scientific Presentation Awards were selected by the session co-chairs and reviewed by the Organizing Committee based on abstracts submitted. All flash talk and short research presentation abstracts were considered for Scientific Presentation awards.

Adriana Aponte Ramos, Undergraduate Student, Inter American University of Puerto Rico, Bayamon Campus, INBRE

Alia Tereza Sadek, Graduate Student, University of South Carolina School of Medicine Greenville, INBRE

Alexa Bostic, Undergraduate Student, West Virginia University

Ana-Maria Dragoi, Junior Faculty Member or Investigator, LSUHSC Shreveport, COBRE

Belinda Joyce Petri, Postdoctoral Researcher, University of Louisville, INBRE

Devin M. Drown, Established Faculty Member or Investigator, University of Alaska Fairbanks, INBRE

Erica J. Johnson, Graduate Student, University of Delaware, COBRE

Erica Sood, Junior Faculty Member or Investigator, Nemours Children's Health, COBRE

Hamed Fayyaz, Graduate Student, University of Delaware, CTR

Hannah Ladwig, Undergraduate Student, Creighton University, INBRE

Heather Drummond, Established Faculty Member or Investigator, University of Mississippi Medical Center, COBRE

Jared C Talbot, Junior Faculty Member or Investigator, University of Maine, COBRE

Karthik Swaminathan, Graduate Student, University of Wyoming, COBRE

Katie Cueva, Junior Faculty Member or Investigator, University of Alaska Fairbanks, INBRE

Khadija Kakar, Graduate Student, University of South Carolina School of Medicine, COBRE

Leya Givvines, Graduate Student, West Virginia School of Osteopathic Medicine, INBRE

Manisha Thakur, Graduate Student, Southern University and A&M college

Martha Rojo, Junior Faculty Member or Investigator, University of Arkansas for Medical Sciences, COBRE

Md Jobayer Hossain, Established Faculty Member or Investigator, Nemours Children’s Health, Wilmington, CTR

Michayla Moore, Graduate Student, MaineHealth Institute for Research (MHIR), COBRE

Moriah Katt, Junior Faculty Member or Investigator, West Virginia University, COBRE

Prateek Verma, Postdoctoral Researcher, University of Arkansas, COBRE

Sai Prashanthi Gumpili, Graduate Student, University of Delaware, INBRE

Steven Ionov, Graduate Student, Dartmouth College, COBRE

Umesh D. Wankhade, Junior Faculty Member or Investigator, University of Arkansas for Medical Sciences, COBRE

Vitoria Mattos Pereira, Graduate Student, University of Wyoming, INBRE

Xhoela Bame, Graduate Student, Dartmouth College, COBRE

Xufang Deng, Junior Faculty Member or Investigator, Oklahoma State University, COBRE

Zim Warda Hasan, Graduate Student, Western Kentucky University, INBRE

VENDORS & SPONSORS

Vendors will be located in the Concourse Foyer during NISBRE2024. We encourage you to stop by and visit their booths to learn more about each of our 2024 sponsors.

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Science and Mentor Award Sponsorship

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Travel Award Sponsorship

Piestar, Inc.

JUNETEENTH EVENTS

In honor of Juneteenth (June 19), we have provided a list of activities in and around the DC area.

Juneteenth Celebration with Playback Theater (Tuesday, June 18th from 3:00PM – 4:00PM) National Archives Museum, 701 Constitution Avenue, NW, Washington, DC 20408

Juneteenth DC Community Festival (Wednesday, June 19th from 11:00AM – 5:00PM) ONE DC Black Workers & Wellness Center located at 2500 Martin Luther King Jr Ave

Fighters for Freedom: William H. Johnson Picturing Justice (Monday-Sunday from 11:30AM – 7:00PM) Smithsonian American Art Museum, 8th and G Streets NW, Washington, DC 20004

Juneteenth Freedom Celebration at Anacostia Community Museum (Wednesday, June 19th from 10:00AM – 5:00PM) 1901 Fort Place SE, Washington, DC 20020

Juneteenth for the City (Wednesday, June 19th from 1:00PM – 6:00PM) Bread for the City's Michelle Obama Southeast Center located at 1700 Marion Barry Ave SE, Washington, DC 20020

Smithsonian National Museum of African American History and Culture (NMAAHC) (Tuesday-Sunday 10:00AM – 5:30PM, Monday 12:00PM – 5:30PM) 1400 Constitution Ave NW, Washington, DC 20560

Special Exhibition: Where we Meet (Tuesday-Sunday from 10:00AM – 5:00PM) The Phillips Collection, 1600 21st Street, NW, Washington, DC

*For a full list of events and other information, please visit **juneteenthdc.org** and **washington.org**.*

NISBRE2024

Detailed Conference Program (ONLINE ONLY)

Organized by Date, Time, and Session, with Presenter Information

SUNDAY, JUNE 16, 2024

9:00AM – 4:00PM Sunday, June 16 Georgetown

Closed Meeting for Grant Administrators, Program Managers, and Evaluators (PEARL)

Organizer: Julie Benson, Associate Director Alaska INBRE, University of Alaska Fairbanks

Organizer: Jessica Garfield, Director of IDeA Research Administration, University of Nebraska, Reno

This pre-conference meeting is open to grant administrators, program managers, and evaluators of COBRE, INBRE, and CTR programs. Join this Program Evaluation and Administration of Research Leaders (PEARL) session to network with others in similar professional roles. Bring your questions and share your experiences related to IDeA program coordination, implementation, and evaluation. We encourage all current PEARL members and any grant administrator, program manager, or evaluator who is interested in learning more about the benefits of PEARL to attend. Please contact the session co-organizers for more information.

11:00AM – 12:00PM Sunday, June 16 Lincoln

Closed Meeting for IDeA COBRE, INBRE, CTR, I-RED Program Directors (NAIPI)

Organizer: Scott Seville, President National Association of IDeA Principal Investigators (NAIPI) Director Wyoming INBRE, University of Wyoming

Speaker: Jessica Molesworth, Executive Director, EPSCoR/IDeA Foundation

Network and connect with other IDeA Directors from across the country. Hear from Dr. Scott Seville, the president of the National Association of IDeA Principal Investigators (NAIPI) and from Jessica Molesworth, the Executive Director of the EPSCoR/IDeA Foundation, on upcoming opportunities and priorities. This is a chance to share your experiences with colleagues and bring questions to ask of this experienced group! Please contact the session co-organizers for more information.

1:00PM – 1:25PM Sunday, June 16 Jefferson

Human Subjects and Clinical Trials Research Workshop

Why Clinical Trials Matter in IDeA States

Organizer: Sally Hodder, Director West Virginia Clinical and Translational Science Institute, Associate Vice President of Clinical and Translational Science, Professor of Medicine and Preeminent Scholar Chair, School of Medicine, West Virginia University

Representation in clinical research leads to improved health outcomes and decreases health inequities. IDeA programs have an opportunity to increase clinical research opportunities in the states they serve. This pre-conference workshop will address various aspects of clinical trial conduct in IDeA states,

including protocol development, navigating the NIH Human Subjects System, and obtaining timely approval for pilot projects.

1:25PM – 2:00PM Sunday, June 16 Jefferson

Human Subjects and Clinical Trials Research Workshop

Patient Perspective from a Survivor

Speaker: Ricki Fairley, Chief Executive Officer, Touch, The Black Breast Cancer Alliance

2:00PM – 4:00PM Sunday, June 16 Monroe

IACUC and Conducting Vertebrate Animal Research Workshop

Moderator: Olga Kovbasnjuk, Program Director, National Institutes of Health
Panelist: Irina Kirpich, Associate Professor, University of Louisville
Panelist: Nicolette Petervary, Director, Division of Policy and Education, Office of Laboratory Animal Welfare, Office of Extramural Research, National Institutes of Health, NIH Office of Laboratory Animal Welfare
Panelist: Johann Urschitz, Assistant Professor, University of Hawaii
Panelist: Kristi Helke, Professor, Chair, Medical University of South Carolina

Learn about application requirements when submitting vertebrate animal proposals. This workshop will provide insights on completing the Vertebrate Animal Section and how to minimize the numbers of animals used while ensuring statistical significance and addressing sex as a biological variable. This session will also include tips for submitting post-award IDeA pilot projects that involve vertebrate animals.

2:00PM – 2:30PM Sunday, June 16 Jefferson

Human Subjects and Clinical Trials Research Workshop

Navigating Human Subjects and Clinical Trials Research Policy

Speaker: Della White, Clinical Research Strategy Coordinator, National Institutes of Health, National Institute of General Medical Sciences

2:30PM – 3:00PM Sunday, June 16 Jefferson

Human Subjects and Clinical Trials Research Workshop

How to Work in NIH Human Subjects System

Speaker: Dawn Corbett, NIH Inclusion Policy Officer, National Institutes of Health, Office of Extramural Research

2:30PM – 3:00PM Sunday, June 16 Lincoln East

Human Subjects and Clinical Trials Research Workshop

Protocol Development

Speaker: Judith Feinberg, Professor of Behavioral Medicine and Psychiatry & Professor of Medicine/Infectious Diseases, West Virginia University
Speaker: Shelley Welch, Senior Director WVCTSI Clinical Trials Center of Excellence, West Virginia University

2:30PM – 3:00PM Sunday, June 16 Lincoln West

Human Subjects and Clinical Trials Research Workshop

Streamlining Post Award Project Submissions

Speaker: Christy Leake, Grants Management Team Leader, National Institutes of Health, National Institute of General Medical Sciences, Grants Administration Branch

3:00PM – 3:30PM Sunday, June 16 Jefferson

Human Subjects and Clinical Trials Research Workshop

How to Work in NIH Human Subjects System

Speaker: Dawn Corbett, NIH Inclusion Policy Officer, National Institutes of Health, Office of Extramural Research

3:00PM – 3:30PM Sunday, June 16 Lincoln East

Human Subjects and Clinical Trials Research Workshop

Protocol Development

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Speaker: Shelley Welch, Senior Director WVCTSI Clinical Trials Center of Excellence, West Virginia University

3:00PM – 3:30PM Sunday, June 16 Lincoln West

Human Subjects and Clinical Trials Research Workshop

Streamlining Post Award Project Submissions

Speaker: Christy Leake, Grants Management Team Leader, National Institutes of Health, National Institute of General Medical Sciences, Grants Administration Branch

3:30PM – 4:15PM Sunday, June 16 Jefferson

Human Subjects and Clinical Trials Research Workshop

Clinical Trials Best Practices

Moderator: Sally Hodder, Director West Virginia Clinical and Translational Science Institute, Associate Vice President of Clinical and Translational Science, Professor of Medicine and Preeminent Scholar Chair, School of Medicine, West Virginia University

Panelist: Carlos Luciano, Professor and Chair or Neurology, Co-Principal Investigator, Hispanic Alliance for Clinical and Translational Research, University of Puerto Rico School of Medicine

Panelist: Clifford Rosen, Director of Clinical and Translational Research and a Senior Scientist at Maine Medical Center's Research Institute

Panelist: Cecilia Shikuma, Professor, Department of Medicine, John A. Burns School of Medicine, University of Hawaii-Manoa, Honolulu

Panelist: Timothy VanWagoner, Associate Professor, Oklahoma University Health Sciences Center Department of Pediatrics, Associate Director Oklahoma Clinical and Translational Science Institute

4:30PM – 6:30PM Sunday, June 16 Heights Courtyard

Welcome Reception

All attendees are invited to join the NISBRE2024 Welcoming Reception. Visit with NIH Program Officers and meet other faculty, staff, and students throughout the IDeA network. Light appetizers will be provided, and a cash bar will be available.

MONDAY, JUNE 17, 2024

8:00AM – 9:00AM Monday, June 17 International Terrace

Breakfast with Small Group Discussions

We encourage you to network with colleagues during breakfast. Tables will be reserved for breakout discussions focused on various topics of interest. No reservations are required. A list of table topics will be available at registration.

9:00AM – 10:15AM Monday, June 17 International Ballroom

Conference Welcome from Dr. Jon Lorsch and Keynote with Dr. Tara Schwetz

Join us for welcoming remarks from Dr. Jon Lorsch, Director of the National Institute of General Medical Sciences. Dr. Tara Schwetz, Deputy Director for Program Coordination, Planning, and Strategic Initiatives of the National Institutes of Health will be giving this year's opening keynote.

Jon Lorsch, Director, National Institute of General Medical Sciences, National Institutes of Health. **Updates from NIGMS**

Tara A. Schwetz, Deputy Director, Program Coordination, Planning, and Strategic Initiatives, National Institutes of Health. **Broadening Our Reach, Strengthening Our Workforce**

10:30AM – 12:30PM Monday, June 17 International Ballroom

Science Highlight Plenary

Organizer: Rick Bevins, Rural Drug Addiction Research Center COBRE PI, University of Nebraska-Lincoln

This two-hour session will highlight cutting-edge research and scientific breakthroughs across a myriad of topics. Join us for this exciting discussion and hear insights from speakers working across IDeA Programs. Plenary speakers include:

Laura Stroud, Professor, Director, Brown Medical School and The Miriam Hospital. **Women's & Perinatal Health: The importance of Stress, Trauma, and Resilience**

Anthony Fehr, Associate Professor, University of Kansas, Department of Molecular Biosciences. **New developments in the function of and drug discovery for the coronavirus macrodomain**

Sally Hodder, Director, West Virginia Clinical and Translational Science Institute Associate Vice President, Clinical and Translational Research, West Virginia Clinical & Translational Science Institute. **IDeA Programs Addressing Rural Health and Health Disparities**

Marcia R. Cruz-Correa, Professor, University of Puerto Rico/School of Medicine. **Molecular Gastric Cancer Disparities in Hispanics: Pathways to Interception**

Gregory Hicks, Distinguished Professor of Health Science & Associate Vice President for Clinical & Translational Research, University of Delaware, College of Health Sciences, Department of Physical Therapy. **Developing a Tailored Rehabilitation Approach for Older Adults with Chronic Low Back Pain: Does the Hip Matter?**

12:30PM – 1:30PM Monday, June 17 International Ballroom

Lunch with Table Topic Discussions

We encourage you to network with colleagues during lunch. Tables will be held for breakout discussions focused on various topics of interest. No reservations are required. A list of table topics will be available at registration.

1:30PM – 3:10PM Monday, June 17 Monroe

Tips for Post-Awards Reporting, Publication Compliance, and RPPR Success

Moderator: Fed Bernal, Acting Chief, Research Advancement Programs Branch, National Institute of General Medical Sciences

Panelist: Yang Zhou, Program Director, National Institutes of Health

Hear from NIH Program Officers about common mistakes in the post-awards reporting process and expectations for citing IDeA grants in publications. Learn about IDeA-specific reporting requirements for the Research Performance Progress Report (RPPR). Hear about how to incorporate information that was once collected via SIRS into the RPPR and bring your questions to this dynamic discussion.

1:30PM – 3:10PM Monday, June 17 Lincoln East

Rural Health and Health Disparities

Co-Chair: Douglas Sawyer, Chief Academic Officer, Maine Medical Center, MaineHealth

Co-Chair: Mark Creager, Professor of Medicine, Dartmouth Hitchcock Medical Center, Geisel School of Medicine at Dartmouth

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Nathan L. Vanderford, University of Kentucky. **Taking ACTION to Reduce Cancer Disparities in Appalachian Kentucky.** Co-Authors: None. COBRE, Short Research Presentation

Katie Cueva, University of Alaska Fairbanks. **The Alaska Native Collaborative Hub for Research on Resilience: Alaska Native youth voices on how their communities support young people.** Co-Authors: Jessica Saniguq Ullrich, Ay'aqulluk Jim Chaliak, Roberta Moto, Evon Peter, Charlene Aqpik Apok, Diane McEachern, Lisa Wexler, James Allen, Jessica Black, Stacy Rasmus. Co-Authors Institutional Affiliations: Not Listed. INBRE, Short Research Presentation

Zugui Zhang, Christiana Care Health System. **The Effectiveness of the Community Health Workers Program in Primary Care in Delaware: Impact on Health Utilities and Outcomes.** Co-Authors: Alexandra Maree Mapp, James T Laughery. Co-Authors Institutional Affiliations: Christiana Care Health System. CTR, Short Research Presentation

Debora Kamin Mukaz, University of Vermont Larner College of Medicine. **Residential Segregation and Thrombo-inflammatory Biomarkers Related to Hypertension in Black and White Americans.** Co-Authors: Andrew D. Sparks, Ryan Packer, Suzanne E. Judd, Virginia J. Howard, April P. Carson, Timothy B.

Plante, D Leann Long, Katharine Cheung, Mary Cushman. Co-Authors Institutional Affiliations: University of Vermont Larner College of Medicine, University of Alabama at Birmingham, University of Mississippi Medical Center, Wake Forest University. COBRE, Short Research Presentation

Martha Rojo, University of Arkansas for Medical Sciences. **Hispanic Faith-based leaders' perspectives on healthy eating interventions in the Hispanic community.** Co-Authors: Hannah Aston, Johnathan Rodriguez, Erickson Feliciano, Carson Guatemala, Janet Lopez. Co-Authors Institutional Affiliations: Not Listed. COBRE, Flash Talk

Emily Zeitler, Dartmouth Health. **Experience of Remote Monitoring of Cardiac Implantable Electronic Devices in Rural New England.** Co-Authors: Laure Bernstein, Jennifer Wenner, Nichole Rogovoy, Mark Creager, Karen Schifferdecker. Co-Authors Institutional Affiliations: Dartmouth Health. COBRE, Flash Talk

Richard Riker, Maine Medical Center. **Evaluating Exception from Informed Consent Community Consultation Surveys Based on Measures of Rurality, Age, and Educational Level.** Co-Authors: Elizabeth Scharnetzki, Amanda Lessard, Catherine Feutz, David Seder, David Gagnon, Frank Chessa. Co-Authors Institutional Affiliations: MaineHealth. COBRE, Flash Talk

1:30PM – 3:10PM Monday, June 17 Lincoln West

Infectious Diseases I

Co-Chair: Anna Dunaevsky, Professor, University of Nebraska Medical Center
Co-Chair: S. Michal Jazwinski, Professor and Director, Tulane University, Deming Department of Medicine

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Xufang Deng, Oklahoma State University. **Design of a SARS-CoV-2 papain-like protease inhibitor with antiviral efficacy in a mouse model.** Co-Authors: Bin Tan, Xiaoming Zhang, Ahmadullah Ansari, Prakash Jadhav, Haozhou Tan, Kan Li, Ashima Chopra, Alexandra Ford, Xiang Chi, Francesc Xavier Ruiz, Eddy Arnold, Xufang Deng, Jun Wang. Co-Authors Institutional Affiliations: Rutgers, The State University of New Jersey, Oklahoma State University. COBRE, Short Research Presentation

For Yue Tso, Louisiana State University Health Sciences Center - New Orleans. **Using CRISPR-Cas9 to Eliminate Kaposi's Sarcoma-Associated Herpesvirus.** Co-Authors: John T West, Charles Wood. Co-Authors Institutional Affiliations: LSU Health Sciences Center. COBRE, Short Research Presentation

Katherine J. Siddle, Brown University. **Clinical, epidemiological and demographic indicators of COVID-19 in Rhode Island.** Co-Authors: Sarah Bowman, Paul Cao, Genevieve Caron, Kristen Carpenter-Azevedo, Elizabeth Chen, Karen Crowley, Glen Gallagher, Edward Hawrot, Richard C. Huard, August Guang, Sarah Ledgerwood, Farahnaz Maroof, Ashok Ragavendran, Vivek Ramanan, Sharon Rounds, Eric Salomaki, Sean Sierra-Patev, Paul Stey. Co-Authors Institutional Affiliations: Rhode Island Department of Health, Brown University, Rhode Island State Health Laboratory. CTR, Short Research Presentation

Rohit K Jangra, LSU Health, Shreveport. **A novel BSL2 system for comprehensive analysis of entry glycoproteins.** Co-Authors: Lohit Khera, Stephanie R. Monticelli, Ramandeep Kaur, Upendra P Lambe, Thomas G. Batchelor, Ana I. Kuehne, Cierra Word, Nahomi Guerra-Pilaquinga, Russell R. Bakken, Andrew S. Herbert. Co-Authors Institutional Affiliations: LSU Health-Shreveport, United States Army Medical Research Institute of Infectious Disease, The Geneva Foundation. COBRE, Short Research Presentation

Steven Ionov, Dartmouth College. **Molecular Analysis of SARS-CoV-2 Vaccine Serum Antibody**

Repertoires in Individuals with Cystic Fibrosis. Co-Authors: Seungmin Shin, Ruth Connor, Jiwon Lee. Co-Authors Institutional Affiliations: Dartmouth College, Dartmouth-Hitchcock Medical Center. COBRE, Flash Talk

Benjamin King, University of Maine. **Inhibition of NADPH Oxidase 2 Improves Survival in Zebrafish Infected with Influenza A Virus.** Co-Authors: Brandy-Lee Soos, Alec Ballinger, Mykayla Weinstein, Julianna Grampone. Co-Authors Institutional Affiliations: University of Maine. COBRE, Flash Talk

Anand Paul, Louisiana State University Health Science Center. **Machine Learning-Enabled Assessment of Healthcare Workforce Demographics and Their Impact on HIV and Infectious Disease Outcomes in Louisiana.** Co-Authors: Lucio Miele, Meredith Clement. Co-Authors Institutional Affiliations: Louisiana State University Health Sciences Center. INBRE, Flash Talk

1:30PM – 3:10PM Monday, June 17 Jefferson East

Artificial Intelligence

Co-Chair: Lucio Miele, Professor, Department Head, Senior Associated Dean of Research, Louisiana State University Health Sciences Center-New Orleans
Co-Chair: Lawrence Cornett, Distinguished Professor, University of Arkansas for Medical Sciences, Department of Physiology and Cell Biology

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Prateek Verma, University of Arkansas. **Evaluation of Large Vision Language Models on Scientific Images.** Co-Authors: Minh-Hao Van, Xintao Wu. Co-Authors Institutional Affiliations: University of Arkansas. COBRE, Short Research Presentation

Russell McCulloh, University of Nebraska Medical Center. **Outlining a vision for a learning research system.** Co-Authors: Ellen Kerns, Jerrod Anzalone, Matthew Rizzo. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. CTR, Short Research Presentation

Indra Neil Sarkar, Brown University. **Establishing A Statewide Learning Health System with OMOP-on-FHIR for High Need Children.** Co-Authors: Elizabeth Chen, Karen Crowley, Paul Stey, Jonah Bradenday, Farahnaz Maroof, Mounika Thakkallapally, Ashok Ragavendran, Edward Hawrot, Sharon I. Rounds. Co-Authors Institutional Affiliations: Brown University. CTR, Short Research Presentation

Shanshan Ding, University of Delaware. **Machine learning and causal inference in high dimensional survival analysis.** Co-Authors: Wei Qian, Zhezhen Jin. Co-Authors Institutional Affiliations: University of Delaware, Columbia University. CTR, Short Research Presentation

Hamed Fayyaz, University of Delaware. **An Interoperable ML Pipeline for Pediatric Obesity Risk Prediction using Commonly Available EHR Data.** Co-Authors: Mehak Gupta, H. Timothy Bunnell, Claudine Jurkovitz Thao-Ly, Thao-Ly Phan, Rahmatollah Beheshti. Co-Authors Institutional Affiliations: Southern Methodist University, Nemours Children's Health, ChristianaCare, University of Delaware. CTR, Flash Talk

Zhicheng Jiao, The Warren Alpert Medical School of Brown University. **Multi-modality AI model for outcome prediction of COVID-19 from chest x-ray.** Co-Authors: Vin Somasundaram, Zhusi Zhong, Scott Collins, Terrence Healey, Michael Atalay. Co-Authors Institutional Affiliations: The Warren Alpert Medical School of Brown University. CTR, Flash Talk

Sabrina Duran, West Virginia University School of Medicine. **Comparing Readability of American**

Academy of Dermatology and AI-generated Patient Education Materials. Co-Authors: Jenna Foster, Andrea Medina Gonzalez, John Nguyen, Diane Wang, Zachary Zinn. Co-Authors Institutional Affiliations: West Virginia University. Flash Talk

1:30PM – 3:10PM Monday, June 17 Georgetown West

Leveraging the NIGMS Sandbox to Advance Biomedical Research Using Cloud Computing

Moderator: Lakshmi Kumar Matukumalli, Program Director, National Institute of General Medical Sciences, National Institutes of Health, Division for Research Capacity Building
Panelist: Nick Weber, Acting Director, Office of Scientific Computing Services, National Institutes of Health, Center for Information Technology
Panelist: Nathan Moore, Data Science Strategy Coordinator, National Institute of General Medical Sciences
Panelist: Benjamin King, Associate Professor, University of Maine
Panelist: Youping Deng, Professor, University of Hawaii
Panelist: Stephanie Byrum, Associate Professor, University of Arkansas for Medical Sciences
Panelist: Kyle Quinn, Professor and COBRE Director, University of Arkansas

Learn more about the NIGMS Sandbox, a cloud-based learning platform that provides educational modules focused on various topics in the biomedical sciences. Hear from investigators who have used the NIGMS Sandbox to extend their research using cloud-based computing. We invite you to attend this session and learn ways cloud computing can transform your research, enhance your team's data analytic capabilities, and increase future data storage and sharing opportunities.

1:30PM – 3:10PM Monday, June 17 Jefferson West

NIH Updates on R-Type Application Requirements

Moderator: Erica Brown, Director, Division of Extramural Activities, National Institute of General Medical Sciences
Panelist: Shannon Doyle, Health Science Policy Analyst, National Institute of General Medical Sciences

Learn about upcoming changes to NIH research grant applications. NIH Program Officers will be on hand to suggest resources for your next application, discuss new requirements important for NIH review, and provide new guidance on pre-/post-award planning. Bring your questions to ask NIH staff during this interactive session.

1:30PM – 3:10PM Monday, June 17 Georgetown East

Planning for Translational Impact in IDeA Programs

Moderator: Joseph Fox, Professor, COBRE PI, University of Delaware
Panelist: Dean Madden, Vice Provost for Research, Professor of Biochemistry & Cell Biology, Dartmouth College/Geisel School of Medicine
Panelist: Alan Tackett, Distinguished Professor, University of Arkansas for Medical Sciences
Panelist: Sally Hodder, Director, West Virginia Clinical and Translational Science Institute Associate Vice President, Clinical and Translational Research, West Virginia Clinical & Translational Science Institute

Hear about innovative ways IDeA Programs are planning for and extending translation opportunities. Learn new strategies for engaging with non-academics to increase translational impact.

3:30PM – 5:10PM Monday, June 17 Monroe

Improving Outcomes for Core Facilities and Increasing Opportunities for Sustainability

Moderator: Olga Kovbasnjuk, Program Director, National Institutes of Health
Panelist: Alan Daugherty, Director, University of Kentucky
Panelist: Melinda Duncan, Associate VP of Research, Professor of Biological Sciences, University of Delaware
Panelist: Pamela Swiatek, Director, Brown University
Panelist: Josh Baker, Director NV INBRE, University of Nevada, Reno
Panelist: Hal Scofield, Professor, University of Oklahoma Health Sciences Center/Oklahoma Medical Research Foundation

Hear about common issues in core facility management, learn ways to build efficiencies in core facility operations, and continue your planning for core sustainability. Join this discussion of core operations, client management, rate structures, compliance considerations, and more. Bring your questions and join in on the discussion.

3:30PM – 5:10PM Monday, June 17 Lincoln East

Cancer and Disease Risk I

Co-Chair: John West, Professor, Louisiana State University Health Sciences Center New Orleans
Co-Chair: Joseph Francis, Professor and Director Center for Comparative Oncology, Louisiana State University

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Harilaos Filippakis, University of New England. **Therapeutic targeting of Tryptophan-mediated macropinocytosis in Tuberous Sclerosis Complex.** Co-Authors: Sarah Lafleur, Windrie Cox, Aidan McGrath-Conwell, Elizabeth P. Henske, Harilaos Filippakis. Co-Authors Institutional Affiliations: University of New England. COBRE, Short Research Presentation

Stephanie M. Dorta-Estremera, University of Puerto Rico Medical Sciences Campus. **Modulating the oral microbiota to enhance anti-tumor immune responses in oropharyngeal cancer.** Co-Authors: Jennifer Diaz-Rivera, Michael Rivera-Rodriguez, Alejandra Rosario-Crespo, Jorge R. Galan-Ortiz, Edna E. Aquino-Pinero, Filipa Godoy-Vitorino, Stephanie M. Dorta-Estremera. Co-Authors Institutional Affiliations: University of Puerto Rico Medical Sciences Campus, Comprehensive Cancer Center UPR, The Alliance. CTR, Short Research Presentation

Thomas Huckaba, Xavier University of Louisiana. **Development and Testing of Proteolysis-Targeting Chimeras (PROTACs) as Therapeutics for Non-Small Cell Lung Cancer.** Co-Authors: Fasial Abedin, Cecily DeFreece, Xianyou Peng, Guangdi Wang. Co-Authors Institutional Affiliations: INBRE, Short Research Presentation

Belinda Joyce Petri, University of Louisville. **Differential m6A modification identified by direct mRNA sequencing in endocrine- resistant and sensitive breast cancer cells.** Co-Authors: Kellianne M. Piell, Eric C. Rouchka, Carolyn M. Klinge. Co-Authors Institutional Affiliations: University of Louisville School of Medicine. INBRE, Short Research Presentation

Emily Tolbert, Kansas State University. **cHPV E6 reduces innate immune signaling.** Co-Authors: Dalton Dacus, Rose Pollina, Nicholas A. Wallace. Co-Authors Institutional Affiliations: Enliven Therapeutics, Kansas State University. COBRE, Flash Talk

Akash J. Vaidya, University of Delaware. **Repurposing Barley-Stripe Mosaic Virus for Cancer Immunotherapy.** Co-Authors: Mruthula Rammohan, Jesal Patel, Evan Gillen, Robyn Logue, Kevin V.

Solomon. Co-Authors Institutional Affiliations: University of Delaware. INBRE, Flash Talk

Hannah Ladwig, Creighton University. **Structural Analysis of Crassostrea gigas OAZ-PK RNA.** Co-Authors: Rhiannon McCracken, Juliane Soukup. Co-Authors Institutional Affiliations: Creighton University. INBRE, Flash Talk

3:30PM – 5:10PM Monday, June 17 Lincoln West

Women's Health

Co-Chair: Ghada Bourjeily, Director of Women's Research, Lifespan / Brown University
Co-Chair: Nalini Santanam, Professor, Joan C Edwards School of Medicine, Marshall University, Department of Biomedical Sciences

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Erica Sood, Nemours Children's Health. HEARTPrep: **A digital health psychosocial intervention for mothers expecting a baby with congenital heart disease.** Co-Authors: Kimberly Canter, Anne E. Kazak, Angel Munoz-Osorio, Alejandra Perez Ramirez. Co-Authors Institutional Affiliations: Nemours Children's Health. COBRE, Short Research Presentation

Leela V. Thomas, Delaware State University. **Influence of social determinants on maternal and infant complications of gestational diabetes mellitus.** Co-Authors: Zugui Zhang, Claudine T. Jurkovitz, Mitchell R. Fawcett, M. James Lenhard. Co-Authors Institutional Affiliations: ChristianaCare Health Services Inc., Sidney Kimmel Medical College. CTR, Short Research Presentation

Elizabeth B. Quigley, University of Wyoming. **Sexually Dimorphic JNK Signaling in the Gonadotrope is Important for Female Fertility Regulation.** Co-Authors: Alexandra Verosky, Brian S. Edwards, Shaihla A. Khan, Ulrich Boehm, Roger J. Davis,Amy M. Navratil. Co-Authors Institutional Affiliations: University of Wyoming, Laramie, University of Colorado, Mayo Clinic, Genus PLC, Saarland University School of Medicine, University of Massachusetts Medical School, Howard Hughes Medical Institute. INBRE, Short Research Presentation

Lisa T. Jansen, University of Arkansas for Medical Sciences - Arkansas Children's Nutrition Center. **Impact of Physical Activity Intervention on Longitudinal Glycemic Patterns in Pregnant Women with Obesity: A CGM Pilot Study.** Co-Authors: Scott Stewart, Lilian Cheak, Precious Jeffrey, Aline Andres. Co-Authors Institutional Affiliations: Arkansas for Medical Sciences, Arkansas Children's Nutrition Center, Arkansas Children's Research Institute. COBRE, Short Research Presentation

Leya Givvines, West Virginia School of Osteopathic Medicine. **Ovariectomy exacerbates plasma IgE and lung eosinophilia, but is not associated with greater vascular endothelial dysfunction in asthmatic mice.** Co-Authors: Abigail R. Patterson, Marina Diioia, Dovenia S. Ponnoth, Shinichi Asano. Co-Authors Institutional Affiliations: West Virginia Wesleyan College, West Virginia School of Osteopathic Medicine. INBRE, Flash Talk

Shyanna Larocque, Turtle Mountain Community College. **Fetal C-Reactive Protein rs1205 Genotype Is Not Associated with Maternal Pre-eclampsia.** Co-Authors: Crystal Azure, Hailey Davis, Craig Poitra, Jackie Poitra, Shayden Standish, Tyler J Parisien, Lyle G. Best. Co-Authors Institutional Affiliations: Turtle Mountain Community College. INBRE, Flash Talk

Lauren Covington, University of Delaware. **Socio-ecological Stressors Among Mothers Experiencing Socioeconomic Disadvantage.** Co-Authors: Destiny Mahmood, Kiara Shay, Emma Archer, Freda Patterson, Emily Hauenstein. Co-Authors Institutional Affiliations: University of Delaware, University of

Virginia. CTR, Flash Talk

3:30PM – 5:10PM Monday, June 17 Jefferson East

Metabolism and Obesity I

Co-Chair: David Rand, Professor and Chair, Brown University Department of Ecology, Evolution and Organismal Biology

Co-Chair: Holly Wichman, Director, University of Idaho / Institute for Modeling Collaboration and Innovation

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Umesh D. Wankhade, Arkansas Children's Nutrition Center, UAMS. **From Conception to Adipose Tissue: Investigating the Role of Housing Temperature on Offspring Response to Dietary Challenge.** Co-Authors: Henry A. Paz, Ying Zhong, James D. Sikes, Reid D. Landes, Roy Morello, Samrat Roy Choudhury. Co-Authors Institutional Affiliations: Arkansas Children's Nutrition Center, University of Arkansas for Medical Sciences, Arkansas Children's Research Institute. COBRE, Short Research Presentation

Matthew D Lynes, MaineHealth Institute for Research. **Peroxiredoxin 2 protects Trpv1+ derived fat cells from excessive reactive oxygen species induced cell death.** Co-Authors: Breanna Morrill, Carolina Cora, Wadak Harbi, Caitlin Ellis, Benjamin Tero, Kimberly Malka, Lucy Liaw. Co-Authors Institutional Affiliations: MaineHealth Institute for Research, University of Southern Maine. COBRE, Short Research Presentation

Caroline de Carvalho Picoli, MaineHealth Institute for Research. **The Gut-Bone Connection: Gastric X/A-like Cells and Skeletal Homeostasis.** Co-Authors: Caroline de Carvalho Picoli, Jeyrie Ramos Aponte, Tiange Feng, Clifford J Rosen, Ziru Li. Co-Authors Institutional Affiliations: MaineHealth Research Institute, MMC Medical School. COBRE, Short Research Presentation

Cammi Valdez, Northeastern State University. **Characterizing a New Longitudinal Mouse Model of Diabetic Retinopathy.** Co-Authors: Cammi Valdez, Erica Dotson, Joshua Butcher, Phillip Coburn. Co-Authors Institutional Affiliations: Northeastern State University, Harold Hamm Diabetes Center, The University of Oklahoma Health Sciences Center, Oklahoma State University, The University of Oklahoma Health Sciences Center. INBRE, Short Research Presentation

Gary ZeRuth, Murray State University. **Gli-similar 3 is essential for proper pancreatic and kidney development in zebrafish.** Co-Authors: None. INBRE, Flash Talk

Vitoria Mattos Pereira, University of Wyoming. **Inhibition of the Cysteine Protease Cathepsin K Attenuates Diabetic Neuropathic Pain.** Co-Authors: Cameron James Campbell, Sreejayan Nair. Co-Authors Institutional Affiliations: University of Wyoming. INBRE, Flash Talk

3:30PM – 5:10PM Monday, June 17 Jefferson West

Innovative Approaches for Recruiting and Preparing New COBRE Project Leaders

Moderator: Fed Bernal, Acting Chief, Research Advancement Programs Branch, National Institute of General Medical Sciences

Panelist: Dean Madden, Vice Provost for Research, Professor of Biochemistry & Cell Biology, Dartmouth College/Geisel School of Medicine

Panelist: Ann West, Professor, Department of Chemistry and Biochemistry

Panelist: Igor Roninson, Professor and Endowed Chair, University of South Carolina

Panelist: Joseph Fox, Professor, COBRE PI, University of Delaware

Join PD/PIs for a discussion of ways they have improved their investigator pipeline in IDeA States, negotiated for hires in a challenging fiscal climate, developed onboarding and training platforms for early state faculty, and created benchmarks and timelines for project leader onboarding.

3:30PM – 5:10PM Monday, June 17 Georgetown East

Resources for Mentors and Mentees: Increasing Inclusiveness and Belongingness

Co-Moderator: Charles Irvin, Professor, University of Vermont
Co-Moderator: Damaris Javier, Associate Director, Research Training Programs, Multiple Principal Investigator, Asynchronous Open Online Course Addressing Structural Racism and Discrimination to Reduce Disparities, Co-Investigator, National Research Mentoring Network- Resource Center (NRMN-RC), Institute for Health Disparities, University of North Texas Health Science Center
Panelist: Nora Dominguez, Director, University of New Mexico / Mentoring Institute
Panelist: Rafael Luna, Head of Biomedical Education & Innovation, Novartis Biomedical Research
Panelist: Gus Kousoulas, Program Director/Principal Investigator Louisiana Biomedical Research Network (LBRN), Head-Department of Pathobiological Sciences (PBS), School of Veterinary Medicine, Louisiana State University

Hear about how to promote inclusiveness and belonging. Successful biomedical research efforts including basic and translational research, education, and training should encourage open communication, active listening, and meaningful engagement to foster a sense of inclusiveness and belonging for all. Learn about important resources for mentors and mentees and join in this important discussion.

3:30PM – 5:10PM Monday, June 17 Georgetown West

Harnessing Shared Resources: National and Regional Resources for Structural Biology and Biomolecular Analysis

Moderator: Paula Flicker, Program Officer, National Institutes of Health, National Institute of General Medical Sciences
Panelist: Ashley Barnes, Health Scientist Administrator (Program Director), National Institutes of Health, National Institute of General Medical Sciences
Panelist: Thomas Cho, Program Director, National Institutes of Health, National Institute of General Medical Sciences
Panelist: Claudia Lopez, Associate Professor, Co-Director Pacific Northwest CryoEM Center (PNCC), Oregon Health & Science University, Pacific Northwest CryoEM Center
Panelist: Nebojsa Bogdanovic, Specialized Faculty Cryo-EM, Florida State University
Panelist: Alan Tackett, Distinguished Professor, University of Arkansas for Medical Sciences

Learn more about NIGMS-supported resource centers for research in structural biology. Hear from NIGMS staff and resource center experts from CryoEM, CryoET, NMR Facilities, and Quantitative Proteomics. We invite you to attend this session to learn how resource centers can be a tool to transform your research and enhance your team's scientific capabilities.

5:15PM - 6:30PM Monday, June 17 International Ballroom

Scientific and Core Poster Session I

Join us in the International Ballroom for this exciting session! Check the Poster Pamphlet (available in

print, on the NISBRE app, and on the conference website) for a list of this year's poster presentations. Posters have been assigned at random to increase opportunities for networking across IDeA-programs and cores. Please remember to vote for your favorite poster(s) in the NISBRE People's Choice Poster Awards available on the NISBRE app. Numerous award categories are available, and winners will be announced during the awards ceremony.

6:30PM - Monday, June 17 Offsite Location

NAIPI National Committee Meeting and Dinner: Closed Session

We invite all NAIPI National Committee Members to join for this closed meeting and dinner following the Poster Session to discuss NAIPI business for the coming year.

Organizer: Scott Seville, President National Association of IDeA Principal Investigators (NAIPI) Director Wyoming INBRE, University of Wyoming

TUESDAY, JUNE 18, 2024

8:00AM – 9:00AM Tuesday, June 18 International Terrace

Breakfast with Small Group Discussions

We encourage you to network with colleagues during breakfast. Tables will be reserved for breakout discussions focused on various topics of interest. No reservations are required. A list of table topics will be available at registration.

9:00AM – 10:00AM Tuesday, June 18 International Ballroom

Keynote with Dr. Gisela Storz

Dr. Gisela Storz is a Senior Investigator and the Associate Scientific Director of the Division of Molecular and Cellular Biology at the National Institute of Child Health and Human Development. She is a member of the National Academy of Sciences. Dr. Storz keynote address will focus on novel gene discovery by the V-SOAR summer program. Additional remarks will be given by Dr. Scott Seville, the president of the National Association of IDeA Principal Investigators (NAIPI).

Gisela Storz, NIH Distinguished Investigator and Associate Scientific Director, Division of Molecular and Cellular Biology, NICHD, NIH. **Novel Gene Discovery by the V-SOAR Summer Program**

Scott Seville, President National Association of IDeA Principal Investigators (NAIPI) Director Wyoming INBRE, University of Wyoming. **Updates from NAIPI**

10:15AM – 12:15PM Tuesday, June 18 International Ballroom

Science Highlight Plenary

Organizer: Gus Kousoulas, Program Director/Principal Investigator Louisiana Biomedical Research Network (LBRN), Head-Department of Pathobiological Sciences (PBS), School of Veterinary Medicine, Louisiana State University

This two-hour session will highlight cutting-edge research and scientific breakthroughs across a myriad of topics. Join us for this exciting discussion and hear insights from speakers working across IDeA Programs. Plenary speakers include:

Jason Pellettieri, Professor, Keene State College. **Regulation of Stem Cell Division During Planarian Regeneration**

Stephania Cormier, Associate VP Research, Director LSU Superfund Research Program, Weiner Endowed Chair and Professor, Louisiana State University. **Unmasking the Link between Air Pollution and Respiratory Viruses**

Mark Nelson, University Distinguished Professor and Chair, Department of Pharmacology, University of Vermont. **Capillaries as a multi-modal sensors of brain activity**

Deborah Stenkamp, Professor, Biological Sciences, University of Idaho. **Development of Vertebrate Color Vision**

Corrie Miller, Assistant Professor, John A Burns School of Medicine, Department of Obstetrics and Gynecology, University of Hawaii. **Social Adversity and Microbial Composition during Pregnancy**

12:15PM – 1:30PM Tuesday, June 18 International Ballroom

Lunch with Table Topic Discussions

We encourage you to network with colleagues during lunch. Tables will be held for breakout discussions focused on various topics of interest. No reservations are required. A list of table topics will be available at registration.

1:30PM – 3:10PM Tuesday, June 18 Monroe

Evaluation and Metric Tracking for Reporting and Sustainability

Moderator: Stephen Kogut, Professor, University of Rhode Island
Panelist: Samuel Robison, Associate Director and Associate Professor of Research, LSU, The Social Research and Evaluation Center and Lutrill & Pearl Payne School of Education
Panelist: Judy Kimberly, Evaluation Director, Brown University
Panelist: Mindy Anderson-Knott, President, Partners for Insightful Evaluation
Panelist: Laura Lessard, Associate Professor, University of Delaware & Delaware INBRE
Panelist: Reagan Curtis, Professor, West Virginia University

Join this panel for tips and tricks in IDeA program evaluation and metric tracking. This information is increasingly important for institutional, state, and federal reporting, with impacts on long-term sustainability. Learn about reporting resources and ask your questions to a broad group of evaluation experts across IDeA mechanisms.

1:30PM – 3:10PM Tuesday, June 18 Lincoln East

Infectious Diseases II

Co-Chair: Lin Liu, Regents Professor and Director, Oklahoma State University
Co-Chair: Scott Hefty, Professor, Chairperson, and CoBRE Director, University of Kansas, Department of Molecular Biosciences

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Kevin Michael Brown, University of Oklahoma Health Sciences Center. **Elucidation of TgPKG kinase substrates required for Toxoplasma motility.** Co-Authors: Gabriel Cabral, Bingjian Ren, Sebastian Nasamu. Co-Authors Institutional Affiliations: University of Oklahoma Health Sciences Center, University

of Geneva. COBRE, Short Research Presentation

Ana-Maria Dragoi, LSUHSC Shreveport. **Interaction of human macrophages with Neisseria gonorrhoeae.** Co-Authors: Maria Dolores Juarez Rodriguez, Stanimir Ivanov. Co-Authors Institutional Affiliations: LSUHSC-Shreveport. COBRE, Short Research Presentation

Avishek Mitra, Oklahoma State University (OSU). **A Novel Class of Channel Forming Membrane Proteins Mediate Heme Iron Acquisition in Mycobacterium tuberculosis.** Co-Authors: Padam Singh. Co-Authors Institutional Affiliations: Oklahoma State University. COBRE, Short Research Presentation

Tirumalai Rangasamy, Louisiana State University. **Development of Small Molecule-based Intervention to Combat the Infection Caused by the Superbug Carbapenem-resistant Klebsiella pneumoniae.** Co-Authors: Kennedy Trahan, Duane Jeansonne, Allyson Mohanty-Aldana, John Le, Amit Sharma, Basel Abuaita, Samithamby Jeyaseelan. Co-Authors Institutional Affiliations: Louisiana State University. COBRE, Short Research Presentation

Bao Vu, University of Oklahoma Health Sciences. **Upc2A: A Key Regulator of Triazole Resistance and Hypoxic Fitness in Candida glabrata.** Co-Authors: None. COBRE, Flash Talk

Manikandan Palrasu, Dept of Pathology, Microbiology and Immunology, School of Medicine, University of South Carolina. **Aryl hydrocarbon receptor transcriptionally regulates beta-defensin-1 and consequently suppresses colonic inflammation during colitis.** Co-Authors: Khadija Kakar, FNU Hamida, Amarnath Satheesh Marudamuthu, Tayler Carter, Kiesha Maria Wilson, Archana Saxena, Xiaoming Yang, Narendra P. Singh, Philip Brandon Busbee, Prakash Nagarkatti, Mitzi Nagarkatti. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine. COBRE, Flash Talk

Alia Tereza Sadek, University of South Carolina School of Medicine Greenville. **Resistance and Intracellular Survival of Atypical Acinetobacter baumannii Isolates from a Fatal Case of Necrotizing Fasciitis.** Co-Authors: Elias M. Wheibe, Kyleigh Connolly, Christine Liu, Chelsea R. Gutierrez, Brock A. Arivett, Ryan F. Relich, Luis A. Actis, Steven Fiester, Maria Soledad Ramirez, Jennifer T. Grier. Co-Authors Institutional Affiliations: INBRE, Flash Talk

1:30PM – 3:10PM Tuesday, June 18 Lincoln West

Environment and Health I

Co-Chair: Timothy VanWagoner, Associate Professor of Pediatrics, OCTSI Sr Associate Director, The University of Oklahoma Health Sciences Center

Co-Chair: Stephania Cormier, Associate VP Research, Director LSU Superfund Research Program, Weiner Endowed Chair and Professor, Louisiana State University

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Manisha Thakur, Southern University and A&M college. **Unraveling the Interplay: Carbon Nanotubes, Inflammation, and Environmental Stressors.** Co-Authors: Sanjay Batra. Co-Authors Institutional Affiliations: Southern University and A&M college. Short Research Presentation

Janeese A Brownlow, PhD, Delaware State University. **An Examination of Neighborhood Disadvantage and Stress on Objective Sleep and Sleep-Related Fears.** Co-Authors: None. INBRE, Short Research Presentation

Emily E. Schmitt, University of Wyoming. **The aging mouse as a novel model of nocturia.** Co-Authors: Danielle R. Bruns, Nicole L. Bedford. Co-Authors Institutional Affiliations: University of Wyoming. INBRE, Short Research Presentation

Alexei G. Basnakian, University of Arkansas for Medical Sciences. **Modification of the TUNEL assay with increased sensitivity to nanoparticles.** Co-Authors: Olena Levurdiak, Shenyang Li, Zach McGowan, Fidaus Razak, Randal S. Shelton, Qinglong Jiang. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences, Central Arkansas Veterans Healthcare System, University of Arkansas in Pine Bluff. COBRE, Short Research Presentation

Alexa Bostic, West Virginia University. **Dielectric Characterization of HL-60 Cells under Microgravity.** Co-Authors: Soumya Srivastava. Co-Authors Institutional Affiliations: Not Listed. Flash Talk

Monica Valentovic, Marshall University School of Medicine. **Cytotoxic Effects of E-Cigarette Flavoring Agent Menthol on Renal Proximal Tubular Epithelial Cells.** Co-Authors: S. E. McGuffey, K.C. Brown. Co-Authors Institutional Affiliations: Marshall University School of Medicine. INBRE, Flash Talk

Dhruthi Mutyala, Southern university and A&M College. **Exosome-Mediated Regulation of Proteasomal Subunits in E-Cigarette Vapor-Induced Inflammation.** Co-Authors: N.Bidarimath, R.Kondati, M.Thakur, S.Batra. Co-Authors Institutional Affiliations: Not Listed. COBRE, Flash Talk

1:30PM – 3:10PM Tuesday, June 18 Jefferson East

Genetics and Genomics

Co-Chair: James Coffman, Associate Professor, MDI Biological Laboratory

Co-Chair: Judith Ross, Director of Clinical Research Nemours Children's Health DE, Nemours Children's Health

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Dylan Feist, Kansas State University. **Fine-tuning of Cell-ECM Assembly by Transglutaminase.** Co-Authors: Erika R. Geisbrecht, Nicole Green. Co-Authors Institutional Affiliations: Kansas State University, Cornell College. INBRE, Short Research Presentation

Jared C Talbot, University of Maine. **Fast-twitch myofibrils grow in proportion with Mylpf dosage.** Co-Authors: Adekeye TE, Teets EM, Tomak E, Sprague K, Waterman S, Varga S, Austin J, Rodriguez-Medio C, Hupper T, Shepherd SJ, Amacher SL, Kelley JB, Talbot JC. Co-Authors Institutional Affiliations: University of Maine, Ohio State University. COBRE, Short Research Presentation

Ethan Hackney, Murray State University. **Assembly of membraneless organelles in Drosophila germ cells.** Co-Authors: Samuel J. Tindell, Alexey L. Arkov. Co-Authors Institutional Affiliations: Murray State University. INBRE, Short Research Presentation

Dionysios Patriarcheas, West Virginia University. **Deciphering Glyphosate Resistance Mechanisms: Insights from S. cerevisiae into Mitochondrial Function and Human Glutamate Transport.** Co-Authors: Jennifer E. G. Gallagher. Co-Authors Institutional Affiliations: West Virginia University. CTR, Flash Talk

Daysha Marie Isaac, Langston University. **Stalk Cell Movement in Drosophila: a model to understand how migrating cells shape tissues and organs.** Co-Authors: Sally Horne-Badovinac, Jocelyn A. Mcdonald. Co-Authors Institutional Affiliations: University of Chicago, Kansas State University. INBRE, Flash Talk

Motoki Takaku, University of North Dakota. **Dissecting cellular reprogramming by genomics and machine learning.** Co-Authors: Mika Saotome, Aerica Nagornyuk, Jill Goodman. Co-Authors Institutional Affiliations: University of North Dakota School of Medicine. COBRE, Flash Talk

Lydia Ostmo, Northeastern State University. **Unraveling the functions of Polymerase Epsilon**

complex in DNA replication and DNA damage. Co-Authors: Brandy Fultz, Sapna Das-Bradoo. Co-Authors Institutional Affiliations: Northeastern State University. INBRE, Flash Talk

1:30PM – 3:10PM Tuesday, June 18 Jefferson West

Planning Ahead for COBRE Phases 2 & 3

Moderator: Fed Bernal, Acting Chief, Research Advancement Programs Branch, National Institute of General Medical Sciences

Panelist: Olga Kovbasnjuk, Program Director, National Institutes of Health

Panelist: Crina Frincu, Program Director, National Institutes of Health, National Institute of General Medical Sciences, Division for Research and Capacity Building

Join us for a discussion on COBRE Phase 2 and Phase 3 planning. Hear about important components of the COBRE Phase 2 and Phase 3 applications. Ask your questions and get advice on how to prepare for future COBRE proposals.

1:30PM – 3:10PM Tuesday, June 18 Georgetown East

Considerations When Applying to Graduate School, Fellowships, and Postdoctoral Research Positions

Moderator: Lucy Liaw, Professor, MaineHealth Institute for Research

Panelist: Kelly Drew, Professor, University of Alaska Fairbanks

Panelist: Nicholas Hubbard, Assistant Professor of Psychology, University of Nebraska-Lincoln, Department of Psychology, Rural Drug Addiction Research Center

Panelist: Donald Sens, Professor, University of North Dakota School of Medicine and Health Sciences

Panelist: Robert Roy, Graduate Student, University of Nebraska-Lincoln

Panelist: Tiange Feng, Postdoctoral Research Fellow, MaineHealth Institute for Research

Panelist: Sarah Rice, Postdoctoral Researcher, University of Alaska Fairbanks

Panelist: Abigail Lind, Undergraduate Student, University of North Dakota

Bring your questions for this interactive Q&A session on applying to graduate school, fellowships, and postdoctoral research positions. Hear from an expert panel of past applicants and awardees on important considerations when choosing a program, questions to ask your top schools, and lessons learned in making the transition to a new institution.

1:30PM – 3:10PM Tuesday, June 18 Georgetown West

IDeA Regional Entrepreneurship Development Program (I-RED)

Co- Moderator: Krishan Arora, Branch Chief, National Institute of General Medical Sciences, National Institutes of Health

Co-Moderator: Eddie Billingslea, Small Business Strategy Coordinator, National Institutes of Health, National Institute of General Medical Sciences

Panelist: Prachee Avasthi, Chief of Science, Arcadia Science

Panelist: John Chavez, Managing Director, New Mexico Start Up Factory

Panelist: Lisa Friis, Professor and Chair, University of Kansas, Mechanical Engineering Department

Panelist: Michael Blaustein, Director, Commercialization Strategy and Business Intelligence, University of Delaware

Panelist: Jackie Willmot, CEO & Co-Founder, XLerateHealth

Build your entrepreneurial skills through I-RED! Learn more about how I-RED can support Small Business

Innovation Research (SBIR) and Small Business Technology Transfer (STTR) programs. Hear from NIH staff, successful entrepreneurs and I-RED awardees, and bring your questions to ask the panel!

2:00PM – 3:15PM Tuesday, June 18 International Terrace

Meet the Funders I: One-on-One Time with Staff from Federal Agencies

Do you have a question for your program officer? Want some advice about the direction of research funding? Does your institution need an expensive instrument and you want to know if NIH or other federal agencies could support it? Want to know more about how to interpret your proposal reviews? Are you interested in obtaining funding from the NIH or other federal agencies but don't know how to proceed? Make time to attend this session where you will be able to ask the questions you've always wanted to ask and find out about receiving NIH or other federal agency support in small roundtable settings that give you one-on-one access to NIH staff from many different Institutes and Centers and staff from other federal agencies.

3:30PM – 4:45PM Tuesday, June 18 International Terrace

Meet the Funders II: One-on-One Time with Staff from Federal Agencies

Do you have a question for your program officer? Want some advice about the direction of research funding? Does your institution need an expensive instrument and you want to know if NIH or other federal agencies could support it? Want to know more about how to interpret your proposal reviews? Are you interested in obtaining funding from the NIH or other federal agencies but don't know how to proceed? Make time to attend this session where you will be able to ask the questions you've always wanted to ask and find out about receiving NIH or other federal agency support in small roundtable settings that give you one-on-one access to NIH staff from many different Institutes and Centers and staff from other federal agencies.

3:30PM – 5:10PM Tuesday, June 18 Monroe

Fiscal Management, Carryover Requests, and No-Cost Extension

Speaker: Christy Leake, Grants Management Team Leader, National Institutes of Health, National Institute of General Medical Sciences, Grants Administration Branch

Hear about the most common questions for fiscal management of COBRE, INBRE, and CTR awards. Learn about what is required for annual reporting, carryover needs, and no-cost extension requests. Ask your questions and get clarification on fiscal policies directly from NIGMS IDeA Program during this informative session!

3:30PM – 5:10PM Tuesday, June 18 Lincoln East

Cardiovascular Biology

Co-Chair: Jimmy Ballard, Professor and Chair, University of Oklahoma Health Sciences
Co-Chair: Richard Lamont, Professor, University of Louisville

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Tasnim Imran, Alpert Medical School of Brown University, Providence VA Medical Center. **Characterizing cardiac microstructure in heart failure with preserved ejection fraction using cardiac magnetic**

resonance diffusion tensor imaging. Co-Authors: Daniel Arcuri, Christopher Nguyen, Reza Avazmohammadi, Michael Atalay, Wen-Chih Wu, Gaurav Choudhary. Co-Authors Institutional Affiliations: Providence VA Medical Center, Rhode Island Hospital, Cleveland Clinic Foundation, Texas A&M University. COBRE, Short Research Presentation

Mabruka Alfaidi, LSHSC. **Interleukin-1 Receptor Activation in Vascular Remodeling and Early Atherosclerosis**. Co-Authors: Siddhartha Gangopadhyay, Evan Kidder, Meleah Pea, Quartina Henderson, Siyuan Cheng, Matthew Woolard, Xiuping Yu, Mabruka Alfaidi. Co-Authors Institutional Affiliations: Feist-Weiller Cancer Center, Center for Cardiovascular Diseases and Science (CCDS), Louisiana State University Health Sciences Center. COBRE, Short Research Presentation

Brigitte E Martin, University of Mississippi Medical Center. **Temporal dynamics of cardiovascular response to influenza infection in mice.** Co-Authors: Kurt C Showmaker, Austin A Medders, Jacqueline B Starrett, Lavanya Challagundla, Michael R Garrett. Co-Authors Institutional Affiliations: The Jackson Laboratory for Genomic Medicine, University of Mississippi Medical Center. COBRE, Short Research Presentation

Michayla Moore, MaineHealth Institute for Research (MHIR). **BMP9/ALK1 Signaling is Required for Transcription and Secretion of Mesenchymal Stem Cell Marker, ISLR (Meflin), in Human Cardiac Progenitor Cells.** Co-Authors: Calvin Vary, Douglas Sawyer. Co-Authors Institutional Affiliations: MaineHealth Institute for Research. COBRE, Short Research Presentation

Carly Michelle Goldstein, PhD, FAACVPR, The Miriam Hospital/Alpert Medical School of Brown University. **Using the Multiphase Optimization Strategy and an Electronic Health Record Review to Refine, Finalize, and Prepare Trauma-Informed Interventions to Increase Phase II Cardiac Rehabilitation Initiation in a Full Factorial Experiment.** Co-Authors: J. Graham Thomas, Benjamin T. Ladd, Wen-Chih Wu. Co-Authors Institutional Affiliations: The Miriam Hospital/Alpert Medical School of Brown University, Providence VA Medical Center. COBRE, Flash Talk

Bedia Akosman, Rhode Island Hospital. **Deciphering the Role of the SOX17/Runx1 Axis in Endothelial Dysfunction and Pulmonary Arterial Hypertension Pathogenesis.** Co-Authors: Eui Young So, Mandy Pereira, Moon-Jung Choi, Euy-Myoung Jeong, James Klinger, Olin Liang. Co-Authors Institutional Affiliations: Rhode Island Hospital, Warren Alpert Medical School of Brown University. COBRE, Flash Talk

Sai Prashanthi Gumpili, University of Delaware. **Risk factors for cardiac events in children and young adults within 6 months following a COVID-19 infection.** Co-Authors: Sai Prashanthi Gumpili, Shubhika Srivastava, Carol Prospero, Ran Zhang, Jobayer Hossain, Suzanne McCahan, Chuming Chen, Julie Cowart, Cathy Wu, H. Timothy Bunnell, Robert Akins, Claudine Jurkovitz. Co-Authors Institutional Affiliations: Nemours Children's Health, University of Delaware, Christiana Care Health Services, Inc. INBRE, Flash Talk

3:30PM – 5:10PM Tuesday, June 18 Lincoln West

Brain Disorders and Mental Health

Co-Chair: A. Courtney DeVries, Professor, West Virginia University, Department of Medicine
Co-Chair: Qian-Quan Sun, Professor and Director of Wyoming Sensory Biology Center, University of Wyoming

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Brad Hubbard, University of Kentucky. **Examining brain capillary-specific mitochondrial dysfunction following mild TBI.** Co-Authors: Velmurugan Gopal Viswanathan, Sarah Tran. Co-Authors Institutional

Affiliations: University of Kentucky. COBRE, Short Research Presentation

Moriah Katt, West Virginia University. **Blood-Brain Barrier Dynamics in Ischemic Stroke.** Co-Authors: None. COBRE, Short Research Presentation

Rammohan Shukla, University of Wyoming. **Ribosomal Dysregulation: An Evolutionarily Conserved Stress Mechanism Reactivates in Human Depression.** Co-Authors: None. COBRE, Short Research Presentation

Anastacia Kudinova, Alpert Medical School of Brown University. **Quadratic association between ecologically assessed sleep duration and next-day suicidal ideation in youth.** Co-Authors: Jacqueline Nesi, Sarah K. Ryan, Ella Diab, Mary A. Carskadon. Co-Authors Institutional Affiliations: Alpert Medical School of Brown University. COBRE, Short Research Presentation

Karthik Swaminathan, University of Wyoming. **Ribosomal Heterogeneity in Stress Neurobiology.** Co-Authors: Rammohan Shukla. Co-Authors Institutional Affiliations: University of Wyoming. COBRE, Flash Talk

Katherine A. Berry, University of Wyoming. **Anxiety on the rocks: College students' anticipatory and compensatory urges to drink in response to a laboratory-based social stressor task.** Co-Authors: Alison Looby. Co-Authors Institutional Affiliations: University of Wyoming. INBRE, Flash Talk

Jee-Yeon Hwang, Creighton University. **TREM1 Signaling as a Therapeutic Target for Global Cerebral Ischemia.** Co-Authors: Hyunha Kim, Rachael Urquhart, Gopal Jadhav. Co-Authors Institutional Affiliations: Creighton University School of Medicine. COBRE, Flash Talk

3:30PM – 5:10PM Tuesday, June 18 Jefferson East

Cancer and Disease Risk II

Co-Chair: Vivian Colón-López, Associate Director, University of Puerto Rico Cancer Center
Co-Chair: Danny Dhanasekaran, Director, Mentoring Translational Cancer Research in Oklahoma (MTCRO) - COBRE & Center for Basic Cancer Research, University of Okalahoma Health Sciences Center, Stephenson Cancer Center

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Omeed Moaven, LSU Health New Orleans. **Novel Therapeutic Avenues Investigating the Use of Engineered Oncolytic Viruses That target Tumor Microenvironment in Modulation and Treatment of Pancreatic Cancer.** Co-Authors: Conner Hartupee, Bolni Marius Nagalo, Mulu Z. Tesfay, Dorota Wyczechowska, Luis Del Valle, Joycelynn Coleman-Barnett, John West, Omeed Moaven. Co-Authors Institutional Affiliations: Louisiana State University (LSU) Health School of Medicine, LSU-LCMC Cancer Center, University of Arkansas for Medical Sciences (UAMS), The Winthrop P. Rockefeller Cancer Institute, Louisiana Cancer Research Center, Louisiana State University Health Sciences Center. COBRE, Short Research Presentation

Md Jobayer Hossain, Nemours Children's Health, Wilmington. **Precision Race-Ethnic Disparity in Mortality Risk in Pediatric Cancers: A Study Using SEER Data.** Co-Authors: Zhaoying Lu, Araf Hossain Jahin. Co-Authors Institutional Affiliations: Nemours Children's Health, University of Delaware. CTR, Short Research Presentation

Maria Jesus Ruiz Echevarria, Oklahoma University Health Sciences, Faculty. **Towards Identifying Novel Therapies for Prostate Cancer.** Co-Authors: Joshua M. Corbin. Co-Authors Institutional Affiliations:

Duke University. INBRE, Short Research Presentation

Yun-Seok Choi, Black Hills State University. **A general method for the development of quantitative biosensors enables the measurement of free Nedd8.** Co-Authors: Zachary Wyatt Davis. Co-Authors Institutional Affiliations: Black Hills State University. INBRE, Short Research Presentation

Adriana Aponte Ramos, Inter American University of Puerto Rico, Bayamon Campus. **Exploring Ergosterol Peroxide's Mechanism of Action on the VCP / ANKZF1 Complex in Triple Negative Breast Cancer Models.** Co-Authors: Michelle Martinez Montemayor. Co-Authors Institutional Affiliations: UCC School of Medicine. CTR, Flash Talk

Sahil Lohana, North Dakota State University. **Validation of novel histone deacetylases (HDAC) specific nanoparticles using HDACs overexpressed human embryonic kidney cells.** Co-Authors: Yogaraj S Ramakrishnan, Premanand Balraj, Md Rakib Hasan Khan, Sanku Mallik, Venkatachalem Sathish, Quadir Mohiuddin. Co-Authors Institutional Affiliations: Not Listed. INBRE, Flash Talk

Raphael Oladokun, West Virginia University. **Dielectrophoretic Characterization and COMSOL Analysis of Late Carcinoma Using PBMCs from MMTV-PyMT (PyMT) and MMTV-WT (WT) Mammary Carcinoma Models.** Co-Authors: Soumya Srivastava. Co-Authors Institutional Affiliations: West Virginia University. INBRE, Flash Talk

3:30PM – 5:10PM Tuesday, June 18 Georgetown East

Tips for Accessing and Utilizing NIH-Supported Repositories and Databases

Moderator: Jean Yuan, Chief, Bioinformatics and Computational Biology Branch, National Institute of General Medical Sciences
Panelist: Xiaoli Zhao, Program Director, National Institute of General Medical Sciences, National Institutes of Health
Panelist: Fred Prior, Distinguished Professor and Department Chair, University of Arkansas for Medical Sciences
Panelist: Sharon Patrick, Service Manager, West Virginia Clinical and Translational Science Institute

Learn more about NIH-supported repositories and databases. Hear from experienced investigators who have utilized these resources in their research. We invite you to attend this session to learn what databases are available, and the process for accessing and utilizing them for your research.

3:30PM – 5:10PM Tuesday, June 18 Georgetown West

Building Capacity and Increasing Competitiveness for NIH's Institutionally-Supported Training Programs

Moderator: Mercedes Rubio, Branch Chief, National Institute for General Medical Sciences
Panelist: Elizabeth Harrington, Associate Dean Office of Graduate Studies, Professor of Medicine, Brown University
Panelist: Nancy DeMore, Professor of Surgery, Medical University of South Carolina
Panelist: Timothy Fields, Director, Kansas Medical Scientist Training Program, Professor and Vice Chair for Research and Faculty Development, Department of Pathology & Laboratory Medicine, University of Kansas Medical Center

Join us for a discussion on building capacity and increasing competitiveness for NIH's institutionally-supported training programs. Hear from NIH staff and funded Investigators from IDeA states as they share important considerations in institutional eligibility and strategies for being successful. Ask your questions and get advice on how to prepare competitive training proposals.

5:15PM - 6:30PM Tuesday, June 18 International Ballroom

Scientific and Core Poster Session II

Join us in the International Ballroom for this exciting session! Check the Poster Pamphlet (available in print, on the NISBRE app, and on the conference website) for a list of this year's poster presentations. Posters have been assigned at random to increase opportunities for networking across IDeA-programs and cores. Please remember to vote for your favorite poster(s) in the NISBRE People's Choice Poster Awards available on the NISBRE app. Numerous award categories are available, and winners will be announced during the awards ceremony.

WEDNESDAY, JUNE 19, 2024

8:00AM - 9:00AM Wednesday, June 19 International Terrace

Breakfast with Small Group Discussions

We encourage you to network with colleagues during breakfast. Tables will be reserved for breakout discussions focused on various topics of interest. No reservations are required. A list of table topics will be available at registration.

9:00AM - 10:00AM Wednesday, June 19 International Ballroom

Keynote with Dr. Kelvin Lee

Dr. Kelvin Lee is the Gore Professor of Chemical and Biomolecular Engineering at the University of Delaware and is Director of NIIMBL: the National Institute for Innovation in Manufacturing Biopharmaceuticals. Dr. Lee's keynote address will cover a series of vignettes that highlight the important role that access to core facilities can play in developing a collaborative research program to address issues in biopharmaceutical development and manufacturing as well as vignettes that illustrate how the power of collaboration can be leveraged to accelerate technological innovation to enhance patient access to medicines.

Kelvin Lee, Gore Professor of Chemical and Biomolecular Engineering, Director National Institute for Innovation in Manufacturing Biopharmaceuticals. **Navigating Technology and Collaboration for Biopharmaceutical Manufacturing Innovation**

10:20AM - 12:00PM Wednesday, June 19 Monroe

Elevating Scholarly Writing

Moderator: Rafael Luna, Head of Biomedical Education & Innovation, Novartis Biomedical Research
Panelist: Amy Franks, Professor and Chair, Department of Pharmacy Practice, UAMS College of Pharmacy, University of Arkansas for Medical Sciences College of Pharmacy
Panelist: Joan Lakoski, Director, Investigator Development and Adjunct Professor, WVU School of Pharmacy, West Virginia University, West Virginia Clinical & Translational Science Institute
Panelist: Judith Weber, Associate Dean for Research and Professor, University of Arkansas for Medical Sciences
Panelist: Charlie Irvin, Professor, University of Vermont
Panelist: Ghada Bourjeily, Director of Women's Research, Lifespan / Brown University

In this session, panelists will offer their experience and expertise in scientific writing and include writing tips and strategies. Panelists will also discuss different models of institutional writing programs and offer

pathways to creating innovative national programs.

10:20AM - 12:00PM Wednesday, June 19 Lincoln East

Environment and Health II

Co-Chair: Donald Sens, Professor, University of North Dakota School of Medicine and Health Sciences
Co-Chair: Sharon Rounds, Program Director/Principal Investigator Advance- Rhode Island-CTR, Associate Dean for Translational Science Professor of Medicine and of Pathology and Laboratory Medicine, The Warren Alpert Medical School of Brown University

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Luz Maria Deardorff, University of Hawai'i Maui College. **Environmental Microbes as Indicators of Human Health Risk After the Lahaina Wildfires.** Co-Authors: Tara Zamani, Michelle Gould, Sally Irwin, Junnie June, Rachel Wilsey, Jennifer Honda. Co-Authors Institutional Affiliations: University of Hawai'i Maui College, University of Texas Health Science Center. INBRE, Short Research Presentation

Zachary Redman, University of Alaska Anchorage. **Toxicokinetic Investigation of Weathered Microplastics and Their Metabolomic Impacts in Bay Mussels.** Co-Authors: Jack Hoen, Monica Brandhuber, Brian DiMento, Logan Weiland, Annette Jarosz, Maile Branson. Co-Authors Institutional Affiliations: UAA Chemistry, Alutiiq Pride Marine Institute. INBRE, Short Research Presentation

Devin M. Drown, University of Alaska Fairbanks. **Impact of Arctic Thaw on Soil Microbial Communities and Emerging Environmental Health Risks.** Co-Authors: Bevyn Cover. Co-Authors Institutional Affiliations: University of Alaska Fairbanks. INBRE, Short Research Presentation

Bikram Subedi, Murray State University. **Wastewater Analysis - Near Real Time Approach of Estimating Substance Use.** Co-Authors: Anita Sapkota, Durga P. Kodati, Landon Jones, Jusdin Kamuf. Co-Authors Institutional Affiliations: Murray State University, INBRE, Short Research Presentation

Zim Warda Hasan, Western Kentucky University. **Effect of Glucocorticoid Blockade on Inflammatory Responses to Acute Sleep Fragmentation in Mice.** Co-Authors: Van Thuan Nguyen, Noah T. Ashley. Co-Authors Institutional Affiliations: Western Kentucky University. INBRE, Flash Talk

Mehtap Haktanir Abul, Alpert Medical School Brown University, Rhode Island Hospital. **Asthma and Sleep-Related Environmental Factors Contributing to Sleep Awakenings in Urban Children with Asthma.** Co-Authors: Sheryl J. Kopel, Shira Dunsiger, Luiz Guzman, Carly Mattice, Sidney Kirchhof, Caroline Gredvig-Ardito, M. Carskadon. Co-Authors Institutional Affiliations: Rhode Island Hospital, Alpert Medical School of Brown University, Bradley-Hasbro Research Center, EP Bradley Hospital Sleep Research Laboratory. CTR, Flash Talk

Sarah Arias, Butler Hospital; Brown University. **Challenges and Considerations when using Electronic Health Record Data for Identification of Suicidal Ideation and Behavior.** Co-Authors: Ivan W. Miller, Charles Eaton, Richard N. Jones, Elizabeth Chen. Co-Authors Institutional Affiliations: Butler Hospital, Brown University. CTR, Flash Talk

10:20AM - 12:00PM Wednesday, June 19 Lincoln West

Metabolism and Obesity II

Co-Chair: Elisabet Børsheim, Arkansas Children's Research Institute, University of Arkansas for Medical Science
Co-Chair: Joey Granger, Professor and Director, The University of Mississippi Medical Center

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Heather Drummond, University of Mississippi Medical Center. **Acid sensing ion channel 2 (ASIC2) deficiency increases light cycle ambulatory activity in mice.** Co-Authors: Kylie M. Larson, Emily Hildebrandt, Jussara do Carmo. Co-Authors Institutional Affiliations: University of Mississippi Medical Center. COBRE, Short Research Presentation

Bhaswati Kashyap, University of Delaware. **Elevated Mitochondrial CD36 and Superoxide Production in Endothelial Cells Exposed to Prolonged High Glucose and Fatty Acids In-vitro.** Co-Authors: Thanh Nguyen, Erica Johnson, Ibra S Fancher. Co-Authors Institutional Affiliations: Not Listed. COBRE, Short Research Presentation

Ibra S Fancher, University of Delaware. **Visceral adipose tissue inhibits endothelial Kir2.1 in obesity via a CD36-dependent mechanism.** Co-Authors: Sabita Rokka, Masoumeh Sadeghinejad, Emma C Hudgins, Erica J Johnson, Thanh T Nguyen. Co-Authors Institutional Affiliations: University of Delaware. COBRE, Short Research Presentation

Christopher Johansen PhD, MPH, University of Nevada, Las Vegas. **Parental acculturation and its association with preschool-aged child's health behaviors among Latinos in Southern Nevada.** Co-Authors: Miguel Fudolig, Liliana Davalos, Brisa Rodriguez, Marissa Martinez. Co-Authors Institutional Affiliations: University of Nevada Las Vegas. INBRE, Short Research Presentation

Andrea Corcoran, Vermont State University - Castleton**. CBD in the landscape: Use tendencies and the need for low-dose human physiology studies.** Co-Authors: None. INBRE, Flash Talk

Erica J. Johnson, University of Delaware. **Subcutaneous adipose arteries exhibit significantly less fatty acid uptake in obesity.** Co-Authors: Thanh Nguyen, Sabita Rokka, Caitlin Halbert, Ibra S. Fancher. Co-Authors Institutional Affiliations: University of Delaware. COBRE, Flash Talk

10:20AM - 12:00PM Wednesday, June 19 Jefferson East

Neuroscience

Co-Chair: Jerome Sanes, Professor, Brown University, Department of Neuroscience
Co-Chair: Jose A. Lasalde-Dominicci, Professor, Director of The University of Puerto Rico COBRE Center for Neuroplasticity, University of Puerto Rico

Join this session of scientific presentations for a mix of short research presentations (15 minutes) and flash talks (5 minutes). See below for a detailed list of presenters and talk titles:

Michael Robichaux, West Virginia University. **Misfolded rhodopsin disrupts the ER secretory pathway to the presynaptic terminals of rod photoreceptors in a retinitis pigmentosa mouse model with retinal neurodegeneration.** Co-Authors: Samantha Thompson, Sophie Crowder, Emily Sechrest, Wen-Tao Deng. Co-Authors Institutional Affiliations: West Virginia University. COBRE, Short Research Presentation

Barbara Gisabella, University of Mississippi Medical Center. **Diurnal Expression Rhythms in the Amygdala of Subjects with Bipolar Disorder, Major Depression and Schizophrenia.** Co-Authors: Barbara Gisabella, Harry Pantazopoulos, Robert McCullumsmith, Michael R. Garrett, Rammohan Shukla. Co-Authors Institutional Affiliations: University of Mississippi Medical Center, University of Toledo, University of Wyoming. COBRE, Short Research Presentation

Maj-Linda B Selenica, University of Kentucky. **Deciphering eIF5A hypusination: Novel Mechanisms that drive TDP-43 neuropathogenesis in Alzheimer Disease and Related Dementia.** Co-Authors:

Maj-Linda B. Selenica, Rohan Desai, Christopher Saunders, Patricia Rocha-Rangel, Ramon Sun, Gopal Viswanathan, Patrick Sullivan, Daniel C. Lee, Maj-Linda B. Selenica. Co-Authors Institutional Affiliations: University of Kentucky, University of Florida**.** COBRE, Short Research Presentation

Xhoela Bame, Dartmouth College. **Mitochondrial network reorganization and transient expansion during oligodendrocyte generation.** Co-Authors: Robert A. Hill. Co-Authors Institutional Affiliations: Dartmouth College. COBRE, Short Research Presentation

Adam C. Nelson, University of Wyoming. **The role of oxytocin neurons of the paraventricular hypothalamic nucleus in social thermoregulation.** Co-Authors: Joe Rogers, Morgane Vandendoren, Jason Landen, Samantha Killmer, Baizar Alamiri, Nicole Bedford. Co-Authors Institutional Affiliations: University of Wyoming. COBRE, Flash Talk

Haiyue Song, Department of Biostatistics, Brown University. **Leverage of Functional Connectivity and Effective Connectivity by Selective Inference with Sample Splitting and fMRI Data.** Co-Authors: Ani Eloyan, Youjin Lee. Co-Authors Institutional Affiliations: Brown University. COBRE, Flash Talk

Khadija Kakar, University of South Carolina School of Medicine. **Protective Effects of Delta-8-THC Against EAE-Induced Enteric Neuropathy and Neuroinflammation through Regulation of miRNA-Mediated Signaling Networks.** Co-Authors: Urmi Halder, Manikandan Palrasu. Co-Authors Institutional Affiliations: Not Listed. COBRE, Flash Talk

10:20AM - 12:00PM Wednesday, June 19 Georgetown East

Using Community-Engagement Approaches to Transform Biomedical Research

Moderator: Clifford Rosen, Professor, MaineHealth Institute for Research
Panelist: Keawe Kaholokula, Contact Multiple Principal Investigator, Professor and Chair, University of Hawaii
Panelist: Keyonna King, Associate Professor, University of Nebraska Medical Center
Panelist: Jennifer Lemacks, Professor, Associate Dean for Research, College of Nursing and Health Professions, School of Health Professions
Panelist: Caroline Compretta, Assistant Vice Chancellor for Research, University of Mississippi Medical Center

Learn how to incorporate cutting-edge community engaged approaches into your research. Join in this discussion highlighting successful examples of community engagement across the IDeA regions. Spend time brainstorming your questions with the panel and leave this session with some new ideas for your research program!

10:20AM - 12:00PM Wednesday, June 19 Jefferson West

Put Your Own Oxygen Mask on First: The ABC's of Well-Being

Organizer: Julie Benson, Associate Director Alaska INBRE, University of Alaska Fairbanks

This session will focus on individual well-being and answer the following questions: What is well-being? What steps can each person take to create wellness every day? Attendees will learn the ABC's of well-being and leave with an action plan to move forward with their individual wellness.

10:20AM - 12:00PM Wednesday, June 19 Georgetown West

Bringing Research into the Classroom: Models of Student Focused Training and Research Experiences

Co-Moderator: Martha Bickford, Professor, University of Louisville

Co-Moderator: John McDowell, Instructor, Delaware Technical Community College
Panelist: Thomas Huckaba, Professor, Xavier University of Louisiana
Panelist: Paul Kim, Associate Professor, Grambling State University
Panelist: Paul Sorgen, Professor, University of Nebraska Medical Center

Learn about innovative ways to bring research into the classroom. Join this panel to discuss successful examples and new avenues to expand research access for undergraduates. Bring your experiences and ask your questions of this expert group!

12:00PM - 1:30PM Wednesday, June 19 International Ballroom

Lunch with Awards Ceremony

Join us for this special lunch event. Winners of NISBRE2024 awards will be announced during the awards ceremony. Award nominees are required to be in attendance to accept their award.

1:30PM - 3:30PM Wednesday, June 19 Jefferson

Grant Writing Workshop: Basic Science Proposals

Moderator: Bill Shuttleworth, Distinguished Professor and Department Chair, University of New Mexico School of Medicine
Panelist: Lisa Cassis, Professor, University of Kentucky
Panelist: Margaret Karagas, Professor and Chair of Epidemiology, Geisel School of Medicine at Dartmouth
Panelist: Susan Lunte, Ralph N. Adams Professor of Chemistry and Pharmaceutical Chemistry, Director of COBRE Center for Molecular Analysis of Disease Pathways, University of Kansas
Panelist: Heather Desaire, Professor, University of Kansas

Join us for a two-hour session with experienced NIH reviewers. Hear experts talk about the review process, give their advice about what are often overlooked sections of an application, and provide general tips for proposal success. Learn about finding relevant grant mechanisms and program announcements and gain insight into the grant review and resubmission processes from the reviewer lens. Bring your questions and join in this exciting session!

1:30PM - 3:30PM Wednesday, June 19 Monroe

Tips and Techniques for Successful Grant Submission: Focus on Behavioral and Biopsychosocial Proposals

Moderator: Stephen Wonderlich, Vice President, Chief of Behavioral Health, Sanford Center for Biobehavioral Research
Panelist: Lori Leibold, Program Director, Boys Town National Research Hospital
Panelist: Laura Stroud, Professor, Director, The Miriam Hospital
Panelist: Judith Weber, Associate Dean for Research and Professor, University of Arkansas for Medical Sciences
Panelist: Curtis Noonan, Professor, University of Montana, Center for Population Health Research

Join us for a two-hour session with experienced NIH reviewers. Hear experts talk about the review process, give their advice about what are often overlooked sections of an application, and provide general tips for proposal success. Learn about finding relevant grant mechanisms and program announcements and gain insight into the grant review and resubmission processes from the reviewer lens. Bring your questions and join in this exciting session!

1:30PM - 3:30PM Wednesday, June 19 Lincoln West

Grant Writing Workshop: Training Mechanisms

Moderator: Stephen Higgins, Professor, Director, University of Vermont

Panelist: Carmen Cadilla, Professor, University of Puerto Rico Medical Sciences Campus

Panelist: Clarissa Henry, Professor, University of Maine

Panelist: Jacqueline Stephens, Professor, Pennington Biomedical Research Center, Adipocyte Biology

Join us for a two-hour session with experienced NIH reviewers. Hear experts talk about the review process, give their advice about what are often overlooked sections of an application, and provide general tips for proposal success. Learn about finding relevant grant mechanisms and program announcements and gain insight into the grant review and resubmission processes from the reviewer lens. Bring your questions and join in this exciting session!

1:30PM - 3:30PM Wednesday, June 19 Lincoln East

Grant Writing Workshop: Fellowship and Early Career Mechanisms

Moderator: Michele McGuirl, Acting Director, Division for Research Capacity Building, National Institutes of Health, National Institute of General Medical Sciences

Panelist: Josiah Hardesty, Assistant Professor, University of Louisville, Department of Pharmacology & Toxicology

Panelist: John Le, Graduate Student, Louisiana State University (School of Veterinary Medicine), Pathobiological Sciences

Panelist: Rebecca Mountain, Staff Scientist, MaineHealth Institute for Research

Panelist: Steven Fiering, Professor Microbiology and Immunology, Program Director, New Hampshire INBRE, Dartmouth, Geisel School of Medicine, Microbiology and Immunology

Join us for a two-hour session with experienced NIH reviewers. Hear experts talk about the review process, give their advice about what are often overlooked sections of an application, and provide general tips for proposal success. Learn about finding relevant grant mechanisms and program announcements and gain insight into the grant review and resubmission processes from the reviewer lens. Bring your questions and join in this exciting session!

4:00PM - 5:00PM Wednesday, June 19 Lincoln East

COBRE Directors Closed Meeting

Co-Organizer: Lucy Liaw, Professor, MaineHealth Institute for Research

Co-Organizer: Rick Bevins, Rural Drug Addiction Research Center COBRE PI, University of Nebraska-Lincoln

Meet with NIGMS Leadership and network with other COBRE Principal Investigators during this NISBRE2024 session. Learn about COBREs in your region, meet COBRE PIs in similar thematic areas, and share resources for COBRE administration. This is a closed meeting for COBRE PIs.

4:00PM - 5:00PM Wednesday, June 19 Georgetown West

INBRE Directors Closed Meeting

Organizer: Carolyn Bohach, Director of Idaho INBRE, University Distinguished Professor, University of Idaho

Speaker: Scott Seville, President National Association of IDeA Principal Investigators (NAIPI) Director Wyoming INBRE, University of Wyoming

Meet with NIGMS Leadership and connect with INBRE Principal Investigators during this NISBRE2024

session. Spend time connecting with INBRE PIs and share resources for INBRE administration. This is a closed meeting for INBRE PIs.

4:00PM - 5:00PM Wednesday, June 19 Georgetown East

CTR Directors Closed Meeting

Organizer: Sharon Rounds, Program Director/Principal Investigator Advance- Rhode Island-CTR, Associate Dean for Translational Science Professor of Medicine and of Pathology and Laboratory Medicine, The Warren Alpert Medical School of Brown University

Meet with NIGMS Leadership and connect with CTR Principal Investigators during this NISBRE2024 session. Spend time connecting with CTR PIs and share resources for INBRE administration. This is a closed meeting for CTR PIs.

NISBRE2024

Short Research Presentation and Flash-Talk Abstracts (ONLINE ONLY)

Organized by Session Topic

SHORT RESEARCH PRESENTATIONS

Artificial Intelligence

Indra Neil Sarkar, Brown University. **Establishing A Statewide Learning Health System with OMOP-on-FHIR for High Need Children.** Co-Authors: Elizabeth Chen, Karen Crowley, Paul Stey, Jonah Bradenday, Farahnaz Maroof, Mounika Thakkallapally, Ashok Ragavendran, Edward Hawrot, Sharon I. Rounds. Co-Authors Institutional Affiliations: Brown University. CTR

The potential of artificial intelligence (AI) in clinical decision-making depends on access to high-quality, diverse, and representative health data. However, a major barrier in developing AI models for health is access to such data. Furthermore, healthcare AI models are often built using data from individual healthcare systems, limiting their scope and introducing biases due to data fragmentation (e.g., in Rhode Island, >2/3rds of health data for individuals are across 2+ electronic health records [EHRs]). To realize the vision of a Learning Health System (LHS) to holistically advance healthcare delivery for a given population, data must be integrated across fragmented healthcare ecosystems to support the development and evaluation of AI models. Health Information Exchanges (HIEs) are positioned to bridge these data gaps. Despite abundant data in HIEs, their inherent data heterogeneity can hinder AI model development. The Fast Healthcare Interoperability Resources (FHIR) is a standard mandated by the 21st Century Cures Act that provides the opportunity to access EHR data in a standards-driven way. Through supplemental NIH/NIGMS funding to advance the use of EHR for Research at Rhode Island's IDeA-CTR program (Advance RI-CTR, U54GM115677), we have expanded our cyberinfrastructure to accommodate HIE data using the Observational Medical Outcomes Partnership (OMOP) Common Data Model alongside FHIR for supporting LHS research. Within the context of studies that we are embarking on a specific population (high-need children), this presentation will provide an overview of the framework that we have developed to improve data quality and expedite AI model development.

Prateek Verma, University of Arkansas. **Evaluation of Large Vision Language Models on Scientific Images.** Co-Authors: Minh-Hao Van, Xintao Wu. Co-Authors Institutional Affiliations: University of Arkansas. COBRE

The application of large vision language models (VLMs) extends beyond everyday imagery and has significant potential in the realm of scientific imaging, encompassing medical, biological, and material sciences. This research delves into the effectiveness of state-of-the-art VLMs, such as LLaVA, Flamingo, and ChatGPT-4, in interpreting a broad spectrum of scientific images, including but not limited to medical X-rays, MRIs, microscope images of cellular structures, and material samples. The study aims to evaluate the models' performance across various tasks such as classification, segmentation, object counting, and visual question answering (VQA). Through extensive testing, we aim to uncover the strengths and limitations of these models in handling the preliminary understanding, intricate detailing, and hierarchical comprehensibility routinely encountered in scientific image analysis. The evaluation inconspicuously highlights the adaptability of these models to different scientific domains, their ability to understand scientific jargon, and their performance in integrating visual and textual information to draw accurate depictions.

Russell McCulloh, University of Nebraska Medical Center. **Outlining a vision for a learning research system.** Co-Authors: Ellen Kerns, Jerrod Anzalone, Matthew Rizzo. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. CTR
Academic medical research operations and administration face organizational inefficiencies that cripple research productivity, collaboration, opportunities, careers, and progress, drain institutional resources, and erode NIH missions. Our interprofessional team at UNMC proposes a learning research system (LRS) that leverages learning health system approaches to ensure that academic institutions complete rigorous, impactful research more efficiently and with maximal individual and community benefit. The LRS accomplishes this using silo-spanning approaches including artificial intelligence (AI)-enabled software tools, systems science, and organizational principles with iterative, actionable feedback loops for continual improvement. A key implementation step is converting research administrative data into a computable format to facilitate data sharing and application of business intelligence approaches to enhance resource allocation. This data can be used to train AI tools that decrease administrative delays and enhance researchers' and research administrators' productivity, accuracy, and quality. Directly aligning with the NIH Directors goals, the LRS can help connect research with primary care to optimize patient outcomes; overcome barriers to research access faced by underrepresented communities; use the EHR to recruit and consent people into studies' in tandem with enhanced data interoperability across EHRs; promote research capacity and efficiency with innovative study designs that address common health issues; and rapidly disseminate evidence to guide decision-making and policy. We will implement solutions using agile development methods, an iterative design approach used in software development. The LRS will enable institutions to design new administrative systems that best align with users' requirements and community values and that can scale to diverse institutional settings.

Shanshan Ding, University of Delaware. **Machine learning and causal inference in high dimensional survival analysis.** Co-Authors: Wei Qian, Zhezhen Jin. Co-Authors Institutional Affiliations: University of Delaware, Columbia University. CTR
High-dimensional survival data holds significant importance in real-world applications such as clinical and medical research on cancer, neurological disorders, cardiovascular diseases, etc. and contemporary mobile health due to its ability to capture complex relationships and provide more comprehensive insights. Classical methods in high-dimensional survival analysis are often within parametric or semiparametric settings, which require certain model assumptions. The goal of this talk is to introduce a unified framework for machine learning (especially nonparametric learning) of high-dimensional survival data via data embedding under various generalized settings. Novel supervised embedding methods will be proposed for dimension reduction of high dimensional survival data. Machine learning methods such as gradient boosting machine, random survival forests, and metalearners will be introduced for modeling and making causal inference for high dimensional survival data after data reduction. In a simulation study and a real-world data example from cancer genomic research, we demonstrate how the proposed methods can be employed for biomarker and risk group identification, as well as to illuminate underlying mechanisms.

Brain Disorders and Mental Health

Anastacia Kudinova, Alpert Medical School of Brown University. **Quadratic association between ecologically assessed sleep duration and next-day suicidal ideation in youth.** Co-Authors: Jacqueline Nesi, Sarah K. Ryan, Ella Diab, Mary A. Carskadon. Co-Authors Institutional Affiliations: Alpert Medical School of Brown University. COBRE
Characterizing the proximal link between sleep duration and suicide risk in children and adolescents is

essential for developing informative, early mobile interventions. We examined the association between ecologically assessed suicidal ideation (SI) and sleep duration in youth recruited after a partial hospitalization program. We also examined contextual factors salient for youth, including nighttime social media use and social media use-related self-referential cognitions. We used ecological momentary assessment (EMA) 3 times/day over 2 weeks in discharged partial hospital patients to assess their levels of SI at home (n=79; 62% assigned F at birth; ages 12-15; mean 13.52; sd 1.14 yr). We also asked youth to report their bedtimes and waketimes every morning for two weeks. Social media use was assessed once via a questionnaire. Using generalized linear mixed models, we showed a significant quadratic effect of sleep duration on next-day SI (B=â€“0.04, SE =0.01, p

Brad Hubbard, University of Kentucky. **Examining brain capillary-specific mitochondrial dysfunction following mild TBI.** Co-Authors: Velmurugan Gopal Viswanathan, Sarah Tran. Co-Authors Institutional Affiliations: University of Kentucky. COBRE
Traumatic brain injury (TBI) is a worldwide epidemic and a major cause of disability, morbidity, and mortality. TBI is a major risk factor for the development of late-life dementia, especially Alzheimer's Disease, and other neurological conditions, such as epilepsy. The most prevalent form of TBI is mild TBI (mTBI), which is characterized by progression of cognitive and psychological deficits accompanied by metabolic and neurovascular dysfunction. There is a lack of studies that investigate mitochondrial and metabolic deficits specifically in the neurovasculature after mTBI. Therefore, we hypothesize that mTBI will produce on-going mitochondrial dysfunction in brain capillaries that can be therapeutically targeted to restore blood-brain barrier (BBB) integrity following mTBI. To first understand brain capillary-specific mitochondrial function and dynamics in response to oxidative stress, we developed a novel ex vivo model in which we used isolated brain capillaries from transgenic mice that express dendra2 green specifically in mitochondria (mtD2g) and generate oxidative stress through lipid peroxidation. Mitochondrial bioenergetics and dynamics were then measured. We found that oxidative stress significantly decreased mitochondrial respiration and volume in brain capillaries. We then used a model of blast-induced mTBI to examine brain capillary-specific mitochondrial function after injury and whether the PDE5 inhibitor sildenafil could modulate these outcomes. At 24h post-injury, isolated brain capillaries were incubated with 1 μM sildenafil. Deficits in maximal mitochondrial respiration of brain capillaries were restored by ex vivo sildenafil treatment. Our findings demonstrate that oxidative stress and mTBI produces mitochondrial dysfunction in brain capillaries, which can be therapeutically targeted.

Moriah Katt, West Virginia University. **Blood-Brain Barrier Dynamics in Ischemic Stroke.** Co-Authors: None. COBRE
The blood-brain barrier (BBB) undergoes significant functional changes in the aftermath of ischemic stroke. These phenotypic changes impair the ability of the BBB to maintain brain homeostasis and prevent further damage to the delicate brain parenchyma. However, there is not complete breakdown of the BBB, making delivery of therapeutics difficult. Development of a human based model is critical for development of novel therapeutics to aid in recovery following an ischemic stroke. Here we have employed a human induced pluripotent stem cell (hiPSC) derived model of the BBB using brain endothelial-like cells (BMECs), pericyte-, and astrocyte-like cells all derived from a single hiPSC line to produce an isogenic model of the BBB in both 2D and 3D. This model was then exposed to simulated ischemia conditions including hypoxia and glucose deprivation. Barrier phenotype is then measured utilizing functional transport experiments as well as protein expression. The hiPSC-derived BBB recapitulates the biphasic opening of the BBB seen in animal models, with increased leakage in hyperacute ischemia, a return to baseline, with a subsequent decline of barrier phenotype and increased leakiness. This is supported by protein expression of tight junction proteins, as well as transcytosis associated proteins. The presence of pericytes and astrocytes supports BMEC phenotype and recovery

following ischemic stroke. Ultimately these results allow us to identify novel therapeutic targets in ischemic stroke for improved patient outcome.

Rammohan Shukla, University of Wyoming. **Ribosomal Dysregulation: An Evolutionarily Conserved Stress Mechanism Reactivates in Human Depression.** Co-Authors: None. COBRE
The heterogeneity in the presentation of Major Depressive Disorder (MDD) poses a significant challenge in understanding its underlying biological mechanisms. To address this gap and establish a conceptual framework aligning animal models with clinical endpoints, our study explores comparative molecular analysis between chronic stress experimental systems and MDD. Transcriptomic profiles from postmortem MDD subjects and mice exposed to chronic variable stress (CVS) were compared, revealing down-regulation of Ribosomal Protein Genes (RPGs) and up-regulation of associated Ribosomal Protein (RP) pseudogenes in both conditions. A seeded gene co-expression analysis, focusing on altered RPGs common between MDD and CVS, unveiled a homeostatic regulation of synaptic changes driven by RP-pseudogenes. In vitro analysis highlighted glucocorticoid-driven endocrine responses to stress as a key factor in RPG dysregulation. In silico assessments indicated a reversal of this dysregulation during MDD remission and selective responsiveness to ketamine, not imipramine. Our findings present compelling evidence that ribosomal dysregulation during stress is a conserved phenotype in both human MDD and chronic stress-exposed mice. This study lays the groundwork for the hypothesis that stress-induced alterations in RPGs, and subsequently ribosomes, contribute to the synaptic dysregulation underlying MDD and chronic stress-related mood disorders.

Cancer and Disease Risk

Belinda Joyce Petri, University of Louisville. **Differential m6A modification identified by direct mRNA sequencing in endocrine- resistant and sensitive breast cancer cells.** Co-Authors: Kellianne M. Piell, Eric C. Rouchka, Carolyn M. Klinge. Co-Authors Institutional Affiliations: University of Louisville School of Medicine. INBRE
Acquired resistance to endocrine therapies (ET) in patients with estrogen receptor Î± (ER+) breast tumors results in metastatic spread. RNA modifications including N6-methyladenosine (m6A) play crucial roles in the post-transcriptional regulation of gene expression and have been implicated in cancer progression. We hypothesized that m6A epitranscriptomic alterations are associated with pathways in ET resistance. Direct-RNA sequencing technology (nanopore) was used to detect and map m6A modifications at single-nucleotide resolution to comprehensively profile m6A modifications in ET-resistant LCC9 and ET -sensitive MCF-7 breast cancer cell lines with or without 4-hydroxytamoxifen (4-OHT) treatment. Additionally, MCF-7 cells were treated with the METTL3 inhibitor STM2457 to identify m6A positions and transcripts directly regulated by METTL3 activity. We incorporated statistical analysis by integrating m6Anet, an existing machine-learning algorithm designed to call m6A modified bases, with a generalized linear model following a binomial distribution analysis to identify significant differential m6A modification ratios (DMR). We identified 61 transcripts with DMR between vehicle-treated LCC9 compared to MCF-7 cells and 323 transcripts with DMRs between 4-OHT-treated LCC9 and MCF-7 cells. Fewer transcripts showed DMR after 4-OHT treatment in MCF-7 (41) versus LCC9 cells (399). Thus, more changes in m6A DMRs were detected in response to 4-OHT in the ET-resistant LCC9 versus ET-sensitive MCF-7 cells with “translation elongation” as the top pathway in enrichment analysis. STM2457 treatment resulted in significant changes to DMRs in MCF-7 cells with or without 4-OHT treatment and altered gene expression patterns associated with “cytosolic ribosome” in enrichment analysis. We identified many genes with multiple m6A modifications, e.g., AMIGO2 with 14 m6A sites at METTL3 target DRACH motifs in MCF-7 cells, compared to no m6A modification in AMIGO2 in LCC9 cells. Our findings reveal distinct m6A modification patterns in ET-resistant LCC9 breast cancer cells compared to their ET-sensitive parental MCF-7 cells and in response to 4-OHT, suggesting a potential role for epitranscriptomic alterations in the

development of ET resistance.

Harilaos Filippakis, University of New England. **Therapeutic targeting of Tryptophan-mediated macropinocytosis in Tuberous Sclerosis Complex.** Co-Authors: Sarah Lafleur, Windrie Cox, Aidan McGrath-Conwell, Elizabeth P. Henske, Harilaos Filippakis. Co-Authors Institutional Affiliations: University of New England. COBRE
Tuberous Sclerosis Complex (TSC) is a multisystem hamartomatous disease that affects the kidneys, brain, heart, skin, and lungs. In TSC, biallelic loss of TSC1/2 leads to constitutive activation of the mammalian target of rapamycin complex 1 (mTORC1). mTORC1 acts as a signaling rheostat via several inter-connected mechanisms, including enhanced glucose and glutamine utilization, nucleic acid, protein, and lipid synthesis. Interestingly TSC2-deficient cells have enhanced macropinocytosis, an actin-dependent endocytic process that facilitates uptake of extracellular material and processing at the lysosome. L-Tryptophan (Trp) is an essential amino acid that plays a critical role in maintaining cellular metabolism and growth. We found that Trp stimulates macropinocytosis ~2.5-fold (p

Maria Jesus Ruiz Echevarria, Oklahoma University Health Sciences, Faculty. **Towards Identifying Novel Therapies for Prostate Cancer.** Co-Authors: Joshua M. Corbin. Co-Authors Institutional Affiliations: Duke University. INBRE
The standard initial treatment for advanced Prostate Cancer (PCa) has been androgen deprivation therapy (ADT) which blocks androgen receptor (AR) signaling. The AR is a ligand-activated nuclear transcription factor that plays a key role in the progression of PCa. However, while ADT is an effective first-line treatment, most patients will eventually relapse with castration resistant PCa, which is often lethal. The identification of novel targets and better therapeutics and/or approaches are critical unmet needs for the management of PCa. The development of resistance to ADT is often accompanied by persistence of AR transcriptional activity, due to adaptation of the AR-signaling pathway. Central to AR-signaling is the recruitment of AR coregulators, which modulate its transcriptional response. Expression of AR coregulators is often de-regulated in PCa, and increased expression generally correlates with aggressive disease and poor clinical outcome. Targeting AR coregulators or their interaction with the AR, are plausible therapeutic approaches for PCa, but so far individual targeting of known AR-coregulators has not been effective, in part due to functional redundancy. We have developed an unbiased shRNA-based negative screen to identify shRNAs that inhibit PCa cell growth and survival (toxic shRNAs). Computational analyses of the group of most toxic shRNAs identified in the screen revealed that each can simultaneously target multiple known AR-coregulatory genes. The implications of these results to the identification of novel targets (including groups of novel AR-coregulators) and therapeutic approaches for PCa will be discussed.

Md Jobayer Hossain, Nemours Chindren's Health, Wilmington. **Precision Race-Ethnic Disparity in Mortality Risk in Pediatric Cancers: A Study Using SEER Data.** Co-Authors: Zhaoying Lu, Araf Hossain Jahin. Co-Authors Institutional Affiliations: Nemours Children's Health, University of Delaware. CTR
Pediatric cancers exhibit significant heterogeneity in etiology, treatment response, and mortality. Mortality risk varies notably by histology-based cancer type, followed by race-ethnicity, posing a serious public health concern. Leveraging a comprehensive SEER dataset of 101,328 pediatric cancer patients diagnosed from 1975 to 2016, we employed frailty models to estimate mortality disparities among race-ethnic groups. Non-Hispanic African American (NHAA) and Hispanic patients faced significantly higher mortality risks than non-Hispanic Caucasians (NH-Caucasians), with NHAA experiencing the highest disparity. NHAA patients face higher mortality risks across all cancer types, with the greatest disparity (adjusted hazard ratio (aHR) between 1.50 and 2.00) in liver, endocrine, acute lymphocytic leukemia, urinary, chronic leukemia, and Hodgkin lymphoma. Moderate disparity (aHR between 1.20 and 1.49) is seen in the brain, CNS, eye, female genital system, AML,

other leukemias, NHL lymphoma, and soft tissue including the heart. Low disparity (1.10-1.19) occurs in bone, joint, and adrenal gland cancers. In Hispanic patients, disparities vary slightly, with ALL and male genital system cancers showing the highest disparity, moderate disparity in 16 cancer types, and low disparity in AML and soft tissue and heart cancers. Hispanic pediatric patients exhibit a survival benefit in the digestive system compared to other groups. Racial/ethnic disparities persist across many cancer types, even after controlling for histological heterogeneity. NHAA experiences the most severe survival disparity, followed by Hispanics. Understanding the estimated disparity in mortality risk can guide public health planners in addressing the modifiable gap in racial disparity in pediatric cancer mortality.

Omeed Moaven, LSU Health New Orleans. **Novel Therapeutic Avenues Investigating the Use of Engineered Oncolytic Viruses That target Tumor Microenvironment in Modulation and Treatment of Pancreatic Cancer.** Co-Authors: Conner Hartupee, Bolni Marius Nagalo, Mulu Z. Tesfay, Dorota Wyczechowska, Luis Del Valle, Joycelynn Coleman-Barnett, John West, Omeed Moaven. Co-Authors Institutional Affiliations: Louisiana State University (LSU) Health School of Medicine, LSU-LCMC Cancer Center, University of Arkansas for Medical Sciences (UAMS), The Winthrop P. Rockefeller Cancer Institute, Louisiana Cancer Research Center, Louisiana State University Health Sciences Center. COBRE
The tumor microenvironment (TME) is a major therapeutic barrier in pancreatic ductal adenocarcinoma (PDAC). Vesicular stomatitis virus (VSV) is an effective oncolytic viral platform for delivery of immunomodulatory and desmoplastic remodeling proteins. The aim of this study is to preclinically investigate the anti-PDAC capacity of a VSV expressing decorin to modify the TME. Protein expression and oncolytic potential of the VSV-decorin construct was comparatively evaluated in vitro versus a wild-type VSV. In vivo studies investigated heterotopic tumor response to intratumoral injections of VSV-decorin versus VSVwt. Tissue samples were stained for Mason's Trichrome, as well as expression of decorin, apoptotic proteins and immune lineage determinants. Cytotoxicity assays of infections at equivalent MOI demonstrated increased cytotoxicity mediated by VSV-decorin (52.1% ±2.2%) vs. VSVwt (63.4% ±3.3%). Expression of decorin protein was validated by immunoblotting indicative of viral replication. Intratumoral decorin expression was verified in treated tissue samples. Tumors evinced reduced Trichrome signifying destruction of peri-tumoral collagen and increased apoptosis. Tumor infiltrating immune cells were significantly increased in the treated immunocompetent animals. The objective response was a smaller significantly softer tumor compared to control treatment as well as the absence of metastatic disease. VSV expressing decorin can successfully remodel the PDAC TME, leading to the breakdown of desmoplastic stroma, promotion of apoptosis and enhancement of tumor toxicity, and immune infiltration. Ongoing research will investigate additional transgene variants, involved mechanisms, and integration with the standard-of-care systemic treatment.

Stephanie M. Dorta-Estremera, University of Puerto Rico Medical Sciences Campus. **Modulating the oral microbiota to enhance anti-tumor immune responses in oropharyngeal cancer.** Co-Authors: Jennifer Diaz-Rivera, Michael Rivera-Rodriguez, Alejandra Rosario-Crespo, Jorge R. Galan-Ortiz, Edna E. Aquino-Pinero, Filipa Godoy-Vitorino, Stephanie M. Dorta-Estremera. Co-Authors Institutional Affiliations: University of Puerto Rico Medical Sciences Campus, Comprehensive Cancer Center UPR, The Alliance. CTR
Patients with oral squamous cell carcinoma (OSCC) often receive antibiotics to prevent infections after surgery. Antibiotic use leads to a decrease in commensal bacteria associated with poor prognosis. Restoring the oral microbiota with probiotic strains might provide a safe and effective therapy for OSCC. Studies to understand the impact of the oral microbiota on intratumoral immune responses and tumor growth in OSCC need to be performed. The goal of this study is to determine the effect of the antibiotic tetracycline, as well as the probiotic Streptococcus salivarius, a commensal oral bacterium, on immune responses and tumor growth in a preclinical model of OSCC during treatment with the immune checkpoint blockade anti-PD-1. Characterization of oral tumor microbiota demonstrated that Streptococcus and Blautia increased significantly in mice

responding to anti-PD-1 therapy compared to non-responders. Topical treatment over the tongue with tetracycline of mice receiving anti-PD-1 led to a reduction in the relative abundance of gut Bifidobacterium and Lactobacillus, accompanied by a reduction in dendritic cell activation, and increase in regulatory T cell frequencies in tumor-draining lymph nodes (tdLNs), and reduction of intratumoral T cells. Topical treatment over the tongue with S. salivarius, induced natural killer cells and CD8+ T cells activation in tdLNs without affecting tumor growth. Surprisingly, intratumoral treatment with S. salivarius led to an increase in CD4+ T cell infiltration into tumors and significant decrease in tumor growth. In conclusion, modulation of the oral microbiota affects intratumoral immune responses and may impact the growth of OSCC in a preclinical model.

Thomas Huckaba, Xavier University of Louisiana. **Development and Testing of Proteolysis-Targeting Chimeras (PROTACs) as Therapeutics for Non-Small Cell Lung Cancer.** Co-Authors: Fasial Abedin, Cecily DeFreece, Xianyou Peng, Guangdi Wang. Co-Authors Institutional Affiliations: Not Listed. INBRE
Non-small cell lung cancer (NSCLC) accounts for the majority (~82%) of all lung cancer diagnoses and can be caused by several distinct mechanisms. One such mechanism is an inversion in Chromosome 2p leading to fusion of the tyrosine kinase domain of the Anaplastic Lymphoma Kinase (ALK) gene with the coiled-coil domain of the echinoderm microtubule-associated protein-like 4 gene (EML4), leading to dimerized, constitutively active tyrosine kinase. While the FDA has approved competitive ALK inhibitors, spontaneous suppressor mutations in the ALK active site limit their efficacy, with 11-month median duration of response. To address this, we developed a series of proteolysis-targeting chimeras (PROTACs) to induce the degradation of the EML4-ALK protein. These heterobifunctional PROTACs are small molecules containing an EML4-ALK targeting motif coupled to an E3 ubiquitin ligase-recruiting ligand. This complex induces the ubiquitination and subsequent proteasome-mediated degradation of the target protein. Through iterative synthesis and testing, we developed a series of early stage, lead PROTAC compounds. In cellular assays, single nanomolar concentrations of PROTACs induce degradation of transformed, NSCLC-causing EML4-ALK fusions, as well as EML4-ALK with suppressor mutations blocking the efficacy of approved therapeutics. Importantly, we observe EML4-ALK degradation for concentrations at or lower than those used for current inhibitors. In an NSCLC mouse xenograft model, oral doses of 10 mg/kg induced complete tumor regression, with a shorter time course to regression and at lower doses than currently approved inhibitors. Here we present ongoing cellular studies of further optimization of our lead compounds against EML4-ALK and drug-resistant ALK suppressor mutations.

Yun-Seok Choi, Black Hills State University. **A general method for the development of quantitative biosensors enables the measurement of free Nedd8.** Co-Authors: Zachary Wyatt Davis. Co-Authors Institutional Affiliations: Black Hills State University. INBRE
Nedd8 regulates cellular signals through conjugation to other proteins. The imbalance of the concentration of free (i.e., unconjugated) Nedd8 to that of conjugated Nedd8 caused by defects in Nedd8-related enzymes or cellular stress are implicated in various diseases. Despite the biological significance of Nedd8, there is currently no method for direct quantification of Nedd8, and this lack is a barrier to study Nedd8 dynamics and its associated enzyme activities. Genetically encoded biosensors are well-established tools for studying dynamic systems like Nedd8 pools, but limitations of current biosensor design methods make them unsuited for quantification of any Nedd8 pool. To solve this problem, we developed a generalizable and modular method for design of a genetically encoded biosensor consisting of a target-binding domain and two reporter domains that interact in the absence of target. Target quantification is based on competition between target binding and the interaction of the two reporter domains. To apply our design strategy to free Nedd8 quantification, we rationally designed a free Nedd8 binder and combined it with FRET-based or split luciferase reporters. Our sensors are capable of quantifying free Nedd8 from nanomolar to micromolar concentrations. The luminescent sensor enables real-time monitoring of deneddylase activity on its physiological substrate,

potentially aiding in developing deneddylase inhibitors for cancer treatments via high-throughput inhibitor screening. Furthermore, our modular design strategy could be implemented to develop genetically encoded quantitative biosensors for other proteins of interest.

Cardiovascular Biology

Brigitte E Martin, University of Mississippi Medical Center. **Temporal dynamics of cardiovascular response to influenza infection in mice.** Co-Authors: Kurt C Showmaker, Austin A Medders, Jacqueline B Starrett, Lavanya Challagundla, Michael R Garrett. Co-Authors Institutional Affiliations: The Jackson Laboratory for Genomic Medicine, University of Mississippi Medical Center. COBRE

There is a growing interest in detecting subtle changes in cardiovascular physiology during viral infections for earlier diagnosis and prognosis. Despite influenza primarily targeting the respiratory system, our previous studies in mice revealed notable alterations in cardiovascular physiology and inflammatory biomarkers. Reductions in activity, blood pressure, and heart rate were observed in females around 3-13 days post-infection (dpi) and in males around 5-12 dpi. Additionally, sex-specific differences in inflammatory marker expression were noted in lung tissues at 7 dpi. In this study, we aim to assess cardiovascular changes and their association with biomarkers during influenza infection. Samples from blood, brain, heart, lung, kidney, and nasal septum were collected at 1, 3, 5, and 9 dpi from both infected and mock-infected mice. Significant body weight loss was observed at 9 dpi in both sexes, with infected females showing increased brain, lung, and kidney weights compared to controls. Histological analyses revealed significant lung injury and heart fibrosis, particularly pronounced in females and slightly elevated in males throughout infection, peaking at 9 dpi. Viral titers were detected in lungs but not heart, indicating indirect cardiovascular effects. We are utilizing single-nuclei RNA sequencing of hearts to analyze both cell-type annotation and transcriptomics. Future studies will explore cardiac function using echocardiography, providing insights into both acute and long-term effects of infection.

Michayla Moore, MaineHealth Institute for Research (MHIR). **BMP9/ALK1 Signaling is Required for Transcription and Secretion of Mesenchymal Stem Cell Marker, ISLR (Meflin), in Human Cardiac Progenitor Cells.** Co-Authors: Calvin Vary, Douglas Sawyer. Co-Authors Institutional Affiliations: MaineHealth Institute for Research. COBRE

Stem/progenitor cell treatments are being investigated as a potential treatment to reverse cardiac remodeling and restore cardiac function in heart disease. However, the molecular mechanisms required for beneficial cell treatment response are not well understood. BMP9 signaling via the ALK1 receptor is a pathway involved in several mechanisms of cardiac repair such as angiogenesis, migration, and proliferation. ISLR (Meflin) is a novel marker of mesenchymal stem cells found to have an important role in maintaining “stemness”, colony formation of stem cells, and inhibiting fibrosis. We identified ISLR as a potential target of BMP9/ALK1 signaling in human highly proliferative cells (hHiPCs) with progenitor capacity isolated from patients undergoing coronary artery bypass graft (CABG) surgery. Using LC-MS/MS analysis of the hHiPC secretome, we find that secretion of ISLR is significantly increased (Fold-change (FC) = 3.1, $p = 0.01$), which corresponds to ISLR mRNA transcription (FC = 2.68, $p = 0.0001$). ISLR upregulation by BMP9 is inhibited upon knockdown and pharmacological inhibition of ALK1 as measured by proteomics ($p = 0.0072$) and RT-qPCR analysis ($p < 0.0001$). Conditioned media collected from BMP9-stimulated hHiPCs improved tube formation highlighting the potential role of this pathway in endothelial cell morphogenesis. Further, ISLR-treated hHiPC clones were analyzed using LC-MS/MS proteomics and STRING. We found ISLR treatment enriched for regulation of cell adhesion, cell migration, and pro-angiogenic proteins, including CXCL12, CD44, MYH9, EMILIN1, and ANXA5. Together, these data lay the foundation for investigating ISLR in potential regulation of stem cell maintenance and repair in heart disease.

Mabruka Alfaidi, LSHSC. **Interleukin-1 Receptor Activation in Vascular Remodeling and Early Atherosclerosis.** Co-Authors: Siddhartha Gangopadhyay, Evan Kidder, Meleah Pea, Quartina Henderson, Siyuan Cheng, Matthew Woolard, Xiuping Yu, Mabruka Alfaidi. Co-Authors Institutional Affiliations: Feist-Weiller Cancer Center, Center for Cardiovascular Diseases and Science (CCDS), Louisiana State University Health Sciences Center. COBRE

Atherosclerosis is a progressive vascular disease caused by endothelial activation secondary to abnormal/disturbed flow patterns of blood flow at specific regions of the affected blood vessels, and other lifestyle/environmental factors. Combined with chronic inflammation of the vessel wall, these factors contribute to the development of plaques and ultimately to the occurrence of myocardial infarctions, strokes, and peripheral vascular diseases. Despite being one of the leading causes of death worldwide, the molecular mechanisms leading to the maintenance of vessel wall inflammation, plaque growth, instability, and rupture are not clearly understood. Here we show that, interleukin receptor associated kinase 1 (IRAK1) signaling is one of the primary drivers of atherosclerosis-associated vascular inflammation and remodeling. In vitro, disturbed flow assays in human aortic endothelial cells (HAoECs) show upregulation of IRAK1 phosphorylation and activation of endothelial to mesenchymal transition (EndMT), establishing the role of IRAK1 signaling in mechanotransduction. Inhibition of IRAK1 signaling in HAoECs lead to reduce the expression of markers of EndMT. Moreover, in a partial carotid ligation model in hyperlipidemic mice, the direct inhibition of IRAK1 signaling via a small molecule inhibitor results in a regression in neointima formation and macrophage recruitment to the plaque area. These findings suggest a crucial role of IRAK1 signaling in EndMT-induced by disturbed flow and potentially provides a cell type specific therapeutic intervention strategy to control disease progression.

Tasnim Imran, Alpert Medical School of Brown University, Providence VA Medical Center. **Characterizing cardiac microstructure in heart failure with preserved ejection fraction using cardiac magnetic resonance diffusion tensor imaging.** Co-Authors: Daniel Arcuri, Christopher Nguyen, Reza Avazmohammadi, Michael Atalay, Wen-Chih Wu, Gaurav Choudhary. Co-Authors Institutional Affiliations: Providence VA Medical Center, Rhode Island Hospital, Cleveland Clinic Foundation, Texas A&M University. COBRE

Background: Heart failure with preserved ejection fraction (HFpEF) is a heterogenous syndrome with limited treatment options, leading to significant morbidity and mortality. In vivo cardiovascular magnetic resonance (CMR) diffusion tensor imaging (DTI) enables the characterization of myocardial fiber architecture. This study aims to utilize CMR DTI to assess microstructural alterations and their association with cardiac function and outcomes in HFpEF.

Methods: Twenty participants (12 with HFpEF and 8 controls without heart failure) underwent CMR DTI, using a free breathing and contrast-free technique. LV short axis slices were acquired; the helix angle transmurality (HAT), slope of the helix angle versus transmural depth from endocardium to epicardium, was calculated from the LV septum. Participants also underwent a 6-minute walk test and a questionnaire (KCCQ) to assess quality of life. Results: Participants had a mean age of 71 years, mean BMI was 34 kg/ m2, 54% had diabetes mellitus and 81% had hypertension. Those with HFpEF had greater mean LV mass indexed to body surface area (66.7 ± 11.7g/m2 vs 58.2 ± 13.8g/m2), greater mean mid-LV native T1 (1267 ± 135ms vs 1207 ± 55ms), and a significantly lower LV septal HAT as compared to controls (65.3^{o} ± 10.0, and 80.0^{o} ± 19.5, respectively, p=0.04). HAT was moderately correlated with KCCQ scores (R2 0.54, p=0.01) and mildly correlated with 6-minute walk test distance (R2 -0.27, p=0.25).

Conclusion: CMR DTI reveals a lower helix angle transmurality (indicating a flatter angle) in patients with HFpEF as compared to controls without heart failure.

Environment and Health

Alexei G. Basnakian, University of Arkansas for Medical Sciences. **Modification of the TUNEL assay with increased sensitivity to nanoparticles.** Co-Authors: Olena Levurdiak, Shenyang Li, Zach McGowan, Fidaus Razak, Randal S. Shelton, Qinglong Jiang. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences, Central Arkansas Veterans Healthcare System, University of Arkansas in Pine Bluff. COBRE
Nanoparticles are recently recognized toxic components of the environment, while methods for quantitative assessment of their toxicity are very limited. The reasons for this include the necessity of colocalizing the nanoparticles with the damaged cells and the low sensitivity of the toxicity methods. The terminal deoxynucleotidyl transferase (TdT) dUTP nick-end labeling (TUNEL) assay seems to ideally fit these requirements because it measures cell death on an individual cell basis, can be combined with the methods to identify nanoparticles in the cells, and can be applied for both in vitro and in vivo studies. The problem with this assay is its low sensitivity to sublethal cell injuries, such as single-strand DNA breaks and gaps. To overcome this limitation, we tested whether an introduction of an in-situ DNA denaturing step before the assay will increase its sensitivity. Out tests included using mouse kidney tissue, cultured rat kidney tubular epithelial NRK-52E cells, and human lung epithelial A549 cells exposed with fluorescent-labeled 3D hollow SnO2 nanobeads and seven other commercially available nanomaterials. The experiments showed the TUNEL modification, which we named a “denatured TUNEL” or dTUNEL, is 2 times more sensitive to nanoparticle-induced injuries in vitro and up to 20 times more sensitive than classical TUNEL to spontaneous injuries in vivo in mouse kidneys. Using this method in 16-well cell culture glass chambers allowed quantitative TUNEL measurements of all tested nanoparticles in the range of 1.5-15 micrograms per sample. The study was supported by NIH 2P20GM109005-06 and VA Merit Review grant to AGB.

Bikram Subedi, Murray State University. **Wastewater Analysis - Near Real Time Approach of Estimating Substance Use.** Co-Authors: Anita Sapkota, Durga P. Kodati, Landon Jones, Jusdin Kamuf. Co-Authors Institutional Affiliations: Murray State University. INBRE
The Centers for Disease Control and Prevention reported 110,000 overdose deaths in the 12 months ending in May 2023, the highest-ever reported overdose death rate. In addition to opioids, cheaper but highly potent synthetic opioids and their analogs continue to pose a serious public health and safety threat. Overdose deaths involving a broad range of synthetic opioids increased by 125% from 2019 to 2023. Wastewater-based epidemiology can provide a more comprehensive, near-real-time, and cost-effective measure of drug consumption in a community to complement conventional methods. We observed higher levels of controlled neuropsychiatric and illicit drug use during mass gatherings such as solar eclipses and July 4th celebrations, basketball and football games, during COVID-19 lockdowns, and recently at rest areas and truck stops along interstate highways. Xylazine-involved deaths have been increasing at alarming rates since 2019 across the eastern and midwestern U.S.; monthly rates of fentanyl mixed with xylazine increased from 2.9% in January 2019 to 10.9% in June 2022. Protonitazene detection in forensic samples increased by 540% (to 179) from 2021 to 2022, indicating a potential protonitazene crisis in the U.S. Our recent studies detecting xylazine and nitazenes in wastewater can provide comprehensive early warnings of substance use in communities.

Devin M. Drown, University of Alaska Fairbanks. **Impact of Arctic Thaw on Soil Microbial Communities and Emerging Environmental Health Risks.** Co-Authors: Bevyn Cover. Co-Authors Institutional Affiliations: University of Alaska Fairbanks. INBRE
Recent decades have seen an increase in global temperatures, especially in high-latitude regions like the Arctic, where temperatures have risen by at least 1.8° C over the past 30 years. This warming trend has significant implications for Arctic soils, including permafrost, which are rich in microbial life. Typically in a dormant state due to the freezing temperatures, these microbes become more active as the permafrost thaws. This activity could pose risks to human and wildlife health, as well as to the stability of ecosystems. Our

research focuses on how the warming of Arctic soils might alter microbial communities, potentially harming the health of ecosystems and increasing health risks for humans and wildlife. We specifically investigate the composition of microbial communities in the upper layers of Arctic soils, as this is key to assessing risks, including the potential release of ancient pathogens. To achieve this, we analyzed soil from three National Wildlife Refuges in Alaska, covering biomes from the Arctic tundra to the boreal forest. We utilized a combination of amplicon-based and long-read metagenomic sequencing data to characterize the soil microbial communities. Our findings indicate that these communities are influenced by geographical location, with soil nutrient composition playing a significant role. Additionally, we found that variation in soil pH structured microbial communities within refuges. Locations with high microbial diversity were found in acidoneutral soils. We leveraged long-read nanopore metagenomic sequencing to assess the presence of antimicrobial resistance genes in these remote environments. With increased community richness, we found increased antimicrobial resistance gene richness. Notably, there were significant differences in the abundance of these genes between refuges, with the highest levels found in the Arctic. This suggests local mechanisms are driving antimicrobial resistance selection. Given the expected expansion of resource exploration in the Arctic, understanding these risks becomes critical. Our project's findings will not only help in identifying potential environmental health risks for workers and residents in northern Alaska but also enhance our understanding of factors that could alter ecosystem health.

Emily E. Schmitt, University of Wyoming. **The aging mouse as a novel model of nocturia.** Co-Authors: Danielle R. Bruns, Nicole L. Bedford. Co-Authors Institutional Affiliations: University of Wyoming. INBRE
Waking at night to urinate (nocturia) is a highly prevalent and morbid problem in older adults and is associated with cardiovascular disease, increased risk of falls, depression, and poor quality of life. Therapeutic interventions are limited, in large part due to poor mechanistic understanding of pathophysiology and lack of an animal model that recapitulates phenotypic characteristics of the disorder. To date, models of nocturia have not addressed two major contributing factors- advanced age and circadian disruption. We aimed to fill this gap and validate the aged (19-21 month old) mouse as a novel model of nocturia that recapitulates impaired circadian control of urination. As expected, circadian rhythms (amplitude) were blunted with age in both sexes. While young males urinated significantly more during their respective day, this effect was blunted in aged males. Expression of the mechanosensor Piezo1 was differentially expressed by day-night in the bladder of young mice and this day-night expression was completely reversed with aging. Expression of clock genes and regulators of volume status in the kidney were also blunted with age. Together, we suggest that the aged mouse is a robust model of circadian disruption of urination (nocturia). Ongoing experiments will aim to test mechanisms of circadian disruption in the bladder and kidney and identify chronotherapy for this unmet need.

Janeese A Brownlow, PhD, Delaware State University. **An Examination of Neighborhood Disadvantage and Stress on Objective Sleep and Sleep-Related Fears.** Co-Authors: None. INBRE
Differential social and contextual environments may contribute to adult sleep health disparities; however, prior studies on neighborhood disadvantage and sleep are limited to self-report sleep data. This study aimed to 1) examine associations between neighborhood disadvantage and objective sleep parameters and 2) investigate relationships between neighborhood stress and sleep-related fears. Data were obtained from participants (N=46; Mean age=34.59, SD=12.74; 63% Female) who completed self-report and objective measures as part of a larger study. The area deprivation index (ADI), a census-based socioeconomic index was used to assess neighborhood disadvantage. The City Stress Inventory examined overall neighborhood stress, to include the neighborhood disorder and exposure to violence subscales. The Fear of Sleep Inventory assessed for sleep-related fears within the sleep environment. Objective sleep was assessed using wrist-based actigraphy. Residing in neighborhoods with greater disadvantage was associated with reduced sleep efficiency

(r=-.347, p=.022), increased wake after sleep onset (r=.322 p=.035) and number of nocturnal arousals (r=.475 p.05). Neighborhood disorder (r=.404, p=.005) and exposure to violence (r=.401, p=.005) were significantly associated with sleep-related fears. A linear regression model indicated that neighborhood disorder and exposure to violence accounted for 19.8% of the variance in sleep-related fears. These findings suggest that neighborhood disadvantage, perceptions of neighborhood characteristics, and exposure to violence may influence adult sleep health. Further research into the mechanisms relating neighborhood disadvantage to sleep efficiency and fragmented sleep is needed to identify specific pathways to protect and promote sleep health. Funder's Acknowledgment: This study was funded by a Center Grant from the National Institute on General Medical Sciences (Grant #P20GM103653). JAB's time was supported by a Center Grant from the National Institute of Minority Health and Health Disparities (Grant # U54MD015959).

Luz Maria Deardorff, University of Hawai'i Maui College**. Environmental Microbes as Indicators of Human Health Risk After the Lahaina Wildfires.** Co-Authors: Tara Zamani, Michelle Gould, Sally Irwin, Junnie June, Rachel Wilsey, Jennifer Honda. Co-Authors Institutional Affiliations: University of Hawai'i Maui College, University of Texas Health Science Center. INBRE
An unintentional consequence of the 2023 Lahaina wildfire may be a novel source of environmental microbes. Hawaii shows the nation's highest disease rates caused by nontuberculous mycobacteria (NTM) with recovery from soil, dust, water and volcanic ash. We hypothesize that environmental monitoring of NTM and indicator bacteria can inform public health risks in burn areas. For this study, a total of 102 environmental samples (soil n=25, ash n=11, dust n=17, water biofilms n=41) were collected from 11 homes, in addition to stream (n=1) and coastal samples (n=7). NTM will be identified by partial rpoB gene sequencing. Stream and coastal water were tested for *Escherichia coli*, *Enterococcus*, and total coliforms. Turbidity, salinity, and pH were also tested. *E. coli* ranged from 102 Colony Forming Units (CFU)/100ml in freshwater and 10-73 CFU/100ml in saltwater. *Enterococcus* was not tested for freshwater but ranged from 10-63 CFU/100ml in saltwater, and >2,420 and 428 CFU/100ml total coliforms were quantified from freshwater and seawater, respectively. Freshwater and seawater turbidity were 1.2 and 0.63 nephelometric turbidity units (NTUs). The average pH and salinity was 7.5 and 0%, and 8.1 and 35% in freshwater vs. seawater. All freshwater samples exceeded the Environmental Protection Agency recommended limits for *E. coli*. Two saltwater samples also exceeded recommendations for *Enterococcus* for recreational waters. Turbidity of all water samples exceeded the Department of Health standard of 0.2 NTUs. Future nutrient analysis may help determine the risk of harmful algal blooms. These results suggest microbiological environmental monitoring is prudent after natural disaster events.

Manisha Thakur, Southern University and A&M college. **Unraveling the Interplay: Carbon Nanotubes, Inflammation, and Environmental Stressors.** Co-Authors: Sanjay Batra. Co-Authors Institutional Affiliations: Southern University and A&M college.
The utilization of carbon nanotubes (CNTs), including single- and multi-walled variants (SWCNTs/MWCNTs), in various industrial and consumer products has sparked concerns regarding potential health hazards upon inhalation. Their expansive surface area and inherent capability to bind to the pollutants or biomolecules introduce complexity, particularly when chemical 'functionalization' alters their physicochemical characteristics. While CNTs offer promise for environmental cleanup, reports indicate heightened responses to allergens, smoke, or pollutants in their vicinity. We conducted preliminary investigations using alveolar epithelial cells (A549) to assess the impact of pristine and functionalized MWCNTs on inflammation. Our results revealed elevated cytokine/chemokine production; the expression of NF-ºB and the receptor for advanced glycation end products (RAGE); danger-associated molecular pattern-HMGB1; and autophagy markers in exposed A549 cells. Moreover, recognizing the intricate cellular signalling network, we explored the influence on the Hippo signalling pathway during MWCNT exposure, observing altered transcription of pathway components thereby underscoring its involvement in mediating key cellular responses. To

comprehend how CNTs modulate inflammation induced by particulate matter like perfluorooctanoic acid (PFOA) with MWCNTs in the vicinity, we conducted in-silico investigations, revealing that pristine MWCNTs augment the binding affinity between PFOA components and inflammatory proteins. This insight aids in unraveling the complexities of nanotube exposure, shedding light on health risks and interactions with environmental pollutants. Furthermore, the study underscores the necessity for comprehensive assessments of nanomaterial exposure consequences, emphasizing the intricate interplay between CNTs, the Hippo signaling pathway, and existing environmental stressors. With the proliferation of CNT applications, ongoing research in this domain is imperative for informed risk management and the development of safe nanomaterials.

Zachary Redman, University of Alaska Anchorage. **Toxicokinetic Investigation of Weathered Microplastics and Their Metabolomic Impacts in Bay Mussels.** Co-Authors: Jack Hoen, Monica Brandhuber, Brian DiMento, Logan Weiland, Annette Jarosz, Maile Branson. Co-Authors Institutional Affiliations: UAA Chemistry, Alutiiq Pride Marine Institute. INBRE
Microplastics (MPs) are plastic particulates with diameters less than 5mm that are formed from the environmental weathering of larger plastic debris. The threat of microplastics (MPs) to the environment and human health is of growing concern due to the frequency of their detection, evidence of toxicity, and potential to function as vectors for secondary contaminants such as plasticizers, heavy metals, pesticides, and polycyclic aromatic hydrocarbons. In this work, we aimed to determine the influence of environmental weathering on the uptake, distribution, and depuration of MPs in bay mussels (Mytilus trossulus, an ecologically, culturally, and nutritionally important species in the sub-Arctic) as well as identify metabolite biomarkers of MP exposure and toxicity. To accomplish this, mussels were exposed to pristine or photochemically weathered iridium-labeled microplastics in 48 hr. laboratory experiments before being moved to clean tanks for a 48 hr. recovery period. Over the course of the experiment, mussels were collected for metabolomics analysis by liquid chromatography coupled to high resolution Orbitrap mass spectrometry and particle toxicokinetics were assessed via detection of iridium labels by inductively coupled plasma mass spectrometry. Results indicate that mussels rapidly respond to weathered MP accumulation, with primary alterations in metabolites associated with oxidative stress pathways; however, no differences were observed between control and pristine MP exposed groups. Future work will leverage these results to evaluate effects of weathering on the toxicity of other plastic types and assess the impacts of weathered MPs in other critical organisms in the Arctic and sub-Arctic domain.

Genetics and Genomics

Dionysios Patriarcheas, West Virginia University. **Deciphering Glyphosate Resistance Mechanisms: Insights from S. cerevisiae into Mitochondrial Function and Human Glutamate Transport**. Co-Authors: Jennifer E. G. Gallagher. Co-Authors Institutional Affiliations: West Virginia University. CTR
Glyphosate remains the most widely used herbicide in the world and reports of toxicity in humans are increasing. Given that glyphosate inhibits the shikimate pathway, which is not present in metazoans, there is currently no established mechanism of action for glyphosate toxicity in humans. Authorities emphasize the data gap and the need to identify the intracellular targets of glyphosate. Using S. cerevisiae as a model organism, we have previously shown that glyphosate is imported into cells using Dip5, a glutamate/aspartate permease, by mimicking the structure of glutamate. Deletion of DIP5 renders yeast resistant to glyphosate. Here we show that deletion of the mitochondrial glutamate transporters AGC1 and YMC1 confers resistance to glyphosate. Our results also indicate that glyphosate affects basal respiration in wildtype yeast, but not DIP5Î”. To further explore whether human glutamate transporters can transport glyphosate, we expressed 15 human glutamate transporters in the resistant DIP5Î” strain. We observed a slight increase in sensitivity in the case of

one transporter. Surprisingly, when we expressed the same transporters in the mitochondrial transporter mutants, we saw a drastic increase in glyphosate resistance in most strains. The human transporters act as a dominant negative allele, suggesting an interaction between Dip5 and another transporter. In summary, our results indicate that glyphosate affects mitochondrial function and suggest that human glutamate transporters confer resistance to glyphosate, possibly through amino acid transport regulation. We anticipate our work to be a starting point for identifying human glyphosate transport and its effects on non-canonical targets of glyphosate.

Dylan Feist, Kansas State University. **Fine-tuning of Cell-ECM Assembly by Transglutaminase**. Co-Authors: Erika R. Geisbrecht, Nicole Green. Co-Authors Institutional Affiliations: Kansas State University, Cornell College. INBRE

The Drosophila melanogaster myotendinous junction (MTJ) is a unique model to understand how secretion and assembly of the extracellular matrix (ECM) contributes to cell adhesion during development and growth. MTJ formation requires myotube targeting to the appropriate tendon cell followed by the secretion and binding of ECM proteins to transmembrane integrin heterodimers on opposing muscle and tendon cells. This stable network not only links the ECM to the internal actin cytoskeleton, but also transmits tension between muscles and tendons to withstand contractile forces. Thus, knowledge of the molecular composition of the MTJ throughout development is essential to understand how forces vary at the muscle-tendon interface. We performed a targeted RNA interference (RNAi) screen to uncover secreted proteins that are required for cell-matrix adhesion in the contractile muscles of third instar larvae (L3). One candidate that emerged is Transglutaminase (Tg), a protein with known scaffold and crosslinking activity. Therefore, our hypothesis that the crosslinking function of Tg is important for maintaining extracellular adhesion and ECM integrity is exciting and may change current dogma suggesting that integrins are the primary mediator for MTJ stability. RNAi knockdown of Tg in the embryonic tendon cells resulted in smaller muscle attachment sites and occasionally led to fully detached muscles by the L3 stage. Preliminary studies indicate that Tg activity is required as an antibody generated against the epsilon-(gamma-glutamyl)lysine-isopeptide bond can be visualized at muscle attachment sites. Current and future experiments will focus on examining Tg mutants and further characterizing if the crosslinking role of Tg is essential through expression of a catalytically inactive Tg.

Ethan Hackney, Murray State University. **Assembly of membraneless organelles in Drosophila germ cells**. Co-Authors: Samuel J. Tindell, Alexey L. Arkov. Co-Authors Institutional Affiliations: Murray State University. INBRE

Membraneless RNA-protein organelles are assembled in many different cell types and their fundamental importance in cellular organization has been highlighted recently. These organelles function in post-transcriptional gene regulation and, also, they have been implicated in neurodegenerative disorders. In Drosophila and other animals, germline (germ) cells form membraneless organelles called germ granules. These granules are assembled at the posterior of an oocyte during germline development and maintained in the early embryo until the formation of primordial germ cells, which give rise to egg and sperm cells. The scaffold protein Tudor is required for the assembly of these germ granules and germline development. This protein contains 11 protein-protein interaction modules called Tudor domains, which bind to other proteins during germ granule assembly. Among Tudor binding partners are Piwi-protein Aubergine, Pyruvate Kinase and ATP-dependent RNA helicase eIF4A. In this work, we are performing systematic molecular and genetic analysis of Tudor protein complex to characterize the mechanisms of assembly of Tudor and its binding partners into germ granules. Interestingly, we have found that different proteins employ distinct mechanisms to associate with Tudor. In particular, different Tudor partners use different number of Tudor domains for interaction or associate with different regions of Tudor scaffold. In addition, our data indicate a varied degree of functional involvement of Tud domains in germline development, suggesting that some Tud domains may

primarily function in non-germline (somatic) cells. Overall, our work aims to provide mechanistic insights into the formation and function of membraneless organelles under normal and pathological conditions.

Jared C Talbot, University of Maine. **Fast-twitch myofibrils grow in proportion with Mylpf dosage**. Co-Authors: Adekeye TE, Teets EM, Tomak E, Sprague K, Waterman S, Varga S, Austin J, Rodriguez-Medio C, Hupper T, Shepherd SJ, Amacher SL, Kelley JB, Talbot JC. Co-Authors Institutional Affiliations: University of Maine, Ohio State University. COBRE
Muscle hypertrophy increases cell size and internally strengthens muscle cells by expanding contractile chains called myofibrils. Although several factors are known to expand muscle cell size, little is known about how myofibril size is controlled. Here we show that Myosin-Light-Chain-Phosporylatable-Fast (Mylpf), controls myofibril assembly in fast-twitch muscle independent of muscle size. The two zebrafish Mylpf genes (mylpfa and mylpfb) are exclusively expressed in fast-twitch muscle. Mylpf gene function is not only necessary and sufficient for fast-twitch myofibril growth, but myofibril growth is also proportionate to the amount of Mylpf protein in this cell type. For instance, these myofibrils are normal in animals mutant for the low-abundance gene mylpfb, severely disrupted in animals mutant for the high-abundance gene mylpfa, and completely missing in the mylpfa;mylpfb double mutant. Myofibril width is increased by transgenic expression of mylpfa-GFP to a degree that linearly correlates with GFP brightness. This transgene restores myofibril width in the mylpfa mutant and increases width in the wild-type sibling. Transgenic expression of human MYLPF-GFP causes the same myofibril increase, indicating functional conservation. However, disease associated alleles of MYLPF are detrimental to myofibril growth in zebrafish. These findings help explain how fast-twitch muscle cells control myofibril growth.

Infectious Diseases

Ana-Maria Dragoi, LSUHSC Shreveport. **Interaction of human macrophages with Neisseria gonorrhoeae.** Co-Authors: Maria Dolores Juarez Rodriguez, Stanimir Ivanov. Co-Authors Institutional Affiliations: LSUHSC-Shreveport. COBRE
The human-adapted pathogen Neisseria gonorrhoeae (Ng) is the etiological agent of the sexually transmitted infection gonorrhea. The ability of Ng to evade the innate and adaptative host immune responses represents a challenge in therapy and vaccine development. Our laboratory showed that Ng can colonize, invade, and replicate inside human macrophages while avoiding killing. Ng invades macrophages through an FMNL3-dependent actin polymerization mechanism and the formation of an invasion platform that induces dynamic filopodia-like protrusions (FLPs) to engage and internalize the Ng colony. Depletion of plasma membrane cholesterol before infection inhibits Ng macrophage invasion and formation of intracellular colonies. In vitro, we demonstrated that macrophage-tethered gonococci resist canonical phagocytosis, replicate to form a microcolony, and recruit both CEACAM1 and CEACAM4 to the invasion platform that mediates internalization of the colony. However, only CEACAM4 is required for efficient bacterial uptake. Nonetheless, the engagement of both CEACAM1 and CEACAM4 by Ng plays a role in the immune response as revealed by the cytokine response regulation in CEACAM1 or CEACAM4-depleted macrophages. Therefore, CEACAM1 and CEACAM4 â€“ ITIM and ITAM-bearing host receptors with immunomodulatory capacity might be critical for the overall immune response modulation and infection outcome. Our work provides new insights into the subversion of immunomodulatory receptors by Ng for macrophage invasion and immune evasion. Ng manipulation of both CEACAM1 and CEACAM4 receptors on macrophages is the first study to investigate how dual engagement of CEACAMs with seemingly opposing functions modulates Ng uptake and immune response in macrophages.

Avishek Mitra, Oklahoma State University (OSU). **A Novel Class of Channel Forming Membrane Proteins Mediate Heme Iron Acquisition in Mycobacterium tuberculosis.** Co-Authors: Padam Singh. Co-Authors

Institutional Affiliations: Oklahoma State University. COBRE
Mycobacterium tuberculosis (Mtb), a lung pathogen, is completely dependent on iron acquisition to colonize and survive with the human host. Like most pathogens Mtb can acquire iron from host heme, which stores >75% of the host iron. However, the importance of Hm iron acquisition (HIA) to Mtb virulence is unknown because we have a very limited understanding of Mtb HIA mechanisms. We have made three crucial discoveries regarding Mtb HIA: 1) HIA across the unique Mtb outer mycomembrane (MOM) progresses through two parallel and functionally distinct pathways. 2) Mtb uses the outer MOM proteins PPE60 and PPE64 for HIA by the two respective pathways. 3) Most importantly, these HIA PPE proteins function as channel proteins for Hm uptake across the outer MOM bilayer. PPE60/64 belong to the PPE (proline-proline-glutamate motif) protein family, which are found exclusively in mycobacteria, and we provide the first direct evidence that mycobacterial PPE proteins can function as channel proteins for nutrient uptake. Most diderm gram-negative bacteria use Î²-barrel channel proteins in their outer membrane for nutrient uptake, but Î²-barrel homologs of any kind have not been discovered in Mtb. We propose that the drastically different architecture of the outer MOM has led Mtb to evolve to use the mycobacteria genus-exclusive PPE proteins as channel proteins in the MOM. Characterizing how PPE proteins function will provide a way forward in developing highly targeted strategies to block Mtb acquisition of Hm, which is a major source of iron in the host.

For Yue Tso, Louisiana State University Health Sciences Center - New Orleans. **Using CRISPR-Cas9 to Eliminate Kaposi's Sarcoma-Associated Herpesvirus.** Co-Authors: John T West, Charles Wood. Co-Authors Institutional Affiliations: LSU Health Sciences Center. COBRE
Kaposi's sarcoma (KS) is one of the most common cancers in sub-Saharan Africa, and is more prevalent in people living with HIV-1 (PLWH) even under anti-retroviral suppression. The etiologic agent for KS is the Kaposi's sarcoma-associated herpesvirus (KSHV). The ability of KSHV to establish life-long latency has been the major challenge for preventing KS development and its treatment. KSHV episomal persistence is highly dependent on its latency genes, one of them is the latency-associated nuclear antigen (LANA). Therefore, we aim to perturb KSHV latency, and perhaps eliminate KS, by targeting LANA and other latency genes using gene-specific CRISPR-Cas9 constructs. As a proof of concept, we delivered a replication-incompetent adenovirus expressing a LANA-specific CRISPR-Cas9 (Ad-CC9-LANA) into various KSHV latently infected cell lines. Delivery resulted in reduced viral copy number as early as 4 days post-transduction with Ad-CC9-LANA. The reduction of KSHV episomal copy number was further confirmed with decreases in LANA mRNA and protein expression. Our results underscore the potential of gene-specific CRISPR-Cas9 disruption of KSHV latency and point to utility of this approach to probe basic mechanisms in KSHV latency. Additional studies are underway to enhance the efficiency of eliminating additional viral latency associated genes and to determine the effects on the infected cultures after editing of these genes. Our approach may also be applicable to other tumorigenic DNA viruses that showed a tendency to hide in the infected cells.

Katherine J. Siddle, Brown University. **Clinical, epidemiological and demographic indicators of COVID-19 in Rhode Island.** Co-Authors: Sarah Bowman, Paul Cao, Genevieve Caron, Kristen Carpenter-Azevedo, Elizabeth Chen, Karen Crowley, Glen Gallagher, Edward Hawrot, Richard C. Huard, August Guang, Sarah Ledgerwood, Farahnaz Maroof, Ashok Ragavendran, Vivek Ramanan, Sharon Rounds, Eric Salomaki, Sean Sierra-Patev, Paul Stey. Co-Authors Institutional Affiliations: Rhode Island Department of Health, Brown University, Rhode Island State Health Laboratory. CTR
Small states present a unique opportunity to comprehensively interrogate the dynamics of infectious disease outbreaks. In a collaboration between Brown University (Advance RI-CTR, U54GM115677) and the Rhode Island Department of Health we established the computational infrastructure for protected data sharing and used this environment to perform a reanalysis of over 25,000 genomes from samples collected in Rhode Island between March 2020 and January 2024 alongside detailed clinical and demographic information. As

convenience sequencing during an outbreak can lead to underrepresentation of certain groups in the available data, we first performed targeted sequencing of 2,500 contemporaneous samples along with 500 retrospective samples, all from Providence County, to improve representation across the most densely populated county and the county with the largest underserved population in the state. We next investigated clinical associations in our dataset, with a focus on disease severity and evidence of accelerated evolution in immunocompromised individuals. Finally, we looked at the broad scale and fine grained epidemiology of SARS-CoV-2 over time across Rhode Island. We compared rates of lineage introduction and establishment regionally, and determined the relative risks associated with a variety of high-contact settings for disease transmission. Together, our results highlight the importance of integrating the extensive genomic datasets made available through nationwide SARS-CoV-2 genomic surveillance efforts with the rich sample-level information stewarded by public health agencies to advance our understanding of viral dynamics and disease.

Kevin Michael Brown, University of Oklahoma Health Sciences Center. **Elucidation of TgPKG kinase substrates required for Toxoplasma motility.** Co-Authors: Gabriel Cabral, Bingjian Ren, Sebastian Nasamu. Co-Authors Institutional Affiliations: University of Oklahoma Health Sciences Center, University of Geneva. COBRE
Toxoplasma is an apicomplexan parasite that infects and persists in a third of humans worldwide. Infections with this parasite can lead to toxoplasmosis, which can be fatal in those that are immunocompromised. Toxoplasmosis also poses a serious threat to vision and mental health in otherwise healthy individuals. Since current drugs cannot cure the infection, new and improved drugs are needed to eliminate the parasite and block pathogenesis. Pathogenesis stems from the lytic lifecycle of the parasite, which requires active motility to invade and egress from host cells. Prior studies have firmly established that cGMP signaling through protein kinase G (PKG) is required for Toxoplasma motility, but the mechanisms by which this kinase controls motility are unclear because its protein substrates have not been identified. With support from the COBRE Oklahoma Center for Microbial Pathogenesis and Immunity, we have screened for putative substrates of PKG in Toxoplasma using multiple proteomic and phosphoproteomic approaches. Based on these data, we hypothesize that PKG phosphorylates multiple essential proteins for motility in Toxoplasma. Currently, we are investigating the role of PKG substrate phosphorylation on specific processes that govern motility such has Ca2+ mobilization and adhesin secretion. Proteins that control parasite motility make attractive targets for novel therapeutic development, a long term goal of our research program.

Rohit K Jangra, LSU Health, Shreveport. **A novel BSL2 system for comprehensive analysis of entry glycoproteins.** Co-Authors: Lohit Khera, Stephanie R. Monticelli, Ramandeep Kaur, Upendra P Lambe, Thomas G. Batchelor, Ana I. Kuehne, Cierra Word, Nahomi Guerra-Pilaquinga, Russell R. Bakken, Andrew S. Herbert. Co-Authors Institutional Affiliations: LSU Health-Shreveport, United States Army Medical Research Institute of Infectious Disease, The Geneva Foundation. COBRE
Hantaviruses are emerging RNA viruses that cause deadly human disease. No FDA-approved vaccines and therapeutics exist against these viruses, and their development is limited by a BSL3 requirement to research pathogenic hantaviruses and the lack of a reverse genetics system. Hantavirus Gn/Gc are the sole virion surface proteins that are necessary and sufficient to mediate cellular entry, and they are also major targets of protective immune responses. Currently available BSL2 systems for studying hantavirus entry are not compatible with a high-throughput analysis of molecular determinants of entry and the antigenicity of Gn/Gc. Here, we have developed a self-replicating BSL2 virus called Sem-HantaVirus (SHV) that expresses Andes hantavirus (ANDV) Gn/Gc. SHVs are infectious, capable of cell-to-cell spread, and display Gn/Gc that is recognized by neutralizing antibodies and host receptor protocadherin-1 (PCDH1). SHVs can be generated at efficiencies compatible with high-throughput deep mutagenesis scanning (DMS) of Gn/Gc's molecular determinants. Through serial passaging in cell culture, we identified adaptive mutations that afforded robust

SHV replication. These mutations rather paradoxically reduced the amount of Gn/Gc incorporation into SHV particles. Importantly, ANDV Gn adaptive mutations identified in SHVs facilitated the generation of SHVs for another closely related hantavirus, Maporal virus. Finally, Syrian hamsters immunized with these SHVs, twice 21 days apart intramuscularly or intraperitoneally, produced neutralizing antibody responses and were protected against a lethal challenge with Andes hantavirus. Thus, we have established a novel virus system for the comprehensive reverse genetic analysis of entry glycoproteins that can be applied to other BSL3/4 agents.

Tirumalai Rangasamy, Louisiana State University. **Development of Small Molecule-based Intervention to Combat the Infection Caused by the Superbug Carbapenem-resistant Klebsiella pneumoniae.** Co-Authors: Kennedy Trahan, Duane Jeansonne, Allyson Mohanty-Aldana, John Le, Amit Sharma, Basel Abuaita, Samithamby Jeyaseelan. Co-Authors Institutional Affiliations: Louisiana State University. COBRE
Rationale: Bacteria that are resistant to carbapenem (superbugs) such as carbapenem-resistant Klebsiella pneumoniae (CRKP) are among the most dangerous to human health. CRKP is widely resistant, often leading to clinical failure even with rescue antimicrobial agents. In this study, we evaluated the antimicrobial properties of sulforaphane, a small molecule activator of Nrf2 against the superbug, CRKP. Methods: We investigated the effects of sulforaphane on the growth of CRKP in vitro. Then, we assessed the intracellular bacterial killing abilities of human alveolar macrophages (hAM) and human monocyte-derived macrophages (hMDM) in vitro. We characterized the presence of CRKP as well as the activation of Nrf2 in CRKP-infected or sulforaphane-treated hAM and hMDM using transmission electron microscopy (TEM) and immunofluorescence labeling with anti-Nrf2 antibody, respectively. We also developed CRKP-induced pneumonia in mice. Results: Treatment with sulforaphane (both 10 μM and 100 μM) significantly inhibited the growth of CRKP at the 5 hour time point. However, both hAM and hMDM were able to kill only 26-30% of the phagocytized CRKP at 5 hour post-infection. TEM images showed the presence of multiple CRKP in infected hAM. Immunofluorescent labeling showed the activation of Nrf2 in both CRKP-infected and sulforaphane-treated hAM and hMDM. Infection with CRKP significantly induced the infiltration of leukocytes and pathologic lesions in the lungs and increased bacterial burdens in the lungs and extrapulmonary organs of mice. Conclusion: Our results highlight the effectiveness of sulforaphane against a clinically relevant superbug, which has the potential to improve the survival of patients infected with CRKP.

Xufang Deng, Oklahoma State University. **Design of a SARS-CoV-2 papain-like protease inhibitor with antiviral efficacy in a mouse model.** Co-Authors: Bin Tan, Xiaoming Zhang, Ahmadullah Ansari, Prakash Jadhav, Haozhou Tan, Kan Li, Ashima Chopra, Alexandra Ford, Xiang Chi, Francesc Xavier Ruiz , Eddy Arnold, Xufang Deng, Jun Wang. Co-Authors Institutional Affiliations: Rutgers, The State University of New Jersey, Oklahoma State University. COBRE
Oral antivirals are urgently needed to combat new SARS-CoV-2 variants and drug-resistant mutants. The papain-like protease (PLpro) is one of two viral cysteine proteases that is encoded by the SARS-CoV-2 genome and cleaves the viral polyproteins. PLpro is vital for viral replication and is a high-profile but challenging drug target. Despite decades of screening and lead optimization, no drug-like PLpro inhibitor has reportedly shown in vivo antiviral efficacy. In this study, we designed and synthesized noncovalent PLpro inhibitors that bind to the newly discovered Val70Ub site and the known BL2 groove pocket of PLpro. The co-crystal structures of PLpro with eight leads revealed their interaction modes. Potent leads inhibited PLpro with inhibitory constant Ki values from 13.2 to 88.2 nM. One of the leads Jun12682 showed potent antiviral activity against wild-type SARS-CoV-2 and the delta and omicron variants (EC50 = 0.25-1.39 μM) and nirmatrelvir-resistant strains (EC50 = 1.22-1.82 μM) in cell cultures. In vitro and in vivo PK optimization identified Jun12682 with high microsomal stability (T1/2 > 60 min) and oral bioavailability of 72.8%. In a mouse model of SARS-CoV-2 infection, oral treatment with 250 mg/kg Jun12682 twice a day for three days after viral inoculation significantly improved survival and reduced lung viral loads and lesions. These data together demonstrate that Jun12682 is the first-

in-class PLpro inhibitor with in vivo antiviral efficacy. It is anticipated that PLpro inhibitors could be used alone or in combination with existing Mpro and RdRp inhibitors to combat new SARS-CoV-2 variants and drug-resistant mutants.

Metabolism and Obesity

Bhaswati Kashyap, University of Delaware. **Elevated Mitochondrial CD36 and Superoxide Production in Endothelial Cells Exposed to Prolonged High Glucose and Fatty Acids In-vitro.** Co-Authors: Thanh Nguyen, Erica Johnson, Ibra S Fancher. Co-Authors Institutional Affiliations: Not Listed. COBRE
Obesity, a complex metabolic disorder, involves various cardiovascular risks like hyperglycemia. Elevated levels of common free fatty acids (FFA) found in human serum were reported to develop inflammation and cause endothelial dysfunction. CD36 is a fatty acid translocase which was previously shown to be upregulated in response to elevated glucose. Furthermore, recent studies have also identified CD36 expression in mitochondria, potentially impacting cellular respiration. To determine if elevated glucose increases mitochondrial CD36 expression, we exposed human adipose microvascular endothelial cells (HAMECs) to elevated glucose with or without free fatty acids (FFA), mimicking obesity and hyperglycemia. Treatments included 1mg/ml glucose and 1mg/ml mannitol (osmotic control) with or without sodium palmitate and BSA conjugate (0.75mM for 6h) for 72 hours. CD36 expression was measured via Western blot, flow cytometry, and immunocytochemistry (ICC). Mitochondrial ROS production was assessed using Mito sox red reagent. Confocal images showed significantly higher fluorescence intensity of MSR in the glucose and FFA treated group. CD36 expression was quantified by isolating mitochondria from HAMECs using TOM40-based magnetic cell sorting. Analysis revealed increased CD36 expression specifically in the mitochondrial fraction of glucose-treated cells, suggesting alterations in mitochondrial respiration due to sustained high glucose levels. Our findings reveal that mitochondrial CD36 expression is elevated in endothelial cells exposed to sustained increases in glucose in vitro, which correlates with increased superoxide production in mitochondria when exposed to fatty acids. Future works will reveal the molecular mechanism behind the increased mitoCD36 on endothelial cell respiration when challenged with fatty acids.

Cammi Valdez, Northeastern State University. **Characterizing a New Longitudinal Mouse Model of Diabetic Retinopathy.** Co-Authors: Cammi Valdez, Erica Dotson, Joshua Butcher, Phillip Coburn. Co-Authors Institutional Affiliations: Northeastern State University, Harold Hamm Diabetes Center, The University of Oklahoma Health Sciences Center, Oklahoma State University, The University of Oklahoma Health Sciences Center. INBRE
As a common complication of diabetes, more than one-third of patients will develop some form of diabetic retinopathy. Microvascular degeneration from hyperglycemic conditions causes diabetic retinopathy. While increased fructose consumption has been documented to cause higher risk of diabetic retinopathy, the mechanism is still poorly understood. Therefore, we propose to investigate the role and mechanistic pathways that drive retinal dysfunction in a diet-induced fructosemia mouse model. Mice were fed control and high fructose diet ad libitum. Weights, non-fasting and fasting blood glucose, and A1C levels were measured every 3 months post-diet induction to assess metabolic health. Funduscopy, fluorescence angiography, and optical coherence tomography were performed to assess in vivo eye health. At 6-months, 12-months, and 18-months post-diet induction, an insulin tolerance test was performed. At 6-months and 18-months post-diet induction, fluorescein dextran heart perfusions were also performed. Fructosemia mice gain significantly more weight that control mice at each time point post-diet induction. Insulin tolerance tests post-diet induction revealed insulin insensitivity in fructosemia mice. At 6-months and 18-months post-diet induction, fructosemia model have increased retinal vascular permeability. At 9-months, 12-months, 15-months, and 18-months post-diet induction, fructosemia mice have increased fasting blood glucose and A1C levels compared to control. Our

data suggests that fructosemia mice are developing metabolic syndrome and the retinal microvasculature is weakening beginning at 6-months post-diet induction and continuing in this longitudinal study. Therefore, this new mouse model of fructosemia may prove promising for studying diabetic retinopathy in a more physiologically relevant system than those currently available.

Caroline de Carvalho Picoli, MaineHealth Institute for Research. **The Gut-Bone Connection: Gastric X/A-like Cells and Skeletal Homeostasis.** Co-Authors: Caroline de Carvalho Picoli, Jeyrie Ramos Aponte, Tiange Feng, Clifford J Rosen, Ziru Li. Co-Authors Institutional Affiliations: MaineHealth Research Institute, MMC Medical School. COBRE

Background- Bariatric surgery is an effective treatment for severe obesity and type 2 diabetes, however, it can lead to side effects such as bone loss and increased fracture risk. While changes in gut hormones and microbiota have been proposed as potential mechanisms, the role of the stomach, the surgical site itself, has been overlooked. Vertical sleeve gastrectomy (VSG), the most commonly performed bariatric procedure, removes most part of the stomach and reduces circulating levels of ghrelin, exclusively produced by gastric X/A-like cells. Our study aims to investigate the roles of gastric X/A-like cells in the context of VSG-induced bone loss. Methods- We employed a VSG mouse model with active ghrelin supplementation and a diphtheria toxin-induced X/A-like cell depletion model. Changes in fat mass, energy expenditure, glucose metabolism, and skeletal parameters were evaluated after four weeks. Results- VSG led to weight loss, decreased ghrelin levels, and induced bone loss in mice, with ~20% reduction in bone parameters. Ghrelin supplementation didn't prevent mice from bone loss. X/A-like cell depletion reduced ghrelin levels (~79% in males, ~59% in females), improved glucose tolerance, and impaired trabecular bone in males, but not females, possibly due to protective effects from estrogen. Take together, X/A-like cell depletion largely recapitulated the glucose and bone phenotypes observed in VSG mice. Conclusions- Ghrelin supplementation alone doesn't rescue VSG-induced bone loss. Depleting X/A-like cells mimics VSG effects on bone and metabolism, suggesting that these cells play a significant role, beyond ghrelin, through other unidentified secretory factors.

Christopher Johansen PhD, MPH, University of Nevada, Las Vegas. **Parental acculturation and its association with preschool-aged child's health behaviors among Latinos in Southern Nevada.** Co-Authors: Miguel Fudolig, Liliana Davalos, Brisa Rodriguez, Marissa Martinez. Co-Authors Institutional Affiliations: University of Nevada Las Vegas. INBRE

Latino children also have a high prevalence of overweight/obesity compared to White children. Previous studies suggest that child's acculturation to the US is associated with health behaviors (nutrition, BMI ,physical activity). The role of parental acculturation remains understudied, with limited studies using validated measures. The objective of this study was to examine parental acculturation and its association with interpersonal factors, and their preschool-aged child's health behaviors. Data were collected and analyzed from 211 Latino parents in Nevada who participated in a self-reported cross-sectional survey in Nevada. Acculturation was measured using Norris' 4-item validated acculturation measure. The mean age of parents was 33.1 (SD=6.7, range=20-51). The average age of their preschool-aged child was 2.9 (SD=0.5, range=2-5). The mean acculturation score was 7.9 (SD=4.4, range=4-20). Approximately 70% of parents were married/living with a partner. Nearly 60% reported the total household income â‰¤ $30,000. About 80% of parents were foreign born and had more than one child. Children were active an average of 4.25 (SD=2.2 range=0-7) days per week. Results suggest that after controlling for covariates, parental acculturation was positively associated with physical activity (r=0.24), increased hydration (r=0.4), consumption of sweetened fruit drinks (r=0.19) and breakfast sweets (r=0.19). Parental acculturation was not associated with child BMI. These findings inform future research on culturally tailored intervention strategies to boost physical activity and decrease sugar-sweetened beverage consumption among Latino preschool-aged children.

Heather Drummond, University of Mississippi Medical Center. **Acid sensing ion channel 2 (ASIC2) deficiency increases light cycle ambulatory activity in mice.** Co-Authors: Kylie M. Larson, Emily Hildebrandt, Jussara do Carmo. Co-Authors Institutional Affiliations: University of Mississippi Medical Center. COBRE
Acid Sensing Ion Channel 2 (ASIC2) is expressed in multiple brain regions that control food intake, body weight, and motor activity. However, the role of ASIC2 in these functions is still undetermined. Thus, we investigated the impact of ASIC2 deficiency on energy balance and motor activity by examining the metabolic and behavioral phenotypes. Male and female wildtype and ASIC2-/- mice (n=5-7) at 16-18 weeks of age on normal chow were placed in metabolic cages (Sable System International). We continuously measured food consumption, motor activity, sleep patterns, oxygen (O2) consumption, carbon dioxide (CO2) production, and energy expenditure for 3 consecutive days following acclimatization. All data were analyzed using a two-way analysis of variance. ASIC2-/- mice weighed slightly less, but had similar lean and fat percentages compared to wildtype animals. We found the sum of all activity was 2-fold higher in male and female ASIC2-/- mice during light, but not dark, cycle. Locomotor budget indicated that ASIC2-/- mice spend more time eating food, touching food, moving around the cage, grooming/scratching and directed ambulatory locomotion. ASIC2-/- mice also ate more food during the light cycle. Accompanying these findings, energy expenditure, O2/ CO2consumption/output were higher in ASIC2-/- mice during the light cycle. These findings suggest that ASIC2-/- mice displayed more activity during the light cycle which likely accounts for the increased metabolic activity. Our results provide evidence for a novel and important role of ASIC2 in controlling energy balance and ambulatory activity. This work was supported by NIH R0HL1630376, P20GM104357, P30GM149404, P20GM121334, and P20GM103476.

Ibra S Fancher, University of Delaware. **Visceral adipose tissue inhibits endothelial Kir2.1 in obesity via a CD36-dependent mechanism.** Co-Authors: Sabita Rokka, Masoumeh Sadeghinejad, Emma C Hudgins, Erica J Johnson, Thanh T Nguyen. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Obesity imposes deficits to adipose tissue and vascular endothelium, yet the role that distinct adipose depots play in mediating endothelial dysfunction in local arteries remains unresolved. We recently showed that obesity impairs endothelial Kir2.1 channels, mediators of NO production, in arteries of visceral adipose tissue (VAT) while Kir2.1 function in subcutaneous adipose tissue (SAT) endothelium remains intact. Therefore, we determined if VAT vs. SAT from lean or diet-induced obese mice affected Kir2.1 channel function in vitro. We found that VAT from obese mice reduces Kir2.1 function without altering channel expression whereas AT from lean mice and SAT from obese mice had no effect on Kir2.1 function as compared to untreated control cells. As Kir2.1 is well-known to be inhibited by fatty acid derivatives and obesity is strongly associated with elevated circulating fatty acids, we next tested the role of the fatty acid translocase CD36 in mediating VAT-induced Kir2.1 dysfunction. We found that downregulation of CD36 restored Kir2.1 currents in endothelial cells exposed to VAT from obese mice. In addition, endothelial cells exposed to VAT from obese mice exhibited a significant increase in CD36-mediated fatty acid uptake. The importance of CD36 in obesity-induced endothelial dysfunction of VAT arteries was further supported in ex vivo pressure myography studies where CD36 ablation rescued the endothelium-dependent response to flow via restoring Kir2.1 and eNOS function. These findings provide new insight into the role of VAT in mediating obesity-induced endothelial dysfunction and suggest a novel role for CD36 as a mediator of endothelial Kir2.1 impairment.

Matthew D Lynes, MaineHealth Institute for Research. **Peroxiredoxin 2 protects Trpv1+ derived fat cells from excessive reactive oxygen species induced cell death.** Co-Authors: Breanna Morrill, Carolina Cora, Wadak Harbi, Caitlin Ellis, Benjamin Tero, Kimberly Malka, Lucy Liaw. Co-Authors Institutional Affiliations: MaineHealth Institute for Research, University of Southern Maine. COBRE
Obesity is a hallmark of a spectrum of disorders collectively referred to as metabolic syndrome and is increasing dramatically, with 573 million obese individuals projected worldwide by 2030. Obesity is driven by

increased adiposity, which occurs when energy intake exceeds energy expenditure, leading to increases and dysfunction in adipose tissue. The major cell type in adipose tissue is the adipocyte, and we recently discovered a previously unknown type of adipocyte derived from vascular smooth muscle (VSM) cells that express the gene Transient receptor potential cation channel subfamily V member 1 (Trpv1). We tested the hypothesis that a protein network underlying cellular function is uniquely expressed in Trpv1+ VSM derived adipocytes. Proteins identified as differentially expressed were validated by qPCR, leading to the identification of the peroxiredoxin family member Prdx2 as enriched in Trpv1+ VSM derived adipocytes. Peroxiredoxin inhibition resulted in excessive reactive oxygen species (ROS) accumulation and cell death. To test the role of Prdx2 in fat cells in vivo, we took a CRISPR approach to specifically edit the Prdx2 gene in Trpv1+ VSM derived adipocytes, resulting in increased blood glucose and expression of pro-inflammatory genes in adipose tissue. Our work suggests Trpv1+ VSM derived adipocytes limit adipose tissue ROS accumulation and inflammation, and future studies will my required to determine if increasing Trpv1+ VSM derived adipocyte activity or number can improve systemic metabolism.

Umesh D. Wankhade, Arkansas Children Nutrition Center, UAMS. **From Conception to Adipose Tissue: Investigating the Role of Housing Temperature on Offspring Response to Dietary Challenge.** Co-Authors: Henry A. Paz, Ying Zhong, James D. Sikes, Reid D. Landes, Roy Morello, Samrat Roy Choudhury. Co-Authors Institutional Affiliations: Arkansas Children’s Nutrition Center, University of Arkansas for Medical Sciences, Arkansas Children's Research Institute. COBRE
Introduction: Temperature can play an important role in the modulation of certain metabolic and physiological processes. Studies in rodents indicate that housing temperature, both preceding conception and during gestation, can have a profound impact on in-utero development and subsequent metabolic programming in next generation of offspring. Here, we investigate how diet-induced metabolic stress is programmed in offspring in response to parental housing temperature. Methods: Male and female mice were housed at either 8°C (cold exposed, CE) or 30°C (Thermoneutral, TN) 1wk prior to conception and 3wk gestation. Sperm samples from male mice were collected, and DNA was isolated to determine epigenetic landscape using Reduced Representation Bisulfite Sequencing (RRBS) assay. Male and female offspring born to CE and TN parents were exposed to control (CEC, TNC) and high-fat diet (CEHF, TNHF) respectively for 12wk, and various metabolic parameters, including body weight and body composition, were measured. Following euthanasia, adipose tissue depots were collected and analyzed. Results: An enduring impact of parental housing temperature was seen in offspring characteristics. Notably, male offspring born to TN parents and fed a high-fat diet (TNHF) exhibited greater body weight gains compared to CEHF counterparts, while in females, higher weight gain was observed in CEHF compared to TNHF. At weaning, there was no difference in body composition amongst the 4 groups (irrespective of sex). However, at 15 weeks of age, TNHF males experienced larger diet-induced fat gain than male CEHF; whereas for females, the diet-induced fat gain did not statistically differ between offspring born to CE- and TN-parents. Histological analyses of adipose tissues depots revealed larger adipocytes in HFD-fed offspring born to TN parents. Additionally, diet-induced differences in Ucp1 expression in brown adipose tissue depended on both parental temperature and offspring sex. And for females, diet-induced expression of both Dio2 in BAT and Ccl4 in iWAT depended on parental temperature exposure, emphasizing the interesting interplay between temperature and diet in shaping adipose tissue. Epigenetic analysis via RRBS highlighted persistent changes in sperm DNA methylation patterns induced by housing temperature, with differentially methylated regions associated with crucial metabolic pathways. Conclusion: Parental housing temperature in rodents exerts a lasting impact on offspring characteristics, notably influencing body weight, fat percentage, and adipose tissue morphology. The intricate interplay of genetic and environmental factors, as highlighted by epigenetic changes, underscores the complexity of metabolic programming. In future, investigating the long-term metabolic consequences of parental housing temperature on offspring health and exploring the molecular mechanisms underlying these

effects could provide valuable insights into strategies for mitigating metabolic disorders in future generations.

Neuroscience

Barbara Gisabella, University of Mississippi Medical Center. **Diurnal Expression Rhythms in the Amygdala of Subjects with Bipolar Disorder, Major Depression and Schizophrenia.** Co-Authors: Barbara Gisabella, Harry Pantazopoulos, Robert McCullumsmith, Michael R. Garrett, Rammohan Shukla. Co-Authors Institutional Affiliations: University of Mississippi Medical Center, University of Toledo, University of Wyoming. COBRE
Recent studies implicate altered diurnal molecular rhythms in cortical regions in subjects with schizophrenia (SZ) and mood disorders. Furthermore, our previous work identified altered diurnal rhythms of somatostatin immunoreactive neurons in the amygdala of subjects with Bipolar Disorder (BD), with decreased somatostatin coinciding with the reported morning peak in severity of depression and anxiety. Diurnal molecular rhythms may be differentially altered between these disorders and potentially associated with changes in metabolic pathways. We used RNAseq profiling in a cohort of subjects with SZ, subjects with BD, subjects with Major Depressive Disorder (MDD), and control subjects (n=15/group) to analyze molecular diurnal expression rhythms across these disorders. The time of death of each subject adjusted for local sunrise time at the date and location of death was used together with nonlinear regression models to analyze diurnal expression rhythms. We observed 2082 rhythmic genes in control subjects, 3059 in subjects with BD, 1586 in subjects with MDD, and 1236 in subjects with SZ. Furthermore, we observed altered diurnal expression rhythms between subjects with BD SZ, and MDD, with a general gain of rhythmicity and altered phase of rhythms in subjects with BD compared to control subjects, and loss of rhythmicity in MDD and SZ. Pathways with altered rhythmicity included several metabolic signaling pathways in each of the disorders. In addition, cellular deconvolution implicated astrocytes, oligodendrocytes, as well as excitatory and inhibitory neurons in these diurnal rhythm alterations. Taken together, our findings suggest differential alterations in diurnal amygdala gene expression rhythms in these disorders with a gain of rhythmicity and altered phase in BD and loss of rhythmicity in MDD and SZ. Altered diurnal expression rhythms may contribute to differentially altered metabolic pathways in BD, MDD, and SZ.

Maj-Linda B Selenica, University of Kentucky. **Deciphering eIF5A hypusination: Novel Mechanisms that drive TDP-43 neuropathogenesis in Alzheimer Disease and Related Dementia.** Co-Authors: Maj-Linda B. Selenica, Rohan Desai, Christopher Saunders, Patricia Rocha-Rangel, Ramon Sun, Gopal Viswanathan, Patrick Sullivan, Daniel C. Lee, Maj-Linda B. Selenica. Co-Authors Institutional Affiliations: University of Kentucky, University of Florida**.** COBRE
TAR DNA-binding protein 43 (TDP-43) pathology is associated with clinical dementia in Alzheimer's disease (AD) patients and limbic-predominant TDP-43 encephalopathy (LATE). Regional decline in glucose metabolic rate is one of the earliest and most consistent features of AD, however the impact of TDP-43 pathology on neurometabolic dysregulation remains poorly understood. We recently reported on the mechanisms by which eukaryotic translation initiation factor 5A (eIF5A) contributes to TDP-43 pathology following cellular stress. eIF5A is the only mammalian protein undergoing conversion of a single lysine to hypusine via deoxyhypusine synthase (DHS) and deoxyhypusine hydroxylase (DOHH) activity. Our analysis revealed induced DHS expression and hypusine levels in the post-mortem AD and AD+LATE brain tissue, further corroborated by us in TDP-43 mouse models. Comprehensive cortical tissue metabolome coverage in a heterozygous TDP-43 mouse model (TARhet) showed increased brain glycolytic rate and TCA cycle metabolite levels, supporting a heightened bioenergetic state. Surprisingly, aberrantly induced neuronal hypusine levels (eIF5AHyp) increased glucose uptake but led to significant reduction in pyruvate/lactate levels. Considering that pyruvate is the primary safeguard against oxidative stress, we propose that induced eIF5AHyp is a metabolic switch in uncoupling the pyruvate entry to TCA cycle and downstream ATP production, suggesting the metabolic profile

observed in vivo. Notably, RNAseq and the NanoStringTM analyses identified disease-associated genes involved in UPR, mitochondrial OXPHOS pathway, and oxidative stress uniquely pertinent to DHS/DOHH expressing mice. Our findings provide pioneering evidence for eIF5AHyp regulation of brain glucose homeostasis and mitochondrial impairment under energy-demanding TDP-43 proteinopathy state in AD and related dementias.

Michael Robichaux, West Virginia University. **Misfolded rhodopsin disrupts the ER secretory pathway to the presynaptic terminals of rod photoreceptors in a retinitis pigmentosa mouse model with retinal neurodegeneration.** Co-Authors: Samantha Thompson, Sophie Crowder, Emily Sechrest, Wen-Tao Deng. Co-Authors Institutional Affiliations: West Virginia University. COBRE
In rod photoreceptors of the retina, an enormous amount of rhodopsin (Rho) protein is synthesized and turned over to maintain healthy visual transduction. To meet this biosynthesis requirement, rods have a complex ER network and secretory trafficking system; however, in cases of retinitis pigmentosa (RP) and other blinding retinal dystrophies, Rho is frequently mistrafficked in the ER across the different rod cellular compartments, including the presynaptic terminal. Rod presynaptic terminals are maintained by transsynaptic proteins like ELFN1 and the dystrophin-dystroglycan complex; however, neither the normal secretory system to rod synaptic terminals nor impact of Rho mislocalization on the terminals is well understood. In this study, we analyzed P23H-hRho-tagRFP-T/+ mice, which have the RP mutant P23H rhodopsin protein fused to an RFP that gets misfolded and mislocalized in the ER throughout all rod compartments, including the rod presynaptic terminals. Using super-resolution microscopy, we found misfolded P23H-Rho localized within presynaptic cytoplasm in close proximity to the synaptic ribbon release site. We found a similar ER accumulation of P23H-Rho in AAV-transfected WT rods. Using conventional EM, we discovered large ER folds corresponding to the mutant protein accumulation; although, the structure of the ribbon appeared unaffected. Using quantitative confocal and western blotting, however, we found significant changes in protein levels of rod synaptic proteins including ELFN1 and dystrophin. Our findings indicate that rods use an ER-based secretory system to supply synaptic terminals. This presynaptic ER is sensitive to overloading by misfolded Rho, which contributes to the disease pathology of RP and other photoreceptor dystrophies.

Xhoela Bame, Dartmouth College. **Mitochondrial network reorganization and transient expansion during oligodendrocyte generation.** Co-Authors: Robert A. Hill. Co-Authors Institutional Affiliations: Dartmouth College. COBRE
Oligodendrocyte precursor cells (OPCs) give rise to myelinating oligodendrocytes of the central nervous system. This process persists throughout life and allows for oligodendrocyte replacement in neurodegenerative diseases and aging. The precise mechanisms that guide OPCs to differentiate into mature oligodendrocytes are poorly understood. Intracellular metabolism and associated mitochondrial dynamics are likely to play key roles in regulating this process. To better understand the physiological and subcellular events that occur within the OPCs as they differentiate into myelinating oligodendrocytes, we determined the mitochondrial distribution and morphometrics across the oligodendrocyte lineage in mouse and human cerebral cortex. During oligodendrocyte generation, mitochondrial content expanded concurrently with a change in subcellular partitioning towards the distal processes. These changes were followed by an abrupt loss of mitochondria in the oligodendrocyte processes and myelin, coinciding with sheath compaction. This reorganization and extensive expansion and depletion took 3 days. Oligodendrocyte mitochondria were stationary over days while OPC mitochondrial motility was modulated by animal arousal state within minutes. Aged OPCs also displayed decreased mitochondrial size, content, and motility. Thus, mitochondrial dynamics are linked to oligodendrocyte generation, dynamically modified by their local microenvironment, and altered in the aging brain.

Rural Health and Health Disparities

Debora Kamin Mukaz, University of Vermont Larner College of Medicine. **Residential Segregation and Thrombo-inflammatory Biomarkers Related to Hypertension in Black and White Americans.** Co-Authors: Andrew D. Sparks, Ryan Packer, Suzanne E. Judd, Virginia J. Howard, April P. Carson, Timothy B. Plante, D Leann Long, Katharine Cheung, Mary Cushman. Co-Authors Institutional Affiliations: University of Vermont Larner College of Medicine, University of Alabama at Birmingham, University of Mississippi Medical Center, Wake Forest University. COBRE

Background: Thrombo-inflammation is involved in hypertension pathogenesis. Black people have higher thrombo-inflammatory biomarkers and hypertension burden than White people. It is unclear whether residential segregation, a driver of health inequities, is associated with thrombo-inflammation and whether it has a differential impact on thrombo-inflammation in Black and White Americans. Methods: This cross-sectional study included 4,362 participants of the biracial REasons for Geographic And Racial Differences in Stroke (REGARDS) cohort. County-level segregation was measured with the (1) dissimilarity index (DI, the difference in racial distribution of census tracts relative to their county), (2) isolation index (ISI, the degree to which Black people are exposed only to one another in a county), and (3) interaction index (ITI, the degree to which Black people are exposed to White people in a county). Linear regression was used to assess correlations of residential segregation indices with 7 thrombo-inflammatory biomarkers associated with hypertension risk: Factor IX, D-dimer, C-reactive protein (CRP), interferon-Î³, tumor necrosis factor-Î±, interleukin-6, and E-selectin. Results: Worse ISI, ITI, and DI were associated with adverse levels of most biomarkers. For example, CRP was 12% (95% CI: 9-16%) higher per SD higher ISI, 5%(95% CI: 1- 8%) higher per SD higher DI, and 9% (95% CI: 6-12%) higher per SD lower ITI. None of the associations differed significantly by race. Conclusions: Multiple thrombo-inflammatory biomarkers important in hypertension were more adverse with greater residential segregation by three metrics, regardless of race. This indicates that residential segregation, a manifestation of structural racism, may become embodied in thrombo-inflammatory processes.

Katie Cueva, University of Alaska Fairbanks. **The Alaska Native Collaborative Hub for Research on Resilience: Alaska Native youth voices on how their communities support young people.** Co-Authors: Jessica Saniguq Ullrich, Ay'aqulluk Jim Chaliak, Roberta Moto, Evon Peter, Charlene Aqpik Apok, Diane McEachern, Lisa Wexler, James Allen, Jessica Black, Stacy Rasmus. Co-Authors Institutional Affiliations: Not Listed. INBRE

Indigenous communities have supported young people to thrive since time immemorial. In Alaska, colonial trauma and ongoing structural racism have contributed to acute health inequities in Alaska Native communities. The Alaska Native Collaborative Hub for Research on Resilience (ANCHRR) is an initiative led by community-based partners and researchers. Through structured interviews in 65 communities, the ANCHRR project identified community-level strengths that protect against suicide, including strong Tribal governance, youth activities, community-led teaching about community history and culture, and opportunities for young people to engage with their culture and spirituality. The authors encouraged young people in three communities identified as highly protective to create digital stories on ways their communities support young people. The project resulted in 26 youth-produced digital stories and 18 photovoice projects, which were all shared in their communities. The involved young people were each invited to be part of a research interview and 22 interviews were conducted. A codebook was developed by two research team members who then independently applied the codebook to the interview notes, then worked together to analyze the data for common themes. In the interviews, youth discussed how their well-being was promoted through social connection, and through a connection to their culture. We will share information about both the digital storytelling, and larger ANCHRR, process and findings. This approach to suicide prevention focused on community strengths, youth voices, and the power of story. Communities can learn from their young people about how to prevent youth suicide.

Nathan L. Vanderford, University of Kentucky. **Taking ACTION to Reduce Cancer Disparities in Appalachian Kentucky.** Co-Authors: None. COBRE
Kentucky has the highest cancer incidence and mortality rates in the US with the highest burden of the disease being localized to the rural, Appalachian region of the state. Residents of Appalachian Kentucky also experience high rates of poverty, low education attainment, limited healthcare access as well as other disparities. Through funding from the National Cancer Institute's Youth Enjoy Science R25 program, the Appalachian Career Training In ONcology (ACTION) Program at the University of Kentucky Markey Cancer Center provides enhanced cancer-focused training for high school and undergraduate students from rural Appalachian Kentucky and works to develop a better understanding of cancer in the community through community outreach and engagement activities. Collaboration with the COBRE-fund Center for Cancer Metabolism at the university has resulted in several students being trained in the area of cancer metabolism. The overarching goal of ACTION is to enhance the diversity of the biomedical workforce by preparing Appalachian Kentucky students for biomedical careers, increase the community's understanding of cancer, and thereby address the cancer and education disparities in Appalachian Kentucky and beyond. This presentation will highlight data describing the cancer disparities in Appalachian Kentucky and describe outcomes of the ACTION program. Program highlights will include summarizing student academic progression and a discussion of special projects that have included the publication of three books containing essays and stories written by ACTION students and a student-driven photovoice project highlighting the causes and consequences of cancer in Appalachian Kentucky.

Zugui Zhang, Christiana Care Health System. **The Effectiveness of the Community Health Workers Program in Primary Care in Delaware: Impact on Health Utilities and Outcomes.** Co-Authors: Alexandra Maree Mapp, James T Laughery. Co-Authors Institutional Affiliations: Christiana Care Health System. CTR
The Community Health Workers (CHW) program, a pivotal component of Delaware's State Healthcare Innovation Plan, aims to bridge communities with healthcare systems and health departments. This study investigates the impact of the CHW program in primary care on health utilities and outcomes based on clinical conditions and social determinants of health. CHWs, program coordinators, and managers, trained in IMPaCT (Individualized Management for Patient-Centered Targets), provided six months of support to enrolled patients using IMPaCT workflow, emphasizing collaborative goal-setting, tailored support, and connection to long-term resources across four areas in Delaware. Data collected from December 2019 to March 2021 for the intervention group and corresponding control group data from primary care sites were analyzed using Generalized Estimating Equations and Difference-in-Difference methods, adjusted for baseline characteristics and social support using propensity scores to address selection bias. Among 471 patients enrolled in the CHW program and 17,172 control group patients, significant improvements were observed in reduced hospital utilities, including number of ambulatory visits (0.51, 95% CI: 0.15 to 0.88, p-value

Women's Health

Elizabeth B. Quigley, University of Wyoming. **Sexually Dimorphic JNK Signaling in the Gonadotrope is Important for Female Fertility Regulation.** Co-Authors: Alexandra Verosky, Brian S. Edwards, Shaihla A. Khan, Ulrich Boehm, Roger J. Davis,Amy M. Navratil. Co-Authors Institutional Affiliations: University of Wyoming, Laramie, University of Colorado, Mayo Clinic, Genus PLC, Saarland University School of Medicine, University of Massachusetts Medical School, Howard Hughes Medical Institute. INBRE
Gonadotrope cells in the anterior pituitary are central regulators of reproductive function. Their activation requires the complex integration of multiple hormones and signaling pathways to initiate distinct gene programs that culminate in the synthesis and secretion of the gonadotropins, luteinizing hormone (LH) and

follicle stimulating hormone (FSH). It is demonstrably clear that males and females require differential patterns of gonadotropin synthesis and secretion to maintain fertility; yet mechanistically, how male vs. female gonadotropes differentially regulate gonadotropin production at the molecular level is unclear. Previous studies in gonadotrope-derived cell lines suggest that c-Jun NH2-terminal kinase (JNK) activation increases the expression of the gonadotropin releasing hormone receptor (Gnrhr), Lhb, and Fshb genes. While informative, this in vitro work does not accurately recapitulate the complex and differential hormonal regulation between the male and female hypothalamic-pituitary-gonadal axis. To specifically address this, we utilized Cre/loxP technology to selectively inactivate JNK 1 and JNK 2 (JNK 1/2) in gonadotrope cells of the anterior pituitary (DKO). Interestingly, our data demonstrates that compared to males who harbor the same deletion, JNK DKO females have elevated serum gonadotropins in diestrus. Consistent with elevated serum gonadotropins, JNK DKO females also have altered estrous cyclicity, enhanced folliculogenesis, and increased ovarian weights. Paradoxically, JNK DKO females skip proestrus and have increased time to first parturition. This intriguing data suggests that JNK regulation likely varies across the estrous cycle. Taken together, our results diverge from previous in vitro findings, and define a sexually dimorphic role for JNK signaling in gonadotropin production.

Erica Sood, Nemours Children's Health. **HEARTPrep: A digital health psychosocial intervention for mothers expecting a baby with congenital heart disease.** Co-Authors: Kimberly Canter, Anne E. Kazak, Angel Munoz-Osorio, Alejandra Perez Ramirez. Co-Authors Institutional Affiliations: Nemours Children's Health. COBRE
Prenatal diagnosis of congenital heart disease (CHD) often leads to anxiety, depression, and traumatic stress in expectant mothers, with long-term implications for the child and family. However, psychosocial intervention is rarely incorporated into prenatal care. This study used a five-phase, user-centered approach to develop HEARTPrep, a digital health psychosocial intervention delivered via mobile app and telehealth to mothers expecting a baby with CHD to promote maternal, family, and child wellbeing. HEARTPrep has three sequential modules (Adjusting, Connecting, Preparing) delivered during pregnancy after prenatal diagnosis of CHD. Phases of intervention development were: (I) Establishing partnerships; (II) Creating content; (III) Developing prototype and testable intervention; (IV) Conducting think aloud testing; and (V) Completing beta testing. Partnerships with parents, clinicians, and design/technology experts were integral throughout the development of HEARTPrep. Feasibility was assessed through enrollment and completion rates. Acceptability was assessed through 20 Likert-scale and five open-ended questions. Ninety percent of recruited mothers enrolled and 80% and 70% completed all three HEARTPrep telehealth sessions and modules, respectively. On a scale from 0 (Not at All) to 4 (Very), mean item acceptability scores ranged from 3.6 - 3.9. Opportunities to process emotions, develop coping skills, learn with their partner, navigate relationships, understand they are not alone, connect with peer support, access resources, and prepare for stressors were described as helpful. These five phases produced a digital health psychosocial intervention with promising feasibility, usability, and acceptability results.

Leela V. Thomas, Delaware State University. **Influence of social determinants on maternal and infant complications of gestational diabetes mellitus.** Co-Authors: Zugui Zhang, Claudine T. Jurkovitz, Mitchell R. Fawcett, M. James Lenhard. Co-Authors Institutional Affiliations: ChristianaCare Health Services Inc., Sidney Kimmel Medical College. CTR
Gestational diabetes mellitus (GDM) has become increasingly prevalent in the past decade, with rates more than doubling. This rise is associated with maternal age, BMI, and race, particularly affecting Asian American individuals. Despite successful maternal glycemic control interventions demonstrated in randomized clinical trials, the incidence of GDM deliveries with complications increased between 2014-2020, notably among Black individuals. We argue that the emphasis on clinical interventions over community-level approaches may

contribute to these disparities. We examined the impact of structural deprivation, racial residential segregation, and income inequality on adverse GDM outcomes. Analyzing data from 2,164 individuals aged 18-51 years with GDM from a large health system's electronic health records (EHR) linked to census-based American Community Survey data, we found significant associations. Results showed that the odds of deliveries with related complications of GDM were 38% higher for individuals residing in areas with a higher percentage of households receiving public assistance (OR=1.38; 95%CI=1.12-1.70), and 25% greater for those living in neighborhoods where the overall unemployment rate was higher (OR=1.25; 95%CI=1.02-1.52). Results revealed elevated odds of delivering infants with low birth weight (4000 grams) was more likely among obese individuals (OR=1.43; CI=1.04-1.97) in those residing in areas with higher percentage of Latino residents (OR=1.45; CI=1.00-2.09). These results underscore the influence of social determinants on GDM outcomes, highlighting the need for comprehensive interventions addressing structural factors alongside clinical management.

Lisa T. Jansen, University of Arkansas for Medical Sciences - Arkansas Children's Nutrition Center. **Impact of Physical Activity Intervention on Longitudinal Glycemic Patterns in Pregnant Women with Obesity: A CGM Pilot Study.** Co-Authors: Scott Stewart, Lilian Cheak, Precious Jeffrey, Aline Andres. Co-Authors Institutional Affiliations: Arkansas for Medical Sciences, Arkansas Children's Nutrition Center, Arkansas Children's Research Institute. COBRE

In the US, >50% of pregnancies occur in women with overweight or obesity, increasing the risk of obesity in their offspring. Insulin sensitivity (IS) plays a crucial role in metabolic health for both mother and fetus, with blood glucose (BG) levels commonly used as an IS indicator. However, traditional spot sampling of BG provides limited insights to metabolic processes. This pilot study aims to investigate how a modifiable lifestyle intervention (physical activity, PA) during pregnancy affects longitudinal glucose patterns using continuous glucose monitoring (CGM). In this ancillary study to a physical activity intervention trial (NCT02125149), 18 women were randomized to either weekly supervised PA sessions (3x 30-45min of moderate intensity exercise), or standard of care (SOC). CGM recorded interstitial glucose values in 15-min intervals across 14-day wear-time periods at each trimester (FreeStyle LibrePro, Abbott, USA).

24-hour glycemic profiles were analyzed from CGM data collected at 12-14, 24-26 and 36-38 weeks of gestation. For SOC participants, glucose levels decreased during the 2nd and 3rd trimester, particularly around 10am and 3pm. No significant changes were observed for PA participants across later trimesters. Compared to PA participants, SOC participants exhibited lower glycemic profiles during late morning and early afternoon in the 2nd and 3rd trimesters.

These findings suggest that weekly moderate-intensity exercise in previously sedentary pregnant women with obesity may maintain 24-hour glycemic profiles. Further research is needed to determine whether this preservation of glycemic profiles influences offspring health outcomes. Funding provided by USDA-ARS 6026-51000-012-06S and NIGMS/NIH, P20GM109096.

FLASH TALK PRESNTATIONS

Artificial Intelligence

Hamed Fayyaz, University of Delaware. **An Interoperable ML Pipeline for Pediatric Obesity Risk Prediction using Commonly Available EHR Data.** Co-Authors: Mehak Gupta, H. Timothy Bunnell, Claudine Jurkovitz Thao-Ly, Thao-Ly Phan, Rahmatollah Beheshti. Co-Authors Institutional Affiliations: Southern Methodist University, Nemours Children's Health, ChristianaCare, University of Delaware. CTR

Reliable prediction of pediatric obesity can offer a valuable resource to the providers helping them engage in timely preventive interventions before the disease is established. Many efforts have been made to develop ML-based predictive models of obesity and some studies report high predictive performances. However, no largely used clinical decision support tool based on these ML models currently exists. This study presents a novel end-to-end pipeline specifically designed for obesity prediction, which supports the entire process of data extraction, inference, and communication via an API or a user interface. By using only routinely recorded data in electronic health records (EHRs), our pipeline uses a diverse expert-curated list of medical facts to predict the risk of developing obesity. We have used input from various stakeholders, including ML scientists, providers, health IT personnel, health administration representatives, and patients throughout our design. By using the Fast Healthcare Interoperability Resources (FHIR) standard in our design procedure, we specifically target facilitating low-effort integration of our pipeline with different EHR systems.

Sabrina Duran, West Virginia University School of Medicine. **Comparing Readability of American Academy of Dermatology and AI-generated Patient Education Materials.** Co-Authors: Jenna Foster, Andrea Medina Gonzalez, John Nguyen, Diane Wang, Zachary Zinn. Co-Authors Institutional Affiliations: West Virginia University.
Patient education material (PEM) is essential for treatment compliance. PEMs from the American Academy of Dermatology (AAD) are currently written above the American Medical Association's recommended reading level of 6th grade. We aim to assess the efficacy of large language model chatbots in making dermatologic information more accessible and understandable. This study aims to compare the readability of AAD PEMs to those of AI chatbots, specifically Open AI's ChatGPT and Google Gemini. PEMs on 10 common AAD topics were generated using ChatGPT 4.0 and Gemini with and without the prompt to produce material at a 6th-grade level (i.e. prompted and unprompted, respectively). AI-generated and their respective AAD PEMs, were compared using: Flesch Reading Ease (FRE), Gunning Fog Index (GFI), Flesch-Kincaid Grade Level, Coleman-Liau index, SMOG Index Score, Automated Readability Index, and Linsear Write Readability Score. A two-sample t-test compared results. The AAD PEMs had a higher mean FRE (66.5) and lower mean GFI (9.73) compared to unprompted ChatGPT (50.4, 11.85) and Gemini (57.2,11.21), indicating AAD's greater readability and comprehension. In its prompted form, ChatGPT consistently generated content that was easiest to read when compared to prompted Gemini and AAD's PEMs (FRE 78.4, p=0.005; GFI 7.66, p

Zhicheng Jiao, The Warren Alpert Medical School of Brown University. **Multi-modality AI model for outcome prediction of COVID-19 from chest x-ray.** Co-Authors: Vin Somasundaram, Zhusi Zhong, Scott Collins, Terrence Healey, Michael Atalay. Co-Authors Institutional Affiliations: The Warren Alpert Medical School of Brown University. CTR
In response to the worldwide COVID-19 pandemic, advanced automated technologies have emerged as valuable tools to aid healthcare professionals in managing increased workload by automatic report generation and prognostic analysis. We propose a multi-modality AI model that facilitates the fusion of imaging information from chest x-rays, free-text radiology reports, and tabular clinical features to estimate the risk of disease progression. Specifically, (1) an imaging branch learns spatial-aware visual information from automatically detected anatomical regions, (2) a state-of-the-art large language model (LLM) strategy is designed to enhance the image-to-text correlation to secure clinically meaningful report generation from raw images, and (3) a multi-modality fusion module is further embedded to integrate the imaging-report branches with clinical measures for further improved patient outcome prediction. Evaluated by the time-to-event analysis metric of the Concordance Index on large-scale datasets, our multi-modality fusion model achieves the best performance of 0.813 on the internal validation set and 0.739 independent external validation set, which is superior to each modality alone, 0.737 and 0.713 on imaging data, 0.739, and 0.703 on clinical measures ($p < 0.05$). Our model also provides a function that presents that visualizes the detected regions of

high progression risks with generated reports to enhance interpretation and trustworthiness of AI models in clinical settings. Besides, given that the x-ray images and reports are widely used in diagnosis and prognosis, the multi-modality framework here could be expanded to a spectrum of chest diseases and improve technical transparency and clinical interpretability in healthcare AI models.

Brain Disorders and Mental Health

Jee-Yeon Hwang, Creighton University. **TREM1 Signaling as a Therapeutic Target for Global Cerebral Ischemia.** Co-Authors: Hyunha Kim, Rachael Urquhart, Gopal Jadhav. Co-Authors Institutional Affiliations: Creighton University School of Medicine. COBRE
Each year, over 200,000 Americans suffer from global cerebral ischemia associated with cardiac arrest, leading to cognitive deficits or death. While current emergency treatments for cardiac arrest focus on restoring cardiac function and blood flow, an effective therapeutic treatment for neurodegeneration and cognitive deficits associated with global cerebral ischemia is a crucial unmet medical need. To elucidate the mechanisms underlying the pathology and identify therapeutic targets for global ischemia, we performed RNA-seq analysis on hippocampal CA1 tissue from a rat model of global ischemia. Bioinformatic analysis of differentially expressed genes revealed that "TREM1 signaling" and "Neuroinflammation" are the top canonical pathways. Our subsequent experiments demonstrated that global ischemia induces activation of TREM1 in infiltrated peripheral immune cells, leading to increased levels of proinflammatory proteins, microglial activation, disruption of the blood-brain barrier (BBB), and reduced expression of BBB tight junction proteins in hippocampal CA1. These findings suggest that global ischemia triggers TREM1-mediated neuroinflammation via BBB integrity loss, ultimately contributing to neuronal death. Furthermore, inhibition of TREM1 significantly attenuated these pathological events and prevented neuronal death. This pilot project, funded by the COBRE program, provided crucial insights into the role of TREM1 as a key player in global ischemia pathology, highlighting its potential as a therapeutic target for this condition.

Karthik Swaminathan, University of Wyoming. **Ribosomal Heterogeneity in Stress Neurobiology.** Co-Authors: Rammohan Shukla. Co-Authors Institutional Affiliations: University of Wyoming. COBRE
In our previous study we have shown that Ribosomal Protein Genes (RPGs) are downregulated in mouse model of chronic variable stress and postmortem brains of individuals who have died during depression episodes. While this response is conserved across species and stressors, it has not been thoroughly studied in mouse models of neuro-translational stress, that recapitulates different aspects of depression. Our ongoing research investigates the patterns of RPG dysregulation in different brain regions of mice under various preclinical stress conditions using available transcriptomic data. The study finds that RPG dysregulation, both up- and down-regulation, is observed in cytoplasmic and mitochondrial RPGs and is more common in chronic stress than in acute or early-life stress. Interestingly, the dysregulated RPGs are significantly associated with post-synaptic gene ontology terms, suggesting their role in synaptic modulation. The study concludes that ribosomal dysregulation is a conserved stress response mechanism during neuro translational stress. The RPG dysregulation could lead to either a global downscaling of ribosome biogenesis or ribosomal heterogeneity, each having a different effect while the variability in RPG dysregulation could potentially serve as a marker of neuronal activity in response to different stress paradigms.

Katherine A. Berry, University of Wyoming. **Anxiety on the rocks: College students' anticipatory and compensatory urges to drink in response to a laboratory-based social stressor task.** Co-Authors: Alison Looby. Co-Authors Institutional Affiliations: University of Wyoming. INBRE
Stressful social and evaluative situations may increase alcohol use among undergraduates as a means of coping in anticipation of the stressful event or to modulate negative affect post-event. This study examined

anticipatory and compensatory urge to drink using a modified Trier Social Stressor Task (TSST) among college student drinkers (N=129, Mage=19.49, 81.4% white non-Hispanic, 62.8% female), based on baseline social anxiety, alcohol coping motives, and type of nonverbal feedback provided during the task. Participants were informed they would give a video-recorded speech that would be evaluated in real-time by two researchers, and were randomized to receive positive or negative nonverbal feedback during their speech. Participants reported urge to drink and completed an alcohol pour task both in anticipation of and following completion of the TSST. All participants reported significantly increased urge to drink from baseline both in anticipation of and following the stressor task. Coping motives and social anxiety predicted stronger anticipatory urge to drink, though there were no significant interactive effects. Conversely, there were no significant predictors on the anticipatory pour task. For compensatory urge to drink and amount poured, there were significant three-way interactions between condition, coping motives, and social anxiety, such that students who received negative feedback and endorsed high coping motives and social anxiety reported the strongest urge and poured the most alcohol after the TSST. Results highlight targets of intervention to reduce problematic alcohol use, including finding alternative ways to manage negative emotion, and indicate the need to attend to anticipatory and compensatory drinking.

Cancer and Disease Risk

Adriana Aponte Ramos, Inter American University of Puerto Rico, Bayamon Campus. **Exploring Ergosterol Peroxide's Mechanism of Action on the VCP / ANKZF1 Complex in Triple Negative Breast Cancer Models.** Co-Authors: Michelle Martinez Montemayor. Co-Authors Institutional Affiliations: UCC School of Medicine. CTR
Triple-Negative Breast Cancer (TNBC) represents a challenging breast cancer subtype due to its high recurrence and mortality rates, aggressive nature, and limited treatment options. We identified the natural product ergosterol peroxide, a steroidal compound found in fungi, as a potent antiproliferative anti-TNBC agent, by inducing ROS and apoptosis. However, EPâ€™s mode of action (MOA) remains to be defined. Oxidative stress in the mitochondria leads to accumulation of damaged proteins, which are normally removed by ubiquitination via the VCP/ANKZF1 complex. Thus, taking advantage of TNBCâ€™s dependency on sterol uptake, removal of misfolded proteins and altered redox homeostasis, we propose that EP serves as a VCP/ANKZF1 complex protein-protein inhibitor (PPI), which will be analyzed via Proximity Ligation Assays (PLA). TNBC (2.0x104) cells/well were seeded in a 8-well chambered slide and incubated at 37°C for 48h. Following cell adhesion, cells were treated with the appropriate effectors for 24h, (i.e., DMSO 0.2%, EP 20Î¼M, and NMS-873 1Î¼M). Subsequently, cells were permeabilized, fixed, then blocked and incubated overnight with the primary antibodies (rabbit anti-human-VCP and mouse anti-human-ANKZF1). Duolink PLA probes were added for 1h, then ligation and amplification steps were performed. Lastly, the slide was mounted for image acquisition using the Cytation-10, and processing using Gen5 software. We are reporting the negative control results which demonstrate PLA signals, indicating PPIs are observed. These are preliminary, and protocol was refined and optimized to conduct on diverse cell lines. This will enable us to comprehend EP's MOA and highlights its potential as a therapeutic agent for TNBC.

Akash J. Vaidya, University of Delaware. **Repurposing Barley-Stripe Mosaic Virus for Cancer Immunotherapy.** Co-Authors: Mruthula Rammohan, Jesal Patel, Evan Gillen, Robyn Logue, Kevin V. Solomon. Co-Authors Institutional Affiliations: University of Delaware. INBRE
Nanoparticle therapies can reprogram tumor-associated macrophages from cancer-supportive to cancer-suppressive (M1) phenotypes. Therapeutic outcomes depend on nanoparticle size, shape, cargo, and surface structure. The special class of rod-shaped plant viruses (RSPVs) allow rare control over all these properties. RSPVs such as tobacco mosaic virus (TMV) are already under investigation for vaccine applications, but their efficacy is limited by the presence of anti-TMV antibodies in human serum. We show that a related RSPV

species, barley-stripe mosaic virus (BSMV), does not suffer from preexisting immunity and thus has immense potential for vaccine development. We leverage a bacterial platform to produce BSMV VLPs, non-infectious analogs in which the viral genome is replaced by a user-defined RNA template, for additional control over particle properties. By decoupling VLP production from native host infectivity, we enable high-density surface functionalization with diverse ligands via direct fusion and post-assembly conjugation methods. Through the introduction of specific residues, we achieve control over surface charge and other physicochemical properties. We also decorate the VLPs with immunogenic ligands including toll-like receptor agonists. Furthermore, we demonstrate that BSMV VLP size and aspect ratio can be tuned by varying the length of the RNA template. The finely tuned, functional VLPs are highly immunogenic and lead to robust M1 activation of murine macrophages. We investigate the mechanism of BSMV VLP immunogenicity, which is partly mediated by toll-like receptors. These scientific and technological advances set the stage for further BSMV VLP development as a nanoparticle platform for cancer immunotherapy and broader vaccine applications.

Emily Tolbert, Kansas State University. **cHPV E6 reduces innate immune signaling.** Co-Authors: Dalton Dacus, Rose Pollina, Nicholas A. Wallace. Co-Authors Institutional Affiliations: Enliven Therapeutics, Kansas State University. COBRE
Each year 3 million Americans are diagnosed with non-melanoma skin cancer (NMSC) and spend approximately $4.8 billion on treatments. Cutaneous human papillomaviruses (cHPV) are hypothesized to promote NMSC by destabilizing the host genome. Supporting this, the E6 protein from these viruses (cHPV E6) dysregulates DNA repair signaling pathways. Inhibition of DNA repair is believed to promote viral replication by promoting cell cycle progression in UV exposed skin. They may also dysregulate other pathways to promote cHPV replication. The cGAS-STING (cyclic GMP-AMP synthase-stimulator of interferon genes) pathway prevents viral infection (and maintains genomic integrity) by activating innate immunity in response to cytoplasmic double stranded DNA (dsDNA). I hypothesize that cHPV E6 also impairs the cGAS-STING innate immune response. To test this, transfected dsDNA was used to simulate cGAS-STING signaling and pathway activation was monitored by immunoblot. This demonstrated that cHPV E6 impairs cGAS-STING signaling downstream of STING activation. Our current efforts use RNA-sequencing to obtain an unbiased measure of how broadly cHPV E6 blocks the innate immune response to cytoplasmic DNA. These data support the hypothesized role of cHPV in NMSC.

Hannah Ladwig, Creighton University. **Structural Analysis of Crassostrea gigas OAZ-PK RNA.** Co-Authors: Rhiannon McCracken, Juliane Soukup. Co-Authors Institutional Affiliations: Creighton University. INBRE
Riboswitches are a type of non-coding RNA that regulate downstream gene expression upon metabolite binding. When a riboswitch interacts with its ligand, it undergoes a conformational change resulting in a change in gene expression. This change in gene expression operates as a feedback mechanism, affecting the same metabolic pathway in which the ligand functions. The Soukup Lab researches potential eukaryotic riboswitches within the Ornithine Decarboxylase Antizyme pseudoknot (OAZ-PK) RNA. One such potential riboswitch is found in the OAZ-PK RNA of a species of oyster, Crassostrea gigas, which is believed to interact with various natural and non-natural polyamines. In-Line Probing (ILP) experiments can be used to analyze the structural changes of this RNA segment upon binding to differing concentrations of these polyamines. Preliminary data from ILP experiments with Crassostrea gigas OAZ-PK RNA indicate that the binding of spermine results in a structural change to the RNA segment, but not other polyamines. Current experiments aim to examine the presence of a structural change upon binding of a closely related polyamine, spermidine. Riboswitches have demonstrated significant impacts on the regulation of metabolic pathways in bacteria, and thus are being used as a target of possible antibiotic treatments. Identification of similar riboswitches in eukaryotic species will provide an opportunity for the development of novel antibiological agents. The project described was supported by an Institutional Development Award (IDeA) from the National Institute of General

Medical Sciences of the National Institutes of Health under Grant # 5P20GM103427.

Raphael Oladokun, West Virginia University. **Dielectrophoretic Characterization and COMSOL Analysis of Late Carcinoma Using PBMCs from MMTV-PyMT (PyMT) and MMTV-WT (WT) Mammary Carcinoma Models.** Co-Authors: Soumya Srivastava. Co-Authors Institutional Affiliations: West Virginia University. INBRE
Peripheral blood mononuclear cells (PBMCs) are specialized immune cells that actively surveil for signs of infection, foreign invaders, and abnormal cells associated with diseases. Inherent interactions occur between PBMCs and proliferating cancer cells, facilitating cellular communication and inducing alterations in the membrane composition of PBMCs. This research utilizes a engineered animal model of spontaneous breast cancer to study these alterations through dielectrophoresis, a dielectric characterization technique using nonuniform fields. The ultimate objective is to apply this knowledge for non-invasive early detection of breast cancer while minimizing false positives and negatives associated with standard screening methods. We probed the dielectric properties of PBMCs from peripheral blood sources of FVB/N MMTV-PyMT+ (late carcinoma, PyMT-PBMC) and FVB/N (wildtype, WT-PBMC) age-matched mice at 14+ weeks using dielectrophoresis in a microfluidic platform. The central hypothesis is that changes triggered in subcellular components like the cytoskeleton, lipid bilayer membrane, and cytoplasm at the onset of carcinoma regulate dielectric properties, affecting bioelectric signals that aid cancer detection. ANOVA results indicate no difference in PyMT-PBMCs crossover frequencies between low conductivity ranges, but differences at 0.01 S/m and 0.05 S/m conductivity levels. WT-PBMCs showed distinct crossover frequencies across the entire conductivity range. Other DEP properties suggest the interaction between PBMCs and cancer cells leads to membrane composition and morphology changes, providing information on how immunosuppressive and chemotactic molecules regulate PBMC responses and behavior. PyMT PBMCs showed increased polarizability, higher membrane capacitance, and folding factor.

Sahil Lohana, North Dakota State University. **Validation of novel histone deacetylases (HDAC) specific nanoparticles using HDACs overexpressed human embryonic kidney cells.** Co-Authors: Yogaraj S Ramakrishnan, Premanand Balraj, Md Rakib Hasan Khan, Sanku Mallik, Venkatachalem Sathish, Quadir Mohiuddin. Co-Authors Institutional Affiliations: Not Listed. INBRE
Introduction: Histone deacetylase (HDAC) is a major enzyme system that is upregulated in numerous disease conditions including cancer. Harnessing the upregulation of HDAC can be a viable tool to design targeted therapy for these diseases. Nanoparticle technology has emerged as a powerful workhorse to suppress the survival of diseased cells selectively. As such, we aim to design a nanoscale, drug delivery platform that responds to HDAC enzymes to initiate drug release. In this poster, we show the pharmacological evidence that HDAC-sensitive nanoparticles are interacting with HDAC enzymes in vitro in time and concentration dependent pattern. Methods: We synthesized HDAC-responsive nanoparticles via developing a block copolymer composed of a poly (ethylene glycol) block and a poly (L-acetylated lysine) block. Abbreviated as PEG-acPLK, these copolymers self-assemble as nanoparticles with negatively charged surface. Using in vitro culture of HEK 293 cells, we showed that the formed nanoparticles interact and interfere with HDAC enzymes. Cells were grown to 80-90% confluency in DMEM media w/ 10% FBS prior to experiments. HEK-293 cells were overexpressed with HDAC 7 & HDAC 8 using Lentiviral vectors. Western blot was done to prove the successful overexpression of the HEK cells. Cytotoxicity assay was done by MTT to analyze the efficacy of HDAC specific nanoparticle on control and overexpressed HEK-293 cells. Results: Our work showed that, PEG-acPLK systems form nanoparticles with a hydrodynamic diameter (RH) of 120-150 nm. The particles were negatively charged on their surface, as such did not produce any non-specific toxicity to cells, such as damage of cell membranes. HEK-293 cells were infected with lentivirus vectors for HDAC 7 and HDAC 8. The medium was changed 8 h after infection. Forty-eight hours after infection, the positive cells were selected with 5 μg/mL puromycin. The lentivirus stable transformants of HEK-293 cells were collected and significant overexpression were confirmed

by western blot. For the cytotoxicity study, control and overexpressed cells were treated with HDAC-nanoparticle and PEG-acPLKC (5 µg/mL to 70 µg/mL) for 24hrs. Both the HDAC-nanoparticle and PEG-acPLC (free form) showed more than 60% of toxicity at the concentration of 20 µg/mL. Whereas the HDAC 7 and 8 overexpressed HEK-293 cells did not showed any effects with nanoparticle and Ae-peg-PLKC, suggesting compensating effect due to highly available HDAC system in place and confirm the effectiveness of the HDAC nanoparticle. Summary and Conclusion: Overall, these results showed that HDAC specific nanoparticle exhibited effects in HEK-293 HDACs overexpressed cells. Further molecular mechanistic studies will help to delineate how the HDAC-responsive particles can be used for drug delivery.

Cardiovascular Biology

Bedia Akosman, Rhode Island Hospital. **Deciphering the Role of the SOX17/Runx1 Axis in Endothelial Dysfunction and Pulmonary Arterial Hypertension Pathogenesis.** Co-Authors: Eui Young So, Mandy Pereira, Moon-Jung Choi, Euy-Myoung Jeong, James Klinger, Olin Liang. Co-Authors Institutional Affiliations: Rhode Island Hospital, Warren Alpert Medical School of Brown University. COBRE
Pulmonary arterial hypertension (PAH) is a progressive and life-threatening condition characterized by distal pulmonary vessel obstruction, vascular remodeling, and increased vascular resistance, yet lacks a definitive cure. Various stressors, such as hypoxia, inflammation, and oxidation can activate genetic processes controlled by specific transcription factors, which typically facilitate vascular repair but may lead to aberrant vascular remodeling if not properly regulated. Among these, SOX17 and its downstream target RUNX1 play crucial roles in PAH. SOX17 is vital for pulmonary vasculature development and post-injury endothelial regeneration, with loss-of-function mutations associated with severe, early-onset PAH. During fetal development, SOX17 directly interacts with Runx1, regulating the endothelial-to-hematopoietic transition to maintain arterial identity. Our earlier research demonstrated the importance of RUNX1 in PAH pathogenesis, showing that endothelial-specific Runx1 deletion can prevent Sugen/Hypoxia-induced PAH in mice. Therefore, we hypothesize that the failure of endothelial SOX17 to repress Runx1 contributes to PAH pathogenesis and aim to elucidate the impact of a compromised SOX17/Runx1 axis on the development of PAH. By utilizing human pulmonary arterial endothelial cells, we observed a transcriptional and phenotypic shift from endothelial to hematopoietic profile following Runx1 overexpression, accompanied by aberrant tube formation, increased proliferation, and enhanced migratory capabilities. In vivo studies revealed that Runx1 inhibitors significantly reverse Sugen/Hypoxia-induced PAH in rats and prevent it in Sox17 enhancer-knockout mice. In conclusion, our findings emphasize the critical role of SOX17/Runx1 axis in endothelial cells and vascular remodeling. Maintaining low Runx1 levels in pulmonary endothelial cells is essential for preserving their identity, suggesting that targeting the SOX17/Runx1 axis holds promise as a therapeutic strategy for PAH.

Carly Michelle Goldstein, PhD, FAACVPR, The Miriam Hospital/Alpert Medical School of Brown University. **Using the Multiphase Optimization Strategy and an Electronic Health Record Review to Refine, Finalize, and Prepare Trauma-Informed Interventions to Increase Phase II Cardiac Rehabilitation Initiation in a Full Factorial Experiment.** Co-Authors: J. Graham Thomas, Benjamin T. Ladd, Wen-Chih Wu. Co-Authors Institutional Affiliations: The Miriam Hospital/Alpert Medical School of Brown University, Providence VA Medical Center. COBRE
Cardiovascular disease (CVD) is the leading cause of death for adults in the United States. Cardiac rehabilitation (CR) is an evidence-based, cost-effective, and widely available program that combines supervised exercise with health behavior change psychoeducation aimed at improving overall health and reducing secondary cardiovascular risk. However, most referred patients do not attend. While some initiation barriers are systemic (e.g., lack of referral), some are person-level, psychosocial, and modifiable; high trauma pathology and low resilience may exacerbate behavioral targets. Interventions to increase CR initiation must

urgently be created to address this public health crisis. The present application finalizes 4 innovative, disseminable intervention components through the Multiphase Optimization Strategy's (MOST) Preparation phase. Following refinements and finalizations based on formative work with CR patients and an electronic health record review to evaluate trauma-related factors in non-initiated patients (Aim 1), the study team will pilot the 4 intervention components in a 24 full factorial configuration designed to evaluate component acceptability, protocol feasibility, and potential changes in behavioral targets, trauma, and resilience (n=32 CR-eligible adults; Aim 2). After final modifications to the components for the future optimization (Aim 3), this STAR COBRE Research Project will result in 4 developed, acceptable intervention components designed to improve CR initiation that will be ready for the MOST Optimization phase. Ultimately, the effective treatment components will form a resource-efficient treatment package. This presentation will share available study findings and detail next steps in this Research Project, which is sponsored by The Miriam Hospital's Stress, Trauma, and Resilience (STAR) COBRE.

Sai Prashanthi Gumpili, University of Delaware. **Risk factors for cardiac events in children and young adults within 6 months following a COVID-19 infection.** Co-Authors: Sai Prashanthi Gumpili, Shubhika Srivastava, Carol Prospero, Ran Zhang, Jobayer Hossain, Suzanne McCahan, Chuming Chen, Julie Cowart, Cathy Wu, H. Timothy Bunnell, Robert Akins, Claudine Jurkovitz. Co-Authors Institutional Affiliations: Nemours Children's Health, University of Delaware, Christiana Care Health Services, Inc. INBRE
Risk factors for cardiac events in children and young adults within 6 months following a COVID-19 infection are still unclear. The risk factors for cardiac events after the onset of COVID infection may differ with time. We sought to identify the risk factors for cardiac events within 30 days (acute phase) and between 31 days and 6 months (follow-up phase) of infection onset. The National COVID Cohort Collaborative data were analyzed to assess baseline risk factors of patients aged 0-30 years with COVID. COVID Severity, Area Deprivation Index (ADI), demographic variables, and pre-existing conditions were included in random forest models to predict cardiac events. We used feature importance and SHAP analysis to assess importance of the risk factors according to age-groups 0-4, 5-17, 18-30 years. A total of 9203 and 12,565 patients had cardiac outcomes in the acute and follow-up phases respectively. During the acute phase, the features common across all age-groups with the highest mean absolute SHAP values were COVID severity, previous arrythmia, race, and ADI. Congenital heart disease (CHD) had also a high SHAP value in age-group 0-4 and gender in age-group 18-30. During follow-up the features with the highest SHAP values common across all age-groups were COVID severity, presence of an acute phase cardiac event, previous arrythmia and race. Other important age-group specific risk factors were CHD for age-group 0-4, ADI for age-group 5-17 and gender for age-group 18-30. COVID severity, previous arrythmia and race are major predictors of cardiac events irrespective of the phase and age.

Environment and Health

Alexa Bostic, West Virginia University. **Dielectric Characterization of HL-60 Cells under Microgravity.** Co-Authors: Soumya Srivastava. Co-Authors Institutional Affiliations: Not Listed.
Space exploration continues to become more advanced as new technology emerges. Organizations such as NASA and SpaceX are seeking to travel further and longer than ever before. With this, many questions are raised on how space travel affects the human body. Even in short-term space travel, microgravity alters the cardiovascular system by reducing circulatory blood volume and blood pressure. When adjusting to Earth's gravitational pull upon return, a newly developed intolerance to Earth's gravity can cause health issues. The effects can also be observed in the musculoskeletal system, ocular system, and more (1). As space exploration rapidly advances, understanding the effects of space travel on the human body is essential. By stimulating microgravity through a clinostat, its effects can be observed without having to send samples to space. HL-60

cells are a human cell line derived from a Caucasian, female patient with acute promyelocytic leukemia. The effects of microgravity on the characteristics of HL-60 cells are relatively unknown. This project utilizes an electrokinetic technique, dielectrophoresis (DEP), to characterize HL-60 cells that have been exposed to microgravity. Using DEP allows the crossover frequency (the frequency at which the cells move towards or away from an electric field) to be analyzed. Analyzing this shows the different dielectric properties of the cells such as conductivity and permittivity. The differences in dielectric properties of cells exposed to microgravity conditions give insight into how microgravity can affect them. Experiments have been conducted using yeast cells exposed to microgravity in a clinostat for 1-5 hours in different medium conductivities ranging from 0.1-0.3 S/m. Exploring the effects of microgravity on HL-60 cells will continue to deepen the understanding of the effects of microgravity on the human body.

Dhruthi Mutyala, Southern university and A&M College. **Exosome-Mediated Regulation of Proteasomal Subunits in E-Cigarette Vapor-Induced Inflammation.** Co-Authors: N.Bidarimath, R.Kondati, M.Thakur, S.Batra. Co-Authors Institutional Affiliations: Not Listed. COBRE
Electronic cigarettes (e-cigs) have become the latest trend among adults and youth alike due to their marketing as a safer alternative to conventional smoking. Recent research suggests that vaping can cause oxidative stress and protein degradation, leading to respiratory diseases. The findings from our laboratory demonstrate the importance of inducible catalytic subunits of 20S proteasome in tobacco-flavored e-cig vapor condensate (TF-ECVC Â± Nicotine) induced inflammation in lung epithelial cells (A549). The substrate binding and commitment of gate (19S) in opening of the 20S proteasome are important in the ubiquitin-mediated degradation of proteins. Our results demonstrate an increase in the transcription/translation of 19S subunits-Rpn13 and Rpn10 in TF-ECVC-challenged cells. Interestingly, exosomes have been shown to harbor 20S proteasomal subunits which are important in maintaining cellular homeostasis. Considering this, we isolated exosomes from tobacco-flavored e-cigs vapor condensate (TF-ECVC Â± Nicotine)-challenged lung epithelial cells (A549) were used to determine the localization of constitutive/immune/19S subunits; along with their specific biomarkers using conventional and/or ELISA-based immunoblot format. Our results demonstrate increased accumulation of constitutive (Î²1, Î²2, Î²5), immune (MECL1), 19S (Rpn13) subunits; along with the exosomal markers CD81, CD63, ALIX in the exosomal fractions of TF-ECVC challenged cells. Overall, our findings provide critical information about the role of exosomes in ECVC-induced inflammation. Therefore, using exosome inhibitors, or employing exosome engineering techniques can be useful to mitigate the harmful/toxic impacts of ECVC.

Mehtap Haktanir Abul, Alpert Medical School Brown University, Rhode Island Hospital. **Asthma and Sleep-Related Environmental Factors Contributing to Sleep Awakenings in Urban Children with Asthma.** Co-Authors: Sheryl J. Kopel, Shira Dunsiger, Luiz Guzman, Carly Mattice, Sidney Kirchhof, Caroline Gredvig-Ardito, M. Carskadon. Co-Authors Institutional Affiliations: Rhode Island Hospital, Alpert Medical School of Brown University, Bradley-Hasbro Research Center, EP Bradley Hospital Sleep Research Laboratory. CTR
that can challenge asthma management and increase awakenings in sleep. We aimed to 1) describe asthma and sleep-related environmental factors in children's homes that can contribute to asthma and sleep outcomes, 2) examine associations between these factors and frequency of nocturnal awakenings and 3) examine whether these associations differ in those with poorly controlled asthma. Methods: 150 urban children 7-9 years old with persistent asthma and their caregivers completed a 16-day observational protocol. Asthma control was assessed via the Asthma Control Test. Asthma and sleep outcomes were evaluated via self/caregiver report and objective (portable handheld spirometer, actigraphy) methods. Assessment of the asthma and sleep environment was also completed. Results: The most prevalent environmental risk factors for asthma and sleep were tobacco smoke (25%), pets (42%), and pests (34%). Sleep hygiene/environmental factors reported by families as challenging included child routinely falling asleep (48%) or sleeping all night

(48%) in a room not intended as their sleep space. Shared sleep space (40%) and lack of protective allergy bedding (40%) were also common challenges. Numerous factors causing objectively measured nighttime awakenings were also reported. Specific analyses examining asthma and sleep environmental factors related to frequency of nighttime awakenings are underway, as well as differences by level of control. Conclusions: Urban children's sleep environment contains asthma and sleep-related factors that interferes with sleep. These disruptors affect both asthma activity and sleep and are areas to target in future multi-component asthma and sleep interventions.

Monica Valentovic, Marshall University School of Medicine. **Cytotoxic Effects of E-Cigarette Flavoring Agent Menthol on Renal Proximal Tubular Epithelial Cells.** Co-Authors: S. E. McGuffey, K.C. Brown. Co-Authors Institutional Affiliations: Marshall University School of Medicine. INBRE
The health effects for E-cigarette and vaping device usage is not well characterized due to the lack of regulation and usage of self prepared juices. Menthol is a flavoring agent contained in vaping products and menthol is detectable in plasma following vaping. The purpose of this project was to evaluate the effect of menthol on renal proximal tubular epithelial cells. The overall hypothesis was that menthol is cytotoxic to renal human (HK-2) cells by impairing mitochondrial function. Human HK-2 cells were plated and equilibrated for 48h. Cells were then exposed to 0-1500 uM menthol for 24h. Studies were conducted as 4 independent experiments with different cell passages. Differences between groups were evaluated using ANOVA followed by a post hoc test. Cytotoxicity was assessed using the MTT assay in which viable cells convert MTT to formazan. Menthol changed MTT in HK-2 cells exposed to 200-1500uM compared to vehicle control (p

Sarah Arias, Butler Hospital, Brown University. **Challenges and Considerations when using Electronic Health Record Data for Identification of Suicidal Ideation and Behavior.** Co-Authors: Ivan W. Miller, Charles Eaton, Richard N. Jones, Elizabeth Chen. Co-Authors Institutional Affiliations: Butler Hospital, Brown University. CTR
Considering that over 75% of individuals receive some form of healthcare prior to suicide1, data in the electronic health record (EHR) can be very informative for suicide detection and prevention efforts. However, leveraging these data for clinical research can be challenging due to barriers associated with locating, accessing, and extracting necessary data.2 Further, there is limited discussion of these challenges and considerations. This pilot work allowed us to navigate data challenges (e.g., extraction, formatting) and considerations when identifying suicide-related visits within our Epic EHR. Data included structured data (six-month visit timeframe) and unstructured data (one-month visit timeframe) from an outpatient Epic EHR system in Rhode Island. Initial patient records were selected based on ICD-10-CM and SNOMED-ST codes. Visits with codes for suicidal ideation or behavior, mental health, or substance use were included. Throughout the process, we encountered barriers ranging from administrative concerns associated with legal and regulatory requirements to staffing changes to data quality issues within the organization. We discuss these challenges in addition to suggestions for how best to navigate these situations. Further, data are provided on our preliminary findings regarding the most frequent locations for documentation of suicidal ideation and behavior both within structured (e.g., ICD codes) and unstructured (e.g., clinical notes) data. A better understanding of the common challenges and solutions associated with working with EHR data can help facilitate effective and efficient use of the EHR for suicide research.

Zim Warda Hasan, Western Kentucky University. **Effect of Glucocorticoid Blockade on Inflammatory Responses to Acute Sleep Fragmentation in Mice.** Co-Authors: Van Thuan Nguyen, Noah T. Ashley. Co-Authors Institutional Affiliations: Western Kentucky University. INBRE
The association between sleep and the immune-endocrine system is well recognized, but the nature of that relationship is poorly understood. Sleep fragmentation induces a pro-inflammatory response in peripheral

tissues and brain, but it also activates the hypothalamic-pituitary-adrenal axis, releasing glucocorticoids. It is unclear whether this rapid release of glucocorticoids acts to potentiate or dampen the inflammatory response in the short term. This study aimed to determine whether blocking or suppressing glucocorticoid activity will affect the inflammatory response from acute sleep fragmentation (ASF). C57BL/6J mice were injected with either 0.9% NaCl (vehicle 1), metyrapone (a glucocorticoid synthesis inhibitor), 2% ethanol in polyethylene glycol (vehicle 2), or mifepristone (a glucocorticoid receptor antagonist) 10 min before the start of ASF or no sleep fragmentation (NSF). After 24 h, samples were collected from brain (prefrontal cortex, hypothalamus, hippocampus) and periphery (liver, spleen, heart, and epididymal white adipose tissue (EWAT)). Proinflammatory gene expression (TNF-Î± and IL-1Î²) was measured, followed by gene expression analysis. Metyrapone treatment affected pro-inflammatory cytokine gene expression during ASF in some peripheral tissues, but not in brain. Metyrapone enhanced proinflammatory cytokine gene expression in heart whereas reduced expression in adipose tissue of mice exposed to ASF. Conversely, mifepristone elevated proinflammatory cytokine gene expression in spleen while decreasing expression in cardiac tissue in mice subjected to ASF. Furthermore, irrespective of sleep fragmentation, mifepristone increased gene expression in spleen, heart, pre-frontal cortex, and hypothalamus. The results provide mixed evidence for pro- and anti-inflammatory functions of corticosterone to regulate inflammatory responses to acute sleep loss.

Genetics and Genomics

Daysha Marie Isaac, Langston University. **Stalk Cell Movement in Drosophila: a model to understand how migrating cells shape tissues and organs.** Co-Authors: Sally Horne-Badovinac, Jocelyn A. Mcdonald. Co-Authors Institutional Affiliations: University of Chicago, Kansas State University. INBRE
Many cells move dynamically during development to form complex tissues and organs. Disruption of cell migration can lead to virous birth defects, including spina bifida, microcephaly (small brain), and congenital heart defects. To better understand how cells move in development, we use a powerful genetic model organism, Drosophila. Many genes required for cell migration are conserved between files and humans, making this a useful system. During fly oogenesis, a string of cells called the stalk forms between egg chambers, future eggs, to form the ovariole. Multiple Ovarioles then buddle together to form the ovary. Loss of the stalk prevents egg formation, but nothing is known about the mechanisms that control stalk movement. In this study, we hypothesized that the stalk activity starts moving early in oogenesis and stops moving at mid-oogenesis. To address this question, we developed methods to image and analyze stalk movement. We report that the conserved STE20-like serine-threonine Kinase Misshapen (MSN) is required, as a knockdown of msn prevents stalk movement. Thus, stalk movement is an active process and occurs from early-to-mid-oogenesis. Future work will focus on how the stalk movement is a new model of tissue migration during development with implications for understanding human birth defects.

Lydia Ostmo, Northeastern State University. **Unraveling the functions of Polymerase Epsilon complex in DNA replication and DNA damage.** Co-Authors: Brandy Fultz, Sapna Das-Bradoo. Co-Authors Institutional Affiliations: Northeastern State University. INBRE
"Polymerase Epsilon (POLE) plays a critical role in DNA replication, essential for cell survival and executing leading strand DNA synthesis. Highly conserved from yeast to humans, it comprises four subunits, with POLE1 in humans and POL2 in yeast acting as the catalytic subunit. Previous research in our lab identified the binding region for an essential replication factor, Minichromosome Maintenance protein 10 (MCM10), in the C-terminal end of yeast Pol2. We have identified mutations in the non-catalytic domain of yeast Pol2 that disrupt its interaction with Mcm10 while still maintaining association with other Polymerase Epsilon subunits. These mutants exhibit delayed DNA replication and impaired recovery after DNA damage. Furthermore, we confirmed that the interaction between MCM10 and POLE1 is conserved in human cells. We have generated

plasmids expressing mutations in the essential, conserved region of the C-terminus of the human POLE1 gene and introduced mutations that have been observed in patients with FILS syndrome (Facial dysmorphism, Immunodeficiency, Livedo, and Short stature). Our study of the FILS mutant in human cells demonstrates its continued ability to bind to MCM10 and is predominantly localized in the nucleus. Two of the POLE1 C-terminal mutants, W1271A and I1358A, also maintained their binding to MCM10. However, the I1358A mutant, along with another mutant, E1428A, showed significantly reduced nuclear localization in human cells compared to wild-type POLE1. We will present a detailed characterization of the yeast and human Polymerase Epsilon mutants that reveal the relevance of the Polymerase Epsilon complex during DNA replication and DNA repair."

Motoki Takaku, University of North Dakota. **Dissecting cellular reprogramming by genomics and machine learning.** Co-Authors: Mika Saotome, Aerica Nagornyuk, Jill Goodman. Co-Authors Institutional Affiliations: University of North Dakota School of Medicine. COBRE
Transcription factors are crucial in regulating gene expression during development and cell reprogramming, typically binding to short DNA sequences to dictate genome localization. Transcription factors selectively target specific loci from huge mammalian genomes containing millions of potential binding sites. Chromatin structure, including nucleosome positioning, was believed to hinder transcription factor binding. However, recent studies indicate that some transcription factors can indeed bind to nucleosomal DNA, challenging conventional views on binding selection mechanisms. In our laboratory, we investigate this paradigm using the mesenchymal-to-epithelial transition (MET) mediated by the pioneer transcription factor GATA3. Employing deep learning to analyze GATA3's localization across the genome, we identified a novel binding motif, indicating GATA3's distinctive interaction with nucleosomes and chromatin via its two zinc finger domains. Our combination of genomic and biochemical methods, including Cryo-EM, has confirmed the importance of this novel binding mechanism in GATA3's function in MET initiation. Our research elucidates the complex interplay between chromatin architecture and transcriptional regulation, demonstrating the value of integrating artificial intelligence with cancer epigenetics to decode sophisticated biological phenomena.

Infectious Diseases

Alia Tereza Sadek, University of South Carolina School of Medicine Greenville. **Resistance and Intracellular Survival of Atypical Acinetobacter baumannii Isolates from a Fatal Case of Necrotizing Fasciitis.** Co-Authors: Elias M. Wheibe, Kyleigh Connolly, Christine Liu, Chelsea R. Gutierrez, Brock A. Arivett, Ryan F. Relich, Luis A. Actis, Steven Fiester, Maria Soledad Ramirez, Jennifer T. Grier. Co-Authors Institutional Affiliations: Not Listed. INBRE
Acinetobacter baumannii is one of the most rapidly-evolving pathogens in the world. Although previously a common cause of nosocomial respiratory and bloodstream infections, atypical strains of A. baumannii have been increasingly isolated from fatal cases of necrotizing fasciitis (NF), or flesh-eating disease, over the past decade. Unlike type strains, these NF A. baumannii (NFAb) strains display distinct genomes and enhanced antibiotic resistance, resulting in limited efficacy of current therapeutics and increased patient mortality. In the present study, we sought to elucidate how two NFAb isolates (NFAb-1 and NFAb-2) obtained from a fatal case of NF respond to environmental stressors, and behave in the host-immune cell niche. To determine environmental resistance, desiccation and transformation assays were performed. To assess host-immune cell entry, isolates were co-incubated with human-derived THP-1 macrophages with or without pre-treatment with Cytochalasin D, an inhibitor of phagocytosis. A colistin-protection assay was performed, allowing for isolation of viable intracellular bacteria and quantification after 24 hours. Intracellular and cell-free bacterial samples were also collected for total RNA sequencing analysis. No significant differences were seen in transformation, but NFAb-1 displayed greater resistance to desiccation. All isolates primarily entered macrophages via

macrophage-driven phagocytosis; however, NFAb isolates displayed greater intracellular entry and survival in host cells, and altered expression of potential virulence factors in the intracellular compartment. Collectively, these results suggest NFAb isolates have the ability to survive across environments, potentially due to mechanisms conferred by altered gene expression.

Anand Paul, Louisiana State University Health Science Center. **Machine Learning-Enabled Assessment of Healthcare Workforce Demographics and Their Impact on HIV and Infectious Disease Outcomes in Louisiana.** Co-Authors: Lucio Miele, Meredith Clement. Co-Authors Institutional Affiliations: Louisiana State University Health Sciences Center. INBRE
The confluence of healthcare workforce demographics and their impact on HIV and infectious diseases in Louisiana is a complex interplay that demands a nuanced examination. This study harnesses the predictive power of machine learning (ML) to analyze and interpret the intricate relationships within demographic data of healthcare providers and their correlation with disease management and outcomes. By employing a Random Forest algorithm, a robust and versatile ML model, we have unearthed patterns and associations that traditional statistical methods may overlook. We used HRSA-AHRF dataset, a compilation of demographic information spanning from 2015 to 2021, underwent a meticulous data cleaning and preparation process, setting a strong foundation for advanced analytics. The EDA phase elucidated key demographic disparities across occupations, highlighting potential areas for strategic intervention. Following this, our Random Forest model identified significant predictors of healthcare delivery effectiveness, focusing on race, age, and gender representation as crucial variables. The model's predictive capacity will be further leveraged to forecast trends and outcomes in HIV and infectious disease prevalence, offering a forward-looking perspective on the state's public health trajectory. The findings point towards the necessity of a diversified workforce that mirrors the state's demographic spectrum, aiming to bolster patient engagement, care compliance, and overall healthcare responsiveness. This research not only emphasizes the importance of demographic inclusivity in healthcare but also demonstrates the transformative potential of ML in shaping public health strategies. As we progress, predictive modeling endeavors will offer actionable insights, guiding Louisiana towards a proactive and preemptive approach in managing HIV and infectious diseases.

Bao Vu, University of Oklahoma Health Sciences. **Upc2A: A Key Regulator of Triazole Resistance and Hypoxic Fitness in Candida glabrata.** Co-Authors: None. COBRE
Triazole drugs (ex: fluconazole) remain the most used anti-fungal chemotherapeutics worldwide. Loss of efficacy of these drugs, often due to the emergence of resistant traits, is a major risk factor of poor patient survival outcome. The pathogenic fungus Candida glabrata exhibits inherent reduced susceptibility to triazoles and often develops high-level resistance during therapy. As a result, the CDC has categorized fluconazole-resistant Candida as a serious threat level pathogen. The transcription factor Upc2A is a key regulator of triazole resistance in C. glabrata. Upc2A regulates gene expression in both the efflux pump and the ergosterol biosynthesis systems, which are crucial in the resistance mechanisms of C. glabrata. Our studies have shown that Upc2A directly regulates genes in both pathways, and isogenic strains lacking the UPC2A gene are more susceptible to triazoles in both wildtype and highly triazole resistance clinical isolates. In addition, Upc2A function is essential for C. glabrata hypoxic growth, and, more importantly, hypoxia significantly enhances triazole efficacy. Together, these findings represent Upc2A as a potential target for antifungal development. Targeting Upc2A function is a promising and unexplored approach to alleviate the triazole resistance problem in C. glabrata and directly inhibits the fungal cell growth under hypoxic conditions, which closely resembles the systemic infection environments within the host.

Benjamin King, University of Maine. **Inhibition of NADPH Oxidase 2 Improves Survival in Zebrafish Infected with Influenza A Virus.** Co-Authors: Brandy-Lee Soos, Alec Ballinger, Mykayla Weinstein, Julianna

Grampone. Co-Authors Institutional Affiliations: University of Maine. COBRE
Influenza A virus (IAV) is a major health concern since it can cause severe lung infections, especially in older adults and individuals with chronic health conditions. The innate immune system is the host's first defense against pathogens, including IAV. The long-term goal of our research is to understand the molecular mechanisms of the innate immune response to IAV infection and use that information to find new antiviral therapeutic targets. Neutrophils have essential roles in innate immunity to bacterial and fungal infections, but their roles in antiviral responses are understudied. Neutrophils generate an inflammatory response following infection, but that response must be carefully regulated. A sufficient level of inflammation is needed to clear infection, but too much inflammation results in a damaging hyperinflammatory response. The zebrafish (Danio rerio) is a powerful vertebrate model system that is used to study IAV infection. Zebrafish larvae are used to study innate immune responses as the adaptive immune system is not active until approximately one month of age. Using zebrafish larvae, we study the roles neutrophils have in controlling IAV infection and how over-activation of neutrophils during IAV infection trigger a damaging hyperinflammatory response. During the inflammatory response, reactive oxygen species (ROS) are produced and released by NADPH oxidase 2 (NOX2) in neutrophils through the respiratory burst response. We hypothesize that reducing the respiratory burst response will limit tissue damage and improve survival. Using RNA sequencing, we found that the oxidative stress response pathway was upregulated in IAV-infected larvae compared to uninfected controls at six hours post infection. We found that treatment with the NOX2 inhibitor, GSK205739, improved survival and the capacity of larvae to generate ROS in IAV-infected larvae compared to controls. These and other studies will help us identify how to limit hyperinflammation during IAV infection.

Manikandan Palrasu, Dept of Pathology, Microbiology and Immunology, School of Medicine, University of South Carolina. **Aryl hydrocarbon receptor transcriptionally regulates beta-defensin-1 and consequently suppresses colonic inflammation during colitis.** Co-Authors: Khadija Kakar, FNU Hamida, Amarnath Satheesh Marudamuthu, Tayler Carter, Kiesha Maria Wilson, Archana Saxena, Xiaoming Yang, Narendra P. Singh, Philip Brandon Busbee, Prakash Nagarkatti, Mitzi Nagarkatti. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine. COBRE
Ulcerative colitis (UC), a chronic inflammatory disease of the colon and rectum, increases the risk of developing colon cancer. The estimated prevalence of UC in North America is 0.4% of the population, with a yearly incidence of 15 per 100,000 people. Microbial, environmental, and host genetic factors are among the several etiologies of colitis. Antimicrobial peptides such as ï¡- and beta-defensins resist microbial colonization of epithelial surfaces in the intestinal or colonic tissue as well regulate mucosal immune response. Dysregulated immune response, often resulting from gut microbial dysbiosis and an impaired AhR (an important environmental sensor) signaling pathway, was recognized to contribute to the development of colitis. In the present study, we investigated how AhR activation regulates beta-defensin1 (BD1) in a murine colitis model. Here, we unexpectedly found that dietary Indole-3-carbinol (I3C), a ligand for the AhR was found to induce AhR and beta-defensin 1(BD1) in colonic epithelial cells isolated from colitis mice. Importantly, BD1 elevation upon I3C treatment was not observed in AhR-null mice, which were more prone to develop colitis, suggesting AhR regulates BD1. This observation was recapitulated upon I3C treatment in colonic cell line, MC38. Moreover, we identified Dioxin Responsive Elements (DREs) in the BD1 promoter which was involved in the upregulation of BD1 by AhR activated by I3C and demonstrated that elevated BD1 was sufficient to suppress colitis. Collectively, these results document a novel role of AhR activation in upregulating BD1, advancing our understanding of how an impaired AhR pathway contributes to the pathogenesis of colitis.

Steven Ionov, Dartmouth College. **Molecular Analysis of SARS-CoV-2 Vaccine Serum Antibody Repertoires in Individuals with Cystic Fibrosis.** Co-Authors: Seungmin Shin, Ruth Connor, Jiwon Lee. Co-Authors Institutional Affiliations: Dartmouth College, Dartmouth-Hitchcock Medical Center. COBRE

Viral infections in people with cystic fibrosis (CF) are associated with pulmonary exacerbations and accelerated disease progression. Though bulk serology data show that vaccines, including those against SARS-CoV-2, induce potent binding and neutralizing antibody responses, humoral and cellular adaptive immune compartments in CF are known to be dysregulated. To better understand vaccine responses in this population, we studied the composition and functional properties of SARS-CoV-2 Spike (S)-specific antibodies of 9 vaccinated individuals with CF. We performed high-resolution proteomics on serum antibodies combined with next-generation sequencing (NGS) of donor-matched B cells to identify and characterize individual antibodies in donor sera. We found that people with CF elicit a diverse S-specific serum repertoire comprised of 54-179 IgG clonotypes, and that antibodies targeting the receptor-binding domain (SRBD) make up the majority of the response. From six donors, we isolated 16 abundant monoclonal antibodies (mAbs), all of which bound Wuhan S with high affinity. Most mAbs bound broadly to the Delta and/or Omicron Variants of Concern, and half were reactive to the distant BA.5 variant. Though most mAbs were non-neutralizing, 4 SRBD mAbs neutralized Wuhan and variants, with IC50's as low as 60 ng/mL. Finally, several mAbs were nearly identical to those found in the B cell and/or serum repertoires of both CF and non-CF individuals, suggesting a convergent antibody response. In sum, our results describe a strong CF SARS-CoV-2 vaccine response at the monoclonal level and suggest that antibodies made by vaccinees with CF are similar to those made by non-CF individuals.

Metabolism and Obesity

Andrea Corcoran, Vermont State University - Castleton. **CBD in the landscape: Use tendencies and the need for low-dose human physiology studies.** Co-Authors: None. INBRE
Recent polls indicate that 14-33% of Americans have used hemp-based products such as cannabidiol (CBD). This non-psychoactive compound is one of 700 chemicals derived from the Cannabis sativa plant and is both legal and widespread for distribution in many states. Despite its prevalent use, few studies have examined the concomitant physiological effects that CBD may have on the cardiovascular and autonomic systems, particularly at recreationally-relevant doses. Additionally, given its rapidly growing popularity, exploring use tendencies and motivation across rural and urban regions becomes increasingly important. Using online surveys, we have been investigating reasons for CBD use, perception of efficacy, and reported use of CBD as an alternative to conventional medical treatment. There is a significant difference in the percentage of respondents who report using CBD as a substitute for medical treatment in rural (37.4%) versus urban (23.6%) respondents ($p < 0.05$). The most frequent reason for use among both rural and urban groups (35.9% and 34.4%) is muscle pain, which is a finding consistent with current literature. Human subjects studies using doses based on those reported by survey participants show that CBD does not appear to have appreciable effects on measured physiological variables (resting heart rate, blood pressure, and heart rate variability) in healthy young adults, though extrapolating these results to an older or unhealthy population should be cautioned. This work contributes to the framework of understanding potential therapeutic uses and/or risk factors of CBD, particularly as it relates to healthy individuals. Additionally, survey results highlight the issue of the use of CBD as a substitute for medical treatment, particularly in rural individuals. Our data supports the need for clinical research on CBD to determine whether it is an effective treatment for the ailments it is commonly used for.

Erica J. Johnson, University of Delaware. **Subcutaneous adipose arteries exhibit significantly less fatty acid uptake in obesity.** Co-Authors: Thanh Nguyen, Sabita Rokka, Caitlin Halbert, Ibra S. Fancher. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Obesity contributes to the development of cardiovascular disease. Arteries of visceral adipose present with endothelial dysfunction whereas subcutaneous adipose arteries remain functional in obesity. Obesity is

associated with elevated long chain fatty acids (LCFAs), contributors to endothelial dysfunction. CD36 facilitates LCFA uptake, which in excess, contributes to endothelial dysfunction. To determine if CD36 contributes to obesity-induced endothelial dysfunction in visceral adipose arteries, visceral and subcutaneous adipose arteries isolated from lean and obese WT and CD36 knockout were mounted for pressure myography. Visceral adipose arteries of obese mice exhibited blunted responses and subcutaneous adipose arteries remained functional. CD36 ablation restored vasodilation in visceral arteries of obese mice, suggesting a role for CD36 in obesity-induced endothelial dysfunction. We next examined endothelial CD36 expression using flow cytometry and immunofluorescence staining in mice and humans. For flow cytometry, arteries were digested and sorted to identify the endothelial cell population (i.e., CD45-CD31+ cells). In both experiments, an antibody that detects an extracellular epitope to CD36 was used to detect expression. Obesity did not alter the expression of CD36 expression in visceral adipose arteries relative to lean controls or subcutaneous arteries from obese mice/humans. Next, endothelial LCFA uptake was assessed at different time points. Subcutaneous arteries from obese mice had decreased LCFA uptake relative to lean controls which may be an underlying mediator for the dichotomy in endothelial dysfunction observed in obesity. Ongoing work in our lab is focused on determining if this is true and if this process is mediated by endothelial CD36.

Gary ZeRuth, Murray State University. **Gli-similar 3 is essential for proper pancreatic and kidney development in zebrafish.** Co-Authors: None. INBRE

The Krüppel-like protein, Gli-similar 3 (Glis3) is a transcription factor that has been implicated in several human pathologies including neonatal diabetes, congenital hypothyroidism, and polycystic kidney disease. Numerous genome-wide association studies (GWAS) have additionally identified Glis3 as a risk locus for the development of type 2 diabetes mellitus. Despite its clinical significance, much remains unknown about the role(s) Glis3 plays during development. In this study, we have characterized developmental expression of glis3 in the zebrafish (Danio rerio) and evaluated the effect of ubiquitous glis3 loss-of-function. In situ hybridization revealed that glis3 was expressed in the pronephros as early as 24 hpf and within the pancreas by 72 hpf. A mutant line of zebrafish that lacks glis3 expression was generated using CRISPR/Cas9 technology and homozygous mutants developed bilateral renal cysts by 15 dpf that progressed in severity with age. Additionally, the hepatopancreatic ductal system failed to undergo branching morphogenesis in glis3 mutants and this phenotype was coincident with a significantly reduced number of secondary pancreatic islets and defective blood glucose metabolism. RNA-seq analysis identified over 300 DEGs in the mutant larvae that included genes implicated in pancreas development, kidney disease, and maintenance of primary cilia. Our results identified novel roles for glis3 directing the specification of endocrine pancreas and anterior enteroendocrine fates from Notch-responsive progenitors along the pancreatic ductal epithelium. Glis3 KO fish could provide key insights into the pathogenesis of diabetes and provide an innovative model to study the mechanisms that promote polycystic kidney disease in the mature kidney.

Vitoria Mattos Pereira, University of Wyoming. **Inhibition of the Cysteine Protease Cathepsin K Attenuates Diabetic Neuropathic Pain.** Co-Authors: Cameron James Campbell, Sreejayan Nair. Co-Authors Institutional Affiliations: University of Wyoming. INBRE

Background and Aim. Diabetic peripheral neuropathy (DPN) is a painful and debilitating complication of diabetes that develops in 30-50% of diabetic patients. The drugs currently available to treat DPN lack specificity and only transiently relieve neuropathic pain. Recent studies demonstrated that the cysteine protease cathepsin K plays a critical role in the development of nociceptive pain. The present study was undertaken to assess the efficacy of cathepsin K inhibition in alleviating DPN. Methods. Five-week-old C57BL/6J mice were rendered diabetic through a single intraperitoneal injection of streptozotocin (STZ, 150 mg/kg), while the control animals received the buffer (n=10 per group). DPN was confirmed in diabetic mice using tactile allodynia test with von Frey filaments. Then, diabetic animals were challenged with a single

intraperitoneal injection of Cathepsin K inhibitor II (0.01 mg/kg, EMD Millipore # 21937). Data were expressed as mean Â± S.E.M and statistically evaluated using the paired Student t-test. Results. STZ injections induced diabetes in the mice as evidenced by elevated blood glucose levels (459.22 ± 35.8 mg/dL). Diabetic mice exhibited mechanical hyposensitivity as indicated by a twofold increase in the von Frey filament threshold (4.75 ± 0.54 g) relative to controls (2.76 ± 0.55 g, p â‰¥ 0.05, n=10). Treatment with cathepsin inhibitor II resulted in a complete reversal of the diabetes-induced mechanical hyposensitivity (2.42 ± 0.60 g, p â‰¥0.05). Conclusion. Inhibition of cathepsin K may represent a viable strategy to treat DPN. Funding Source: Institutional Development Awards (IDeA) from the NIGMS of the NIH under grant number P20GM121310.

Neuroscience

Adam C. Nelson, University of Wyoming. **The role of oxytocin neurons of the paraventricular hypothalamic nucleus in social thermoregulation.** Co-Authors: Joe Rogers, Morgane Vandendoren, Jason Landen, Samantha Killmer, Baizar Alamiri, Nicole Bedford. Co-Authors Institutional Affiliations: University of Wyoming. COBRE
Thermoregulation is vital for maintaining homeostasis, but is also associated with affective and behavioral states. Yet, how body temperature (Tb) is modulated by social interaction, and the underlying neural pathways, is poorly understood. We developed a paradigm and computational tools to determine the relationship between huddling behavior and Tb in adult mice. In female groups, but not male groups, huddling is associated with the lowest observable Tb and Tb-variance. At room temperature, but not at thermoneutral temperatures, active-huddling has a bidirectional effect on Tb: it is cooling prior to, but warming after, bouts of quiescent-huddling. Based on patterns of huddling-associated Cfos activity, we investigate oxytocin neurons of the paraventricular hypothalamus (PNVOT) as a mechanism driving social thermoregulation. We performed chemogenetic experiments using DREADDs and the ligand DZC at different ambient temperatures. In females, activation of PVNOT results in increased Tb and disrupted thermotaxis. In males, both excitation and inhibition of PVNOT results in decreased body temperature, with no effect on thermotaxis. Our results suggest the presence of multiple populations of PVNOT neurons controlling thermoregulation. In fiber photometry experiments, PVNOT neural activity correlates with both social condition and ambient temperature. Large calcium transients occur more frequently in paired and warm conditions, as compared to solo and cool conditions, and more frequently during quiescent-huddling compared to other behavioral states. Together, our results suggest that huddling substates acutely adjust Tb and point towards a role of PVNOT neurons in behavioral thermoregulation.

Haiyue Song, Department of Biostatistics, Brown University. **Leverage of Functional Connectivity and Effective Connectivity by Selective Inference with Sample Splitting and fMRI Data.** Co-Authors: Ani Eloyan, Youjin Lee. Co-Authors Institutional Affiliations: Brown University. COBRE
Effective connectivity research investigates whether and to what extent functional activity in one brain region directly impacts the physiological activity in other brain regions. One general approach for studying effective connectivity is the conditional Granger causality that applies a vector autoregressive model to time-series data from each brain region while conditioning on potential confounding time courses. In practice, however, it is challenging to select potential confounders in time-series settings. For example, the human brain consists of numerous regions, each of which can confound the causal relationships between other pairs of regions. This may render potential conditioning set in identifying effective connectivity between a pair of regions “possibly unnecessarily” high-dimensional. To address these challenges, we propose using the sample splitting method that leverages a measure used for functional connectivity to select conditioning time courses from one part of the data. With these pre-selected time courses in the conditioning set, we then apply the conditional Granger causality with the other part of the data to infer the temporal influence from one region to another. We

demonstrate, both in theory and simulations, that the proposed sample splitting is asymptotically valid under certain conditions, effectively controlling type-I error rates. We apply our proposed approach to the resting-state fMRI data from the Alzheimer's Disease Neuroimaging Initiative to examine the effective connectivity between the brain regions after controlling for potential confounding.

Khadija Kakar, University of South Carolina School of Medicine. **Protective Effects of Delta-8-THC Against EAE-Induced Enteric Neuropathy and Neuroinflammation through Regulation of miRNA-Mediated Signaling Networks.** Co-Authors: Urmi Halder, Manikandan Palrasu. Co-Authors Institutional Affiliations: Not Listed. COBRE
Multiple sclerosis has long been associated with neurological symptoms, yet the connection between neuroinflammation and enteric neuropathy remains understudied. To test the complex brain-gut connection, we administered delta-8-THCÂ (10mg/kg)Â i.pÂ into mice with Experimental Autoimmune Encephalomyelitis (EAE),Â an animal model of MS. We observed that treatment significantly reduced the clinical score and reversed the weight loss in treated groupÂ by suppression of proinflammatory Th1 phenotypes such as Tbet and IFN-g and increase anti-inflammatory phenotype such as Tregs and IL-10. miRNAseq analysis of brain infiltrating CD4+ cells revealedÂ that the decrease in neuroinflammation following treatment was associated with the downregulation of miRNAs,Â involved in Pyroptosis and Th1 pathway regulation. TheÂ EAE mice exhibit persistent gastrointestinal symptoms. To investigate bowel dysfunction miRNAseq analysis was performed for colonic and ileal tissues and contents. A highlyÂ dysregulated miRNA6538 was found in all four miRNAseq analyses.Â miRNA6538 downregulation in colonic and ileal tissues, along with ileal content in delta-8-THC-treated EAE mice, suggests a protective role against EAE-induced bowel symptoms while itsÂ upregulation in colonic content could be due to the shedding of cells as a part of homeostasis during cellular turnover. In summary, delta-8-THC's suppression of EAE involves a dual impact on the brain and gut, showing its potential as a therapeutic strategy for mitigating neurodegenerative disorders

Rural Health and Health Disparities

Emily Zeitler, Dartmouth Health. **Experience of Remote Monitoring of Cardiac Implantable Electronic Devices in Rural New England.** Co-Authors: Laure Bernstein, Jennifer Wenner, Nichole Rogovoy, Mark Creager, Karen Schifferdecker. Co-Authors Institutional Affiliations: Dartmouth Health. COBRE
Background: Remote monitoring (RM) of cardiac implantable electronic devices (CIEDs) is the standard of care to supplement in-person evaluation. However, little is known about the delivery and experience of RM care in rural areas. Methods: Semi-structured interviews were conducted with individual patients with a CIED and with physicians practicing primary care, cardiology, or cardiac electrophysiology (EP) in rural New England to elicit experiences with RM and facilitators and barriers to effective RM use. To date, 13 patients and 8 physicians have been interviewed. Results: Preliminary results from patient interviews show that patients identified RM as easy to use and that it instilled confidence in their care, with the primary barrier to RM being a lack of internet or phone connectivity. Non-EP physicians generally reported limited involvement or awareness of CIED care but understood how to access expert CIED and RM-related care through direct contact with CIED-trained physicians and staff of CIED management clinics as needed. Efficient and accessible CIED clinic managers were repeatedly identified by interviewees as being critical to the success of RM care. Conclusions: These findings suggest that effective CIED RM can be achieved in rural areas but there are opportunities to improve continuity of care by enhanced internet access or phone connectivity. Furthermore, supporting and fully staffing CIED RM clinics facilitates care for patients and communications with their non-EP physicians. This has important implications for other aspects of care delivery in rural geographies that depend on or would be enhanced by technology-based interactions.

Martha Rojo, University of Arkansas for Medical Sciences. **Hispanic Faith-based leaders' perspectives on healthy eating interventions in the Hispanic community.** Co-Authors: Hannah Aston, Johnathan Rodriguez, Erickson Feliciano, Carson Guatemala, Janet Lopez. Co-Authors Institutional Affiliations: Not Listed. COBRE
Introduction/Background: Childhood obesity has emerged as a significant public health concern in the US. While obesity has increased among all ethnicities, there is a notable disparity when comparing minority children, such as Hispanics, to their Caucasian counterparts. One setting that has been underutilized in addressing this concern is faith-based organizations (FBOs). Recognizing their unique role, we explored the prospect of leveraging these settings to combat childhood obesity, particularly in the Hispanic community. Methods: Using a mixed-methods approach, we conducted an online survey to reach faith-based leaders in a Southern state. We also conducted interviews to assess the feasibility of developing and implementing an obesity-prevention intervention in FBOs, employing purposive and snowball sampling techniques to enhance recruitment. The interviews, averaging 23 minutes, were conducted in Spanish or English. All were audio-recorded, transcribed, and uploaded to MAXQDA for data management. We utilized descriptive statistics and thematic analysis. Results: We received 52 completed surveys; 42% were from Catholic facilities, 15% Baptist, 15% non-denominational, 15% 'other' and 12% Pentecostal. Seventy-nine percent of church facilities had a kitchen, but only 8% offered cooking classes; 63% had outside space, but only 19% offered physical activity classes. All had Spanish-speaking staff on site. We completed 27 interviews. The main themes were (1) Feasibility of intervention, (2) Barriers to healthy food preparation, (3) Components of healthy eating interventions, and (4) Cultural considerations for improving healthy eating. Discussion: Faith-based leaders acknowledge childhood obesity as a problem and believe in the effectiveness of obesity-prevention interventions in FBOs. They made recommendations for developing such interventions.

Richard Riker, Maine Medical Center. **Evaluating Exception From Informed Consent Community Consultation Surveys Based on Measures of Rurality, Age, and Educational Level.** Co-Authors: Elizabeth Scharnetzki, Amanda Lessard, Catherine Feutz, David Seder, David Gagnon, Frank Chessa. Co-Authors Institutional Affiliations: MaineHealth. COBRE
The Exception from Informed Consent (EFIC) pathway for emergency research requires community consultation prior to initiating studies. Prior reports identify community consultation acceptance rates, but the impact of rurality on acceptance and attitudes toward EFIC have not been reported. Maine is the most rural state in the nation, representing an opportunity to evaluate this issue. A retrospective analysis of 1,704 deidentified community consultation surveys from two cardiac arrest studies evaluated EFIC acceptability and reasons for acceptability. Respondent zip codes were converted into two Rural Urban Commuting Area (RUCA) code classification schemes (WWAMI and Roundtable). Descriptive analyses, including Fisher's Exact test evaluated acceptability and selected reasons by RUCA scheme and category, age, and education level. Most respondents (92.7%) felt the EFIC pathway for research consent was acceptable, with similar rates between trials (96.6% vs 91.9%) which were higher than reported rates (86.5%). Neither RUCA classification scheme identified differing rates of acceptability (WWAMI: range 89.5-94.1% p=0.08; Roundtable: 85.7-100% p=0.41). Acceptability differed significantly as a function of age and education level, p

Women's Health

Leya Givvines, West Virginia School of Osteopathic Medicine. **Ovariectomy exacerbates plasma IgE and lung eosinophilia, but is not associated with greater vascular endothelial dysfunction in asthmatic mice.** Co-Authors: Abigail R. Patterson, Marina Diioia, Dovenia S. Ponnoth, Shinichi Asano. Co-Authors Institutional Affiliations: West Virginia Wesleyan College, West Virginia School of Osteopathic Medicine. INBRE
Sex is an important biological variable in cardiovascular disease (CVD). Females suffer from a more severe form of asthma than males, and recent clinical evidence suggests that female-specific asthma symptoms are

associated with increased CVD risk. However, the mechanisms underlying the sex specific pathophysiology of asthma associated CVD are unknown. The goal of this study was to determine whether ovariectomy (OVX) of mice with asthma alters blood biomarkers and vascular reactivity. We utilized an ovalbumin-induced asthma model in C57/BL6 mice which were randomly assigned to 4 groups: 1) sham female control (CON), 2) OVX CON, 3) sham female asthma, and 4) OVX asthma. In the lung, eosinophil population was higher in OVX asthma mice than sham female asthma mice. Similarly, the OVX asthma group had significantly higher plasma anti-OVA IgE (Sham asthma: 9 ± 2 vs. OVX asthma: 28 ± 2 ng/ml, p

Shyanna Larocque, Turtle Mountain Community College. **Fetal C-Reactive Protein rs1205 Genotype Is Not Associated with Maternal Pre-eclampsia.** Co-Authors: Crystal Azure, Hailey Davis, Craig Poitra, Jackie Poitra, Shayden Standish, Tyler J Parisien, Lyle G. Best. Co-Authors Institutional Affiliations: Turtle Mountain Community College. INBRE
Background and Purpose: Pre-eclampsia is a multifactorial obstetric complication, likely involving immune dysfunction; and annually results in approximately 60,000 maternal deaths, world-wide. We have previously identified rs1205 and two other C-reactive protein (CRP) gene variants, the maternal genotypes of which, are associated with the risk of pre-eclampsia (PE). These findings have been replicated in two non-American Indian populations. Most analyses of genetic PE risk assume that maternal genotype confers risk, whereas the fetal genotype may be determinative and the maternal genotype simply correlated with fetal genotype. Method: Relevant institutional IRBs and the Tribal Nations approved this research; and all participants provided informed, written consent. We enrolled only offspring of mothers known to be heterozygous for the rs1205 variant of CRP and experiencing either PE affected or normal pregnancies, thus eliminating the maternal genetic influence of this variant. Offspring were then genotyped using TaqMan assays to determine if fetal rs1205 genotype was associated with PE. Results were evaluated using standard chi-square and logistic regression tests. Results: Offspring of 26 of 36 normal pregnancies and 11 of 20 PE pregnancies carried the rs1205 T allele in a dominant genotype (Fisher's exact chi square p=0.192). Multivariate logistic regression analysis adjusted for maternal age, nulliparity and BMI resulted in an odds ratio of 0.433, p=0.210, 95% CI 0.117-1.603. Conclusion: Among 53 women, all heterozygous for the rs1205 allele, neither chi-square nor multivariate adjusted logistic analysis suggest an association between PE and fetal T allele dominant genotypes.

Lauren Covington, University of Delaware. **Socio-ecological Stressors Among Mothers Experiencing Socioeconomic Disadvantage.** Co-Authors: Destiny Mahmood, Kiara Shay, Emma Archer, Freda Patterson, Emily Hauenstein. Co-Authors Institutional Affiliations: University of Delaware, University of Virginia. CTR
Background: Parenting toddlers is stressful and for socioeconomically disadvantaged mothers, stress can be exacerbated by insufficient resources. We aimed to identify the experience of daily stressors, their severity, and the effectiveness of stress management strategies used by disadvantaged mothers over a two-week period.
Methods: We enrolled 54 mother-toddler dyads who were eligible for federally funded programs (e.g., WIC, Medicaid) into our Family Stress and Sleep study. Mothers completed two-weeks of daily electronic diaries reporting experienced stressors, their severity, stress management strategies and their effectiveness. We quantified reported daily stressors, their severity, management strategies and effectiveness. We used qualitative content analysis to assess mothers' overall stress experience. Results: Mothers (62% Black, mean age 33 ï‚± 5 years) reported school and/or work (22%), interpersonal issues (20%) and household management (10%) as their top three daily stressors. One-quarter of mothers rated their daily stress as moderate-to-high. Mothers described mindfulness techniques (25%, e.g., positive self-talk, meditation, breathing), distraction (20%, e.g., music, screentime, 'keeping busy') and self-care (15%, e.g., nap/rest, treat oneself) as their top stress management strategies, but reported only a 25% success rate in effectively decreasing their stress. Our

qualitative results indicate that the stressors mothers encounter are viewed as out of their control, and while they employed healthy coping strategies, they were not effective in decreasing their feelings of stress. Conclusions: Mothers of toddlers experiencing socioeconomic disadvantage feel stressed out daily. Healthy stress management strategies are not effective. Future work is needed to better understand how mothers are employing such strategies.

NISBRE2024

Poster Presentation Abstracts (ONLINE ONLY)

Organized by Poster Number

Posters are listed by assigned poster number. Please note that odd numbered posters will be presented on Monday, June 17, 2024 from 5:15 - 6:30PM ET and even numbered posters will be presented on Tuesday, June 18, 2024 from 5:15 - 6:30PM ET. All posters will be displayed in the International Ballroom. Please remember to vote for your favorite poster(s) in the NISBRE People's Choice Poster Awards available on the NISBRE app. Numerous award categories are available.

POSTER PRESENTATIONS

1. Maryam Khodaverdi, West Virginia Clinical and Translational Science Institute. **Bot Or Not: Machine Learning Approaches for Identifying Artificial Intelligence Bots in Online Survey Research.** Co-Authors: Kacie Kidd, Brad Price. Co-Authors Institutional Affiliations: West Virginia University. CTR Surveys have long been a tool for collecting cross sectional data and being a source of multidirectional bias. Transition from paper to online survey predominance has led to additional challenges including increased malicious respondents, particularly in the setting of incentivized survey instruments. The last two years have seen a marked rise in the accessibility of artificial intelligence (AI) platforms allowing bot masters to deploy volumes of human-like bot respondents in the hopes of receiving payment from researchers. This study identifies AI bots in online survey responses utilizing an approach combining machine learning and natural language processing. We implement bag of words approach and dimension reduction techniques on a widely distributed online survey (n=4,781) to define relevant, high frequency words. A Support Vector Machine Classifier with Adaptive Synthetic Sampling to deal with the high number of bots that are encountered in the survey. Results show that our method is able to identify bots with 97% total accuracy (n=957). Specifically, the method is able to identify bots with 99% and humans with 62% precision respectively. Our approach serves as a much-needed strategy for confronting a new era in online survey research wherein seemingly human AI bot respondents have the potential to fully disrupt data collection and interpretation, or worse, lead to false conclusions. Use of a machine learning algorithm as employed in this study to develop predictive analytics allowing for the reliable separation of human from AI bot may well be central to the future of online survey research.

2. Lorraine S. Evangelista, University of Nevada, Las Vegas. **Promoting community engagement and capacity building to address health disparities in diverse communities in the Mountain West Region: Experiences of the Community Engagement and Outreach Team.** Co-Authors: Reimund Serafica, Francisco S. Sy, Joseph Guerrero Lopez, Rebecca Palacios, Tony Ward, Jeffery Chaichana Peterson, Judith Owens-Manley. Co-Authors Institutional Affiliations: University of Nevada Las Vegas, Public Health Sciences at NMSU, University of Montana, University of Alaska Anchorage. CTR Introduction: Community engagement can increase health disparities research. Collaboration with the community promotes trust in researchers. The cultural and geographical diversity of the communities in the Mountain West Clinical and Translational Research Infrastructure Network (MW CTR-IN), consisting of 13 state universities from seven states, made community engagement and capacity-building

challenging. We describe the formation of the Community Engagement and Outreach Core, evaluate how it overcomes barriers to engaging and reaching diverse communities, and summarize factors essential to successful academic research-community collaborations. Methods: Three Regional Community Advisory Boards (CABs) were formed, with clearly defined roles and responsibilities to set the basis for team objectives, efficiency, and responsibility. Community participation in local activities was encouraged through regular meetings. A comprehensive community needs assessment and asset mapping provided essential resources and services to optimize networking, and facilitate development of community engaged research pilot projects. Results: Academic-community collaborations were established to effectively address the team's strengths, priorities, available resources, and needs. The team promoted open communication to improve transparency, accountability, and trust. They developed and implemented strategies to overcome challenges, negotiating and supporting research in community engagement, and establishing infrastructure for building practice-based research networks. Conclusion: Implementing a stakeholder engagement strategy that facilitates collaboration between CABs and academic researchers has effectively addressed challenges and potential solutions. It capitalizes on the combined knowledge and expertise of community and academic partners. The collaborations established over the past five years have effectively increased the research capacity of the community and academic partners in the Mountain West region.

3. Laura Enid Marrero-Jimenez, University of Puerto Rico at Cayey. **Role of diet modification on Chronic Ethanol Tolerance Development.** Co-Authors: Priscilla M. Gutierrez Ortiz, Enrique Rodriguez Borrero. Co-Authors Institutional Affiliations: University of Puerto Rico at Cayey. INBRE
Alcohol Use Disorder (AUD) is an extended global health challenge. Considered a brain disorder, AUD can be mild, moderate, or severe. Repeated alcohol consumption leads to the development of tolerance, expressed as a reduced response to a normally consumed dose of alcohol. Tolerance has been characterized as Acute, Rapid, and Chronic. It is speculated that prolonged exposure to alcohol over prolonged periods could be a leading factor in alcohol resistance development. Lasting changes in the brain caused by alcohol abuse perpetuate AUD and make individuals vulnerable to relapse. The Characterization of AUD in mammals has been extremely difficult because of complex genomes, behaviors, and physiological diversity within their brain. D. melanogaster serves as a powerful, inexpensive, and simpler model to study AUD. Our goal is to explore the impact of chronic ethanol exposure on tolerance development. Flies were exposed to 50% ethanol vapor for 5 consecutive days. Control flies were exposed to water vapor for 4 days and on the 5th, day were exposed to 50% ethanol, and the difference in sedation time and recovery time was scored. Our findings suggest that flies chronically exposed to ethanol develop higher ethanol tolerance when 1st exposure and 5th exposure were compared. Also, our preliminary data suggest that a High Protein Diet increases the sedation time during ethanol chronic exposure. Further experimentation will include other diet modification and microbiome disruption to study their influence chronic tolerance development.

4. Jacob K. Clerc, Presbyterian College. **Investigating the Unjamming Transition for the Development of a Soft-Robotic Gripper.** Co-Authors: Ashton J. Shannon, Eli T. Owens. Co-Authors Institutional Affiliations: Presbyterian College. INBRE
As innovations are made in the field of prosthetics, the quality/cost ratio continually increases. While opensourced prosthetics exist, most lack the ability to grip abnormal objects or require arduous coding efforts to do so. Therefore, there is a need for affordable prostheses that can perform everyday tasks. Various styles of grippers exist, including both hard-robotic and soft-robotic designs. Our efforts have been focused on a softrobotic design, particularly a â€œmalleable gripper.â€• This design autonomously conforms to objects of all geometries, and then grasps the object through the use of a granular material.

Granular materials exhibit properties of solids, liquids, and gasses; and they can transition between phases athermally. We can exploit this behavior by having our confined granular material conform to the shape of an object while in the liquid state. We then induce jamming to make the granular material solid and grasp the object. This has been previously accomplished with pneumatic grippers which jam the granular materials by removing the air from a membrane. Though useful, pneumatic designs can be cumbersome and sluggish which has led us to explore the advantages of magnetically induced jamming. We can take advantage of iron filings, which can be manipulated using a magnetic field, as our granular material. Solenoids can be used to produce magnetic fields which then pull the filings together causing them to jamâ€"gripping the object within the granular material. This project design furthers the affordability of prosthetics through the creation of a low cost, opensourced universal gripper.

5. Cody Casey, Coastal Carolina University. **Two new candidate alleles for TANGO2 in Drosophila melanogaster model.** Co-Authors: Jay DeLoriea, Paria Asadi, Djenann Saint-Dic, Michael Sacher, Chiara Gamberi. Co-Authors Institutional Affiliations: Coastal Carolina University, Concordia University. INBRE Rare autosomal recessive TANGO2 deficiency disease (TDD) affects over 8,000 people worldwide and results in intellectual and multi-organ neurodevelopmental delays, seizures and often lethal acute metabolic and cardiac crises induced by diet or stress. First reported in 2016, TDD is caused by mutations in the Transport and Golgi Organization 2 gene. Recent findings and the observations that TANGO2 orthologs have been conserved from humans to the fly, and possibly bacteria, implies that the TANGO2 protein may play vital, yet unknown cellular functions related to lipid metabolism. We have published a new Drosophila TDD model that recapitulates critical aspects of the TDD pathology and indicated that vitamin B5 rescued the TDD defect, that was confirmed in TDD-affected individuals. The only TANGO2 allele in Drosophila, TANGO2[G517], is caused by a transposon insertion that reduces TANGO2 mRNA expression by 97%. The effects of genes and corresponding phenotypes in health and disease are studied using key tools like mutant collections and allelic series. We used the CRISPR-Cas9 system to generate novel null alleles of TANGO2. Constructs expressing CRISPR, Cas-9 and TANGO2 guide RNAs under GAL4 control were introduced by genetic crossing to incite insertion/deletion damage at the TANGO2 locus. Three-hundred-and-twelve single fly knockout candidates were isolated and tested that yielded two deletion lines. Once fully characterized, the two candidate null allele lines will be instrumental in studying the TDD phenotypes, defining the molecular defects underlying the pathology, and eventually find cures for TDD.

6. Reece A. Garcia, Southeastern Oklahoma State University. **Protein and natural product characterization of redbud trees.** Co-Authors: Anna J. Ritter, Kaisey L. Jones, Asuncion Eleazar Rubio, Cooper McKinney, Nancy L. Paiva. Co-Authors Institutional Affiliations: Not listed. INBRE Redbud (Cercis canadensis) seeds and flowers were eaten by Native American tribes in Oklahoma and across the US, and the bark or twigs were used to prepare medicinal drinks. Previous studies in our lab have analyzed some of the properties of the proteins in these tissues, and we would like to isolate and analyze either genomic or cDNA clones encoding key proteins identified earlier, such as seed storage proteins, lectins, and condensed tannin- or anthocyanin-related biosynthetic genes. Here we emphasize our findings on the amino acid and total protein content of redbud seeds and anthocyanin content of flowers. Oven-dried immature beans were powdered and processed by 3 methods to measure all 20 amino acids and total protein. SDS-PAGE was used to characterize protein banding patterns, for comparison to commercial legumes. Redbud seeds contained 15-16%(w/w dry weight) total protein and were rich in most essential amino acids. Abundant protein bands at 65, 52, 35,17,18 kDa accumulate late in seed development. Amino acid profiles confirm that immature redbud seeds should provide a useful source of essential amino acids. Acetone extracts of young flowers were purified through reverse phase

(C18-Si) columns for the major pick/purple pigments, and analyzed by UV-Vis spectroscopy and LC-MS. Spectra were consistent with anthocyanins and their glycosides, which serve as beneficial antioxidants in human diets. Funding was provided by NIH/NIGMS award P20GM103447 for OK-INBRE Summer Intern and SMaRT Interns, NASA Oklahoma Space Grant Consortium, and Ronald E. McNair Post-Baccalaureate Achievement Program at Southeastern Oklahoma State University.

7. Brigette M Romero Carpio, University of Delaware. **Proteasome inhibitors dysregulate circRNA expression in human iPSC-derived cardiomyocytes.** Co-Authors: Grace Davis, Theresa Edery, Vijay Parashar, Chi Keung Lam, Mona Batish. Co-Authors Institutional Affiliations: University of Delaware COBRE

Cardiovascular diseases (CVD) are responsible for approximately 17.9 million deaths annually, establishing them as the leading cause of mortality worldwide. Circular RNAs (circRNAs) play a crucial role in the propagation and progression of CVDs, being five times more stable than linear RNAs. This enhanced stability renders circRNAs excellent candidates for diagnostic biomarkers and therapeutic targets. Our goal is to determine the expression levels of circNFIX and circZNF609 in human cardiomyocytes treated with different concentrations of proteasome inhibitors (PIs). CircNFIX and circZNF609 have been associated with acute ischemic heart disease and myocardial infarction, respectively. Total RNA was isolated from two iPSC-CM cell lines, and cDNA was synthesized from each sample. Each cell line was validated in triplicate, consisting of a control group (with no treatment) and six groups treated with different concentrations of proteasome inhibitors (Carfilzomib - 25 and 250 nM, Bortezomib - 25 and 250 nM, and Ixazomib - 25 and 250 nM). The expression level of circRNAs was measured by qRT-PCR using divergent primers. The fold change of the treated samples was calculated relative to the control, with 18S serving as the housekeeping gene for normalization. The expression of circNFIX and circZNF609 was significantly upregulated following treatment with Carfilzomib, Bortezomib, and Ixazomib in iPSC-CM cell lines. The highest doses of PI led to notable alterations in circRNA expression. Thus, reducing the expression of these circRNAs could potentially mitigate PI-induced cardiotoxicity by decreasing cardiomyocyte apoptosis and ROS apoptosis.

8. Derald E. Wentzien, Delaware State University. **The Creation of a Dashboard to Track the Accomplishments of the Research Capacity Core at Delaware State University.** Co-Authors: None. INBRE

AUTHOR: Derald E. Wentzien AFFILIATION: Delaware State University PURPOSE: The Research Infrastructure Core is an important component of any core supported by a grant designed to offer technical support and resources to researchers. The makeup of any Research Infrastructure Core varies between institutions and is based on the disciplines, skill sets and needs of researchers. In 2022 Delaware State University established an Interdisciplinary Health Equity Research (IHER) Center from a Research Centers in Minority Institutions (RCMI) grant. The Core was established to strengthen DSU's research infrastructure for biomedical, social and behavioral research related to health disparities and health equity. The Research Infrastructure Core, called The Research Capacity, is comprised of three cores, a Qualitative Research and Evaluation Core, a Microscopy Core, and a Cell Electrophysiology Core. Each core has a lead to manage the functionality and day-to-day operations of the cores. As the core director for the Research Capacity Core it is essential that an effective tool is used to compile the accomplishments of each core to facilitate easy tracking and reporting. METHODS AND RESULTS: Although Tableau and Power BI are powerful tools to create dashboards, an Excel dashboard was created to track the accomplishments of the three cores. Excel was selected since all research faculty are familiar with Excel and it was easy to create a separate sheet for each core based on their individual functionality. Each core lead is responsible for updating the information for their core. Linking the

sheets in an Excel dashboard provides one central location for easy tracking and updating. DISCUSSION AND CONCLUSION: The Excel dashboard was created based on a criterion of ease of use, effective presentation of the accomplishments, and usefulness in generative year end reports. Future use of the dashboard will be assessed to analyze the effectiveness of the dashboard.

9. Marla Berry, University of Hawaii at Manoa. **Consortium of Research Advancement Facilities and Training (CRAFT) at the University of Hawaii Precision Nutrition COBRE.** Co-Authors: Alexander Culley, Youping Deng, Alika Maunakea, Elaine Mirkin, Rachel Novotny, Lucia Seale, Joanne Yew. Co-Authors Institutional Affiliations: University of Hawaii. COBRE
To enable Precision Nutrition, access to the capabilities of multiple disciplinary fields is essential. CRAFT integrates new and established Core components under a unified administrative structure, providing a single point-of-contact resource offering multiple layers of â€˜omics and analytical approaches and tools enabling research in Precision Nutrition. CRAFT is overseen by an Executive Committee consisting of the COBRE PI, Program Coordinators and Core Directors. A centralized online portal catalogs users, services provided, costs incurred, and user satisfaction with service, education and training, providing timely and objective evaluation of Cores. Each core is allocated a baseline budget, with additional funding distributed annually among the Cores based on performance and need to maximize resource flexibility. This structure ensures long-term strategic planning that includes institutionalizing Core support beyond the end of the award period. Components of CRAFT include: Bioinformatics, data analysis, curation, management, and secure archival storage for high-throughput, large or complex datasets; Epigenomics, Genomics, Metagenomics and Transcriptomics; Metabolomics and Lipidomics; Histopathology; Confocal Microscopy, Scanning and Transmission Electron Microscopy; Flow-FACS; Dietary assessment tool development, Anthropometric analysis; Study design and statistical analysis; Metabolic Phenotyping; Analyses of functional respiration, glycolysis and Î²-oxidation; Cardiovascular function and Neurobehavior/motor function. Working alongside the Community Engagement and Outreach Core, CRAFT supports investigator interactions with community members including those affected by health disparities. This innovative approach extends the impact of CRAFT beyond the UH academic community and provides a novel model for Precision Nutrition.

10. Ryan Michael Taitano, University of Delaware. **Experimental Approaches to Quantify the Influence of Pathological Hemodynamics On Astrocyte Dysfunction.** Co-Authors: John Slater, Sam Freeman, Rishahbh Singh. Co-Authors Institutional Affiliations: Not listed. COBRE
Dementia has been estimated to affect up to 7% of individuals above the age of 65 years worldwide, and up to 8-10% in developed countries. With rising health care costs and no known cure, there is a critical need to understand the potential mechanisms. Recent evidence suggests that age-related stiffening of the large elastic arteries is a major contributor. Under normal conditions, elastic arteries dampen the pulsatile flow from the heart resulting in non-pulsatile, continuous flow in cerebral microvasculature. Arterial dampening diminishes with age-related stiffening, resulting in pulsatile flow and higher pulse pressures in cerebral Âµvasculature leading to brain injury. While most hypotheses focus on shear-induced injury mechanisms, endothelial cells and neurons are also sensitive to strain. Therefore, we hypothesize that induction of cyclic strain due to arterial stiffening can result in astrocyte dysfunction. In this study, we developed an in vitro microfluidic hydrogel model, with collagen and poly-ethylene diacrylate (PEGDA), to recapitulate a cylindrical blood brain barrier (BBB). Using this platform, we first encapsulated hippocampal astrocytes (HAs) into the base hydrogel and investigated their viability in response to mechanical strain controlled by a pneumatic pressure controller. Specifically, we characterize the vessel diameter strain and 3D hydrogel strain as a function of applied pressure in cyclic

and continuous forms in both collagen and PEGDA devices. Additionally, we investigate the HA viability in response to the different pressure conditions and as a function of distance from the microvessel.

11. Ricky Wiggins, Jr., Louisiana State University Health Sciences Center-Shreveport. **Advancing High-Capacity Flow Cytometry: Development of Antibody Tracking and Sharing Software for Efficient Cost Sharing and Collaboration.** Co-Authors: Sushma Bharrhan, Jian Wang, Marcin Sypniewski, Rona S. Scott, Matthew D. Woolard, Andrew D. Yurochko. Co-Authors Institutional Affiliations: Not listed. COBRE
Advancements in flow cytometry technology have enabled a growing array of antibody and fluorochrome combinations for scientific inquiry. However, this expanded capability brings technical and financial challenges. The upfront investment in antibodies and panels can be prohibitive, discouraging experimentation. As more labs adopt flow cytometry, redundancy and waste in antibody use increase. Our solution, integrated within an immunophenotyping core facility, addresses these issues by facilitating cost sharing and easing financial barriers. We have developed a user-friendly computer program tailored to our campus environment for antibody sharing and tracking. This project uses a Python flask-based web application that aims to make managing a wide array of antibody and fluorochrome combinations much more accessible to access. Python is a popular choice based on its simplicity and extensive libraries. In addition, the program uses various web technologies such as HTML and CSS to meet user-friendly requirements and Flask, a lightweight modular microweb framework, to handle HTTP requests. The core component of this web application is the MySQL relational database that stores the antibody information in tables that are connected via logical relationships. The application uses refined search capabilities to allow the user efficient navigation through all the combinations of entities in the database with relative ease. This program streamlines antibody identification and usage monitoring, benefiting the core facility and individual researchers. Moreover, our system is adaptable for broader use, serving as a cataloging and sharing tool for laboratories seeking efficient antibody management and collaboration within their institutions.

12. Jesse J. Halverson, Mayville State University. **Ecology and Blood Feeding Preferences of Mosquitoes in Traill Co., ND.** Co-Authors: Madisen Knudsvig, Gavin Bohlman, Taylor Painter, Keylim Rivera, Joseph Mehus. Co-Authors Institutional Affiliations: Mayville State University. INBRE
Mosquito feeding preference is a key component to understanding disease transmission patterns not only locally, but worldwide. As an example, when West Nile virus entered the United States, the public at large was unaware of the vectors of the virus, but also did not understand how a â€œbird virusâ€• was making its way into human hosts. This project investigates host feeding preferences of local mosquitoes. Mosquito collections began the first week in June, 2022. Using CO2-baited Sentinel and Mosquitaire traps, a total of 46,021 mosquitoes were collected, of that 734 (~1.6%) were engorged. Aedes vexans represented 497(67.7%), and Culex tarsalis represented 109 (14.8%) of the total engorged mosquitoes. Approximately 300 bloodmeals were selected to be sent to UND for molecular identification; to date 85 samples have been identified to species though PCR. Most samples selected for PCR were species other than Ae. vexans and Ae. excrucians as previous studies have shown preference for White-tailed Deer (Odocoileus virginianus). Of the 85 hosts identified so far, 40 (47.1%) were collected from rural, wooded or farmstead sites. The remainder of the bloodmeals were from mosquitoes collect in and around Mayville, North Dakota. Thirty of the 85 samples were found in floodwater mosquitoes; 55 from standing water mosquitoes. All bloodmeals originating from floodwater mosquitoes were from mammals (White-tailed Deer, Eastern Cottontail, Goat), while the standing water mosquitoes demonstrated a high diversity of hosts (White-tailed Deer, Cow, Sheep, Human, American Robin, Green Heron, Common Grackle, Chipping Sparrow, American Crow, Mourning Dove, and House Wren).

13. Keshab Subedi, CHRStianacare Health System. **Risk Factors and Implications of Leaving Without Treatment from the Emergency Department.** Co-Authors: Keshab Subedi. Co-Authors Institutional Affiliations: Not Listed. CTR

Background: Patients who leave without treatment from ED may experience delayed diagnosis and treatment. Multitudes of hospital and patient-level factors and circumstantial conditions could affect the patient's decision to leave without treatment from ED. Objective: We aim to identify and quantify the effect of patent- and hospital-level factors on the likelihood of leaving without treatment (LWOT), and to evaluate the effect of LWOT on ED recidivism and inpatient admission. Methods: This is a retrospective analysis using the data from the electronic health records (EHR) of patients presented at three EDs of Christiana Care Health Systems from 1 January 2020 through 30 August 202. Logistic regression models and Random Forest models were fit to estimate the effect of several factors on LWOT, and to identify the most important predictors of LWOT. Results: There were 267,845 ED encounters during the study period with a LWOT rate of 4.96%. Diagnosis of COVID-19, insurance: self-pay, arrival mode: police, door-to-doctor time, and number of ED visits in the prior 30 days were the top five predictors of LWOT. Compared to the patients with commercial insurance, the odds of LWOT were 2.65, 1.98, and 1.37 times higher among patients without insurance coverage, patients with Medicaid, and patients with Medicare, respectively. An hour increase in daily median door-to-doctor time was associated with 82% increased odds of LWOT. Conclusion: Door-to-doctor time is the most important modifiable factors associated with LWOT. System level interventions aimed at improving patient flow and reducing the ED wait time are important to improve LWOT rates.

14. DaShan Osborne, Delaware State University. **Effects of aging on cholinergic synaptic release in the central nervous system DaShan Osborne and Hakeem Lawal Neuroscience Program, Department of Biological Sciences, Delaware State University Dover, DE.** Co-Authors: Hakeem Lawal. Co-Authors Institutional Affiliations: Delaware State University. INBRE

Acetylcholine (ACh) is a ubiquitous chemical found in both the central nervous system (CNS) and peripheral nervous system (PNS). In the CNS, ACh is synthesized in the cytoplasm of cholinergic neurons and stored in synaptic vesicles. Vesicular Acetylcholine Transporter (VAChT) is a protein that transports ACh from the cytoplasm to the synaptic vesicles. Despite the wealth of knowledge regarding the regulation of ACh synaptic transmission, including the fact that cholinergic decline is an important feature of aging, not much is understood about how cholinergic release is mediated late in the lifespan or the role of VAChT in that process. We are interested in systematically determining how ACh synapses are altered during aging, and what role changes in expression or function of VAChT may play in that process. Here we use Drosophila melanogaster as a model, and immunohistochemistry to visualize age related changes in the expression of VAChT, as well as changes in its localization to synaptic vesicles relative to the plasma membrane. For this study, Drosophila were separated into 3 age groups (0-7 days old; 28 days old; 56 days old), as well as male and female, per age group. The brains were dissected and visualized under a fluorescent microscope. Data from this study are still in the gathering stages. We hypothesize that there will be a change in the expression and localization of VAChT as the neurons age. Future studies will focus on synaptic physiology, and how agerelated changes and the overexpression of VAChT, affect synaptic vesicle localization and synaptic transmission.

15. Timothy E. Burdick, Dartmouth Health & Geisel School of Medicine. **Adding geocoded social determinants of health to the EHR and data warehouse.** Co-Authors: Jennifer A. Snide, Mathan M. Thillaiyapillai, John F. Duggan, Dustin S. Ray. Co-Authors Institutional Affiliations: Dartmouth Health. COBRE

The Dartmouth Health COBRE (Rural Healthcare Delivery Science) Statistics, Informatics, and Qualitative Methods Core recently added geocoded social determinants of health (SDoH) data to the electronic health record (EHR) and to the enterprise data warehouse (EDW) at the individual patient record level. From the patient home address (street address, city, state, and 5-digit zip code), we could generate a 9-digit zip code. The 9-digit zip could then be linked to community-level SDoH data. Specifically, we added to each patient record three indices: (1) Area Deprivation Index, (2) Social Deprivation Index, and (3) Social Vulnerability Index. Similarly, we linked patients to a rural-urban commuting area (RUCA) code. By querying the EDW, we can provide researchers information about the community associated with the patient address, including composite measures of rurality, economy, education, housing, food access, and other SDoH. The community SDoH can be correlated with clinical measures such as diabetes control, cancer stages, lung disease, and health care delivery utilization.

16. Erica Ashley Farris, University of Wyoming. **Myeloid Iron TfR1 Uptake Effect on Infection Behavior and Dissemination.** Co-Authors: Tathagato Roy, Jason Gigly. Co-Authors Institutional Affiliations: Not Listed. INBRE

Toxoplasma gondii (T. gondii) infection is a major health concern for the developing fetus and people with compromised immune systems. T. gondii disseminates to the heart and brain where it encysts into a chronic infection for life. The myeloid compartment includes innate immune cells important for early control of infection. Myeloid cells also regulate host infection behavior or ability to resist the infection. Evidence also suggests a role in T. gondii dissemination due to changes in cell motility and adherence. Factors regulating host infection behavior and parasite dissemination are unclear. Previous data from our lab demonstrates limiting host iron in vivo decreases infection behavior and increases parasite dissemination to the brain. Therefore, we hypothesize iron is critical for myeloid regulation of infection behavior and T. gondii dissemination. To test this hypothesis, mice whose myeloid cells lack the expression of the key host protein for cellular iron uptake, the Transferrin receptor 1 (TfR1) (LysMCre X TfR1 flox/flox, cMTfR1KD) were infected with T. gondii. We measured infection behavior parameters: body temperature, blood glucose, weight, sickness score, and survival in cMTfR1KD compared to wild type controls (WT). Brain T. gondii cyst burdens were also measured. We did not detect differences in infection behavior between cMTfR1KD and WT animals. However, we observed female cMTfR1KD mice had higher cyst burdens compared to female WT, male cMTfR1KD, and male WT mice. Our findings reveal myeloid TfR1 iron uptake does not impact infection behavior, yet, does impact parasite dissemination only in females.

17. Kurt Wulser, University of Nebraska-Lincoln. **Nebraska Center for Integrated Biomolecular Communication (NCIBC) - Systems Biology Core Facility (SBC).** Co-Authors: Adam Caprez, Darcy Cochran, Jared Hass, Micah Jeppesen, Martha Morton, Robert Powers, Jean-Jack Riethoven, Kurt Wulser. Co-Authors Institutional Affiliations: University of Nebraska-Lincoln. COBRE

The Nebraska Center for Integrated Biomolecular Communication (NCIBC) Systems Biology Core Facility (SBC) has been strategically designed to: 1.) Enhance existing technology and enable the application of omics and instrumentation methodology among users. 2.) Provide the necessary skills, tools, and training for systems biology analysis by investigators and other core facility users. Thus, SBC is expected to enhance infrastructure in an area of critical importance to NCIBC researchers requiring streamlined access to lipidomics, metabolomics, proteomics, chemical analysis and structural biology instrumentation and techniques, and statistical and bioinformatics methodology. SBC is a collaborative core facility that works closely with investigators to help them achieve their scientific goals, therefore SBC is much more than a service facility. The SBC facility provides analytical instrumentation that includes nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry, and expert services

to researchers from both academia and industry. Samples that SBC can be expected to handle include: 1.) Life and food sciences such as plant/ animal cells lysates, serum, urine, and micro-organisms such as bacteria, and yeasts, and food and beverages. 2.) Chemical and material sciences such as synthetic and natural compounds, polymers, rare-earth materials, nanoparticles, and nanofibers. 3.) Electrical engineering, chemical engineering, biomedical engineering, physics, and mechanical engineering. 4.) Assistance with experimental design, new methodology development, and troubleshooting existing projects. The core has also been actively participating in undergraduate/graduate training and outreach education programs. The goal of NCIBC SBC is to enhance collaboration amongst faculty while enabling projects to adopt new technologies. Staff member train users and also collaborate on projects to enhance research and broaden research skills. Acknowledgements: The Nebraska Center for Integrated Biomolecular Communication (NCIBC) is supported by NIH NIGMS P20 GM113126.

18. Jefxander Carrasquillo-Villafañe, Ana G. Mendez University, Carolina Campus. **Perspective of high school students, teachers, and parents on academic performance during the COVID-19 school lockdown.** Co-Authors: Nilda G. Medina Santiago. Co-Authors Institutional Affiliations: Ana G. Mendez University. INBRE
The COVID-19 pandemic caused many changes in students' educational experience, such as relying on distance learning, as well as teacher and school staff shortages. It is important to understand the challenges that these students went through on their day-to-day basis regarding their performance in school before, during and after the lockdown. The main goal of this research is to explore the perspective of children, teachers, and parents on academic performance of high school students in the context of the confinement due to the pandemic. Therefore, the initial objective of the study was to develop a set of questionnaires as a preliminary step to explore the challenges that the children, teachers, and parents must deal with regarding the academic performance of the students due to the confinement of the pandemic. Three questionnaires were developed for each group (Parents, Teachers, and Students) consisting of approximately 12 to 15 items, depending on the group, focusing on motivation, educational barriers, grades, attendance, involvement, and communication. They were evaluated by 6 judges, including teachers, psychologists, and parents, and their recommendations were incorporated in the final versions. Questionnaires will be administered during recruitment via social media, email, and in-person. As future work, descriptive analysis will be performed with the data collected about the experience of managing these challenges and how participants believe it has affected academic performance. The results of this study may contribute to develop innovative ways for parents, teachers and even students to better approach these challenges during similar situations in the future.

19. Irina Kirpich, University of Louisville. **Bioactive lipid mediators in alcohol-associated liver disease: potential therapeutic targets and biomarkers of disease severity.** Co-Authors: Dennis Warner, Craig McClain. Co-Authors Institutional Affiliations: University of Louisville. COBRE
Background/Aims: Alcohol-associated liver disease (ALD) is a global healthcare challenge. Mechanisms and mediators of ALD development/progression are not well-understood and effective therapeutic options are limited. Various bioactive lipid mediators have recently emerged as important factors in ALD pathogenesis. The current study aimed to examine alterations in lipid metabolites, specifically linoleic acid (LA)-derived oxylipins, in heavy drinking individuals with and without liver injury, and to evaluate associations between these molecules and markers of liver injury and systemic inflammation. Our ultimate goal was to identify candidate lipid mediators/pathways for their potential to serve as biomarkers of clinical diagnosis/prognosis. Methods: Plasma oxylipin analysis was performed in heavy drinking individuals without (n=15) or with mild ALD (n=33), 18 patients with moderate alcohol-

associated hepatitis (mAH), and 29 socially drinking but otherwise healthy volunteers. Results: Lipoxygenase-derived metabolites, 13-HODE and 13-oxoODE, were markedly elevated only in mAH patients. The CYP450-derived epoxides, 9,10-EpOME and 12,13-EpOME were decreased in all patients regardless the presence or the absence of liver injury. Oxylipins derived via soluble epoxide hydrolase (sEH) pathway, 9,10-DiHOME and 12,13-DiHOME, were elevated in the mAH group compared to patients with mild liver injury. Multivariable regression analysis in mAH revealed that 13-HODE and 12,13-EpOME (elevated and decreased, respectively), in combination with elevated IL-1Î² as independent predictors, can effectively predict altered liver function as defined by elevated bilirubin levels. Conclusion: The current study provided evidence that specific changes in LA-derived oxylipins can differentiate mild ALD from more severe ALD stage, and identified sEH as a potential pathogenic pathway in ALD.

20. Katherine Muksuris, West Virginia University. **Noninvasive Neuromodulation for Parkinson's Disease: Insights from animal models.** Co-Authors: Mariya Cherkasova. Co-Authors Institutional Affiliations: West Virginia University.
Parkinson's Disease (PD) is a debilitating neurodegenerative movement disorder that affects over 6 million people worldwide. The loss of dopamine producing neurons in the substantia nigra pars compacta (SNc) results in the cardinal motor symptoms of PD such as bradykinesia, rigidity, and tremor, with nonmotor functions, such as mood and cognition, also frequently affected. Dopamine replacement therapy is the mainstay treatment for PD. Among adjunctive treatments, noninvasive neuromodulation approaches have been investigated. We will present an overview of the following noninvasive neuromodulation treatments that have been investigated for both motor and nonmotor symptoms of PD: transcranial magnetic stimulation (TMS), transcranial direct current stimulation (tDCS), electroconvulsive therapy (ECT), and focused ultrasound (FUS). The overview will focus on the evidence of efficacy in human patients, as well as the putative underlying mechanisms of these forms of neuromodulation gleaned primarily from studies in animal models of PD. These mechanisms include the preservation of the integrity of SNc neurons, increases in neurotropic factors in the SNc and striatum, and anti-inflammatory and antioxidant effects which may contribute to the preservation of neurons in the SNc. The implications of these findings for further research and clinical practice will be discussed.

21. Christopher Lee, University of South Carolina. **Reducing diagnostic barriers of Trypanosoma cruzi using convolutional neural network applied image classification in blood smears captured through mobile phone images.** Co-Authors: Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina. INBRE
Chagas disease, caused by the parasite Trypanosoma cruzi (T.cruzi), is a significant public health challenge in endemic regions with an estimated 70 million at-risk of acquiring incident disease. Traditional diagnostic methods are non-specific requiring specialized equipment and multiple testing platforms thereby making them inaccessible in low-resource areas. This study proposes a novel smartphone-based acute disease screening method for biological samples that could be employed in resource limited areas to bridge the gaps leading to missed diagnosis. Specifically, we propose a novel convolutional neural network (CNN) architecture for the automated classification of T.cruzi in blood smear images. Utilizing deep learning, this model distinguished between positive and negative parasitemia incidences with high accuracy and minimized error. The dataset was composed of augmented thin blood smear microscope images, totaling 2,718 positive and 3,180 negative images. The developed custom CNN model included four convolutional blocks with increasing complexity filters, dropout regularization, and a final fully connected layer for binary classification. A stratified shuffle split approach was taken for data partitioning, the Adam optimizer and a ReduceLROnPlateau learning rate scheduler was used to optimize the training process. The results indicate that the CNN model achieved a

robust performance with an accuracy of 91.26%, precision of 86.67%, recall of 95.76%, and an area under the ROC curve of 0.94. These findings support the utility of this deep learning architecture as an effective tool for acute Chagas disease diagnostics, offering a scalable solution to augment clinical decision making and potentially reduce the misdiagnosed burden of this neglected tropical disease. These results warrant future field adaptation studies.

22. Peter R. McDonald, University of Kansas. **Flow Cytometry Core: A Chemical Biology of Infectious Disease COBRE Core Laboratory.** Co-Authors: Robin C. Orozco, P. Scott Hefty. Co-Authors Institutional Affiliations: University of Kansas. COBRE
The University of Kansas Flow Cytometry Core provides access to flow cytometry and cell sorting instrumentation and expertise to researchers. Services and training are provided for flow cytometry: cell sorting and multi-parametric analysis of individual cells in solution, calculated from their fluorescent or light scattering characteristics. The FCC provides assistance in sample processing, data analysis, instrument training, software support, method and grant assistance, manuscript support, and consulting. The FCC is a 980 ft2 BSL-2 facility equipped with a BD FACSymphonyâ„¢ S6 Cell Sorter, a BD FACSAriaâ„¢ Fusion cell sorter, a Cytekâ„¢ Aurora Spectral Flow Cytometer, and other supplemental assay instrumentation. The Cytekâ„¢ Aurora full-spectrum flow cytometer enables tube-based and 96-well plate based spectral cytometry, with 5 lasers to allow analysis of 30+ colors. The BD FACS instruments allow measurement and sorting of up to 6 resolved populations of cells simultaneously, based on up to 50 parameters of detection using 18 simultaneous fluorochromes. The facility is equipped to handle BSL-2 samples and perform aseptic and single cell sorting into tubes or 96-well plates. The FCC will equip CBID researchers with tools directly applicable to infectious disease research, such as identifying and characterizing infectious agents such as bacteria and parasites, quantification and sorting of cells infected with microbial pathogens, and assessing chemical probe efficacy against infectious agents. The FCC resources enable monitoring immune responses and activation status associated with infection, and measuring changes in cellular phenotypes in response to compound treatment. The FCC seeks to assist collaborators in achieving their research goals.

23. Madison Olson, University of Wyoming at Casper. **Investigating Cardiac Function Through the Study of Myocardial Citrullination Patterns in Mice: Effects of Age and Gender on Cardiac Peptidyl Arginine Deiminase/PAD Expression.** Co-Authors: Chavely Cruz Cardenas, Mason Agor, Trevor Hible, Abby Boatman, Brian Cherrington, Danielle Bruns, Florence Teule-Finley. Co-Authors Institutional Affiliations: University of Wyoming at Casper, University of Wyoming. INBRE
Cardiac aging phenotypes, sex specific epidemiology, and clinical treatment outcomes are related to changes in how the aging process and how the heart interacts with testosterone and estrogen. Despite knowledge of differences in the cardiac aging process between men and women, the molecular mechanisms underlying the sex differences in cardiac aging remain unclear. Citrullination is a form of post-translational modification (PTM) that directly affects cardiac function by altering myocardial proteins, but it is relatively understudied. Citrullination converts arginine amino acid residues to citrulline using peptidyl arginine deiminase (PAD) enzymes. PADs have been widely studied in reproduction, but their expressions and functions in relation to aging have not been characterized. It is known that estrogen stimulates PAD2 expression while testosterone represses it, resulting in sex differences of citrullinated proteins. Preliminary data show that sex hormone regulation of PAD2 expression changes with age, thus resulting in sex differences in cardiac aging phenotypes. The purpose of this study is to gain an understanding of the role of citrullinated myocardial proteins relating to the differentiation of cardiac aging between both sexes, as well as the mechanisms of this hormonally driven process to evaluate if PAD-mediated protein citrullination leads to sex differences in cardiac aging.

24. Taren Swindle, Arkansas Children's Research Institute. **Center for Childhood Obesity Prevention-Community Engagement Core Services.** Co-Authors: Anna Huff Davis, Sharon Sanders. Co-Authors Institutional Affiliations: Not Listed. COBRE

The Center for Childhood Obesity Prevention Community Engagement Core (CCOP-CEC) provides services and activities to support CCOP investigators and other child health focused investigators in effectively engaging communities in their research. The CCOP-CEC aims to develop infrastructure for the Core, provide child health focused CE services to investigators, and build the CE research capacity of investigators and community partners. Services offered through the Core include but are not limited to consultations, community connections, capacity building for CE research, and recruitment support. The Core developed training programs such as the CE 101 Workshop, CE 201 Workshop, CE 101 Bootcamp, and the Dos and Don'ts of CE Workshop for child health research (adapted by the University of Arkansas for Medical Sciences Translational Research Institute CEC) to facilitate community connections and build capacity for CE research. The Core also launched a digital toolkit for investigators, monthly Community of Practice, Bidirectional Experience (windshield tour), and the Give-Get-Grid workshop to enhance community-academic partnership collaborations (adapted from the Kellogg Foundation's Community Partnerships for Health Professions Education Grant). Since 2021, the CCOP-CEC observed a 150% increase in CCOP investigators utilizing CE services and approaches. The Core has provided 14 CE consultation services for research projects which yielded outcomes of eight recruitment activities, 12 qualitative interviews, and 17 community connections for investigators. The CEC collaborates with a highly engaged 15-member Community Advisory Board quarterly and established relationships with16 additional resource partners (community and academic) across the state of Arkansas which has leveraged the success of multiple CE efforts.

25. Gian DePamphilis, Butler Hospital. **Puff, Puff, or Pass? The use of Tetrahydrocannabinol (THC) During Repetitive Transcranial Magnetic Stimulation (rTMS) for Treatment Resistant Depression (TRD).** Co-Authors: Eric Tirrell, E. Frances Kronenberg, Noah Vaughan, Lauren Hindley, Megan Vigne, Joshua Brown, Andrew M. Fukuda, Linda L. Carpenter. Co-Authors Institutional Affiliations: Butler Hospital, McLean Hospital. COBRE

Repetitive transcranial magnetic stimulation (rTMS) is an effective treatment option for individuals with treatment resistant depression (TRD). Although depression is among one of the most common reasons for cannabis use, it is unclear whether these products have a positive, deleterious, or neutral effect on rTMS treatment outcomes. THC use forms were retrospectively collected via clinician interviews at the Butler Hospital TMS Clinic/Neuromodulation Facility, indicating 39 patients who self-reported intermittent/stable THC use throughout treatment (at least 3x/week). To investigate the influence of THC on clinical outcomes between users and non-users, a researcher blinded to treatment outcomes created a matched data set of 39 patients with no intentions to use THC during their course of rTMS. The matched controls were selected based on age, sex, baseline depression severity as measured by the Inventory of Depressive Symptomatology, Self-Report (IDS-SR) scale, and any history of past psychiatric hospitalizations or electroconvulsive therapy (ECT). Qualitative reports of nine adverse events potentially related to THC use throughout a rTMS treatment course were also gathered through medical chart reviews. Chi-square analysis revealed no association in response/remission rates between active users and non-users. Additionally, independent samples t-tests indicated no difference in percent IDS-SR improvements over a treatment course between groups. Results suggest active THC use likely does not play a role in the efficacy of this treatment; however, users and clinicians alike should approach concurrent THC and rTMS with caution given the adverse events that have been reported.

26. Maycie Schultz, University of Wyoming. **Investigating Cellular Gene Expression, Function, and Diversity Differences in 5xFAD Mice Using Single-Cell RNAseq (scRNAseq) Methodology.** Co-Authors: Derek Walton , Madeline Bershinsky, Albert Allotey, Jared Bushman, Qian-Quan Sun. Co-Authors Institutional Affiliations: Not Listed. COBRE
Listed as the 6th leading cause of death, Alzheimer's Disease (AD) is the most common form of dementia affecting 1 in 10 people over the age of 65. Although largely prevalent, little is known about AD onset. Here, pre-symptomatic 5XFAD mouse model was used to investigate early features of the medial Prefrontal Cortex (mPFC) and Anterior Cingulate Cortex (ACC). The ACC, which connects to the mPFC, has shown evidence in contribution to spatial cognition, navigation, and spatial processing. Thus, investigation of these regions may provide clearer documentation of memory system abnormality. In terms of the mouse model, 5xFAD mice contain five AD-linked mutations and mimic AD-phenotypes. Additionally, 5xFAD mice present early and progressive histological signs of AD including amyloid plaques, gliosis, and neuronal death.Using single-cell RNAseq (scRNAseq) methodology, mPFC and ACC single-cell samples are hybridized to probe pairs. During extension, unique barcodes, and unique molecular identifiers (UMIs) are generated and sequencing libraries analyzed. The scRNAseq data reveals a comprehensive view of cellular diversity, gene expression in specific cell types, and cell modifications by 5xFAD. Using this technique, key information involving differentially expressed genes and cellular function can be assessed between control and 5xFAD mice.

27. Ariana Negroni-Santiago, University of Puerto Rico. **Insights into Stomach Ulcers Treatment using H2S, Hemoglobin I, and Collagen Moiety.** Co-Authors: Juryanis Velez-Rodriguez, Nicolas I Bauza-Reyes, Cacimar A. Ramos-Alvarez, Juan Lopez-Garriga. Co-Authors Institutional Affiliations: Not Listed. INBRE
Studies have highlighted the therapeutic potential of modulating Hydrogen Sulfide (H2S) synthesis. But reliable measurement in living organisms remains a challenge due to stability, toxicity, and release control concerns. Stomach ulcers present an opportunity for H2S treatment. With the goal of uncovering potential physiological functions for ulcer treatment, this study aims to examine the structural changes of the MbFeIIISH2 complex within collagen, the reaction of HbI-SH2, and the formation of sulfuric absent groups. Hemoglobin I (HbI), sourced from the purification and characterization of Lucina pectinata's ctenidia through published methodology, was chosen as the protein for H2S delivery system. X-ray Absorption Spectroscopy (XAS) at the SLAC National Accelerator Laboratory was used to discern their molecular structures of the reactions of Human Hemoglobin (Hb), Equine Myoglobin (Mb), and HbI with H2S. Furthermore, diverse reaction sets involving Hb and Mb with H2S in different states were analysed at the Crystallography Center at the Hauptam-Woodward Institute at Buffalo, NY, for advanced analysis at the synchrotron facility at SLAC for X-ray analysis. Results reveal that encapsulating MethMb in liquid collagen has structural changes upon interaction with H2S, leading to SulfMb formation. On the other hand, protein crystallization attempts to study Sulf-Hb encountered resolution issues due to mosaicity. These findings provide insights into potential stomach ulcer treatments. Future plans include optimizing protein collection via E. coli expression and completing data analysis from XAS, along with crystallization method optimization.

28. Elizabeth Reisher, University of Nebraska Medical Center. **Untangling Rurality in Health Research: A Review of Definitions and Their Use in Electronic Health Record Research.** Co-Authors: Jerrod Anzalone. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. CTR
Rurality represents a complex interplay of demographics, economic resources, and population density. Rural populations have been described as facing health disparities, including access to care and differences in health outcomes. Varying definitions of rurality could result in differing outcomes in studies and impact the generalizability of findings to rural communities. This study aimed to identify how

rurality is defined in observational cohort studies using electronic health record (EHR) literature and understand gaps in addressing rurality in research. A literature search was conducted using PubMed to identify studies assessing rural populations using EHR or Real-World Data (RWD) from January 1, 2000, to October 31, 2023. 510 articles were identified and refined using text mining to select studies that only used patient-level EHR data, resulting in a total of 36 articles included in the review. Studies drastically varied in terms of how rural was defined. 10 provided no definition, 17 used Rural-Urban Commuting Area (RUCA) codes, 3 used the National Center for Health Statistics (NCHS) classification, 2 used the Federal Office of Rural Health Policy (FORHP) guidelines, 1 used the Census definition, 1 used the Office of Management and Budget (OMB) standards, and 2 used the Veterans Affairs Urban-Rural-Highly Rural classification. Many studies did not justify the selected rural definition, and several did not report the geographic unit used to assign residential rurality. Rural definition criteria vary widely; careful consideration of definition use is necessary to ensure rigorous study design.

29. Aditya Khanna, Brown University School of Public Health. **Integrated Network Analysis of RADx-UP Data to Increase COVID-19 Testing and Vaccination Among Persons Involved with Criminal Legal Systems (PCLS).** Co-Authors: Rosemarie A Martin. Co-Authors Institutional Affiliations: Not Listed. COBRE

Background: US criminal legal settings (CLS) have large COVID-19 outbreaks. Persons involved with CLS (PCLS) additionally experience significant barriers to health care upon release, returning to environments impacted by lower vaccine access, fewer testing facilities, medical mistrust, and higher COVID-19 prevalence. A complex interplay between individual, social network and structural factors drives adverse health outcomes, but their interaction is not routinely examined. Methods: To address this gap, we are leveraging two existing RADx-UP studies: (1) the Community Network Driven COVID-19 Testing Among Most Vulnerable Populations in the Central United States (C3) study which collected longitudinal social network data on testing, vaccination and health behaviors among PCLS in five US states; (2) the COVID19 Testing and Prevention in Correctional Settings (CTC) study that assessed mitigation strategies for PCLS in three US states. Using these data, we are parameterizing an agent-based network model (ABNM) to simulate interaction between the multilevel factors identified above. Anticipated Results: The proposed modeling will quantify the impact of network-level influences on COVID-19 testing, vaccination, and health behaviors among PCLS and their network communities. Building upon this analysis, an integrated, validated, dynamic ABNM platform will provide a basis to simulate counterfactual scenarios for COVID-19 testing and vaccination. Simulation output analyses will provide an assessment of the potential effects of interventions on testing, vaccination and COVID-19 incidence in PCLS populations and their networks. Discussion: : Through ongoing conversations with state public health departments and community-based organizations, we are building comprehensive tool for pandemic planning.

30. Caleb Esteban, Ponce Health Sciences University/Ponce Research Institute. **Metabolic Syndrome Risk among Hispanic Sexual Minorities in Puerto Rico.** Co-Authors: Alixida Ramos-Pibernus, Idhaliz Flores, Eddiel Hernandez-Lopez. Co-Authors Institutional Affiliations: Ponce Health Sciences University. CTR AIMS. This project aimed to describe the percent of participants with metabolic syndrome (as defined by the World Health Organization) risk and high risk, and to analyze significant differences in risk by sexual orientation (gay/lesbian vs. bisexual+) among Hispanic sexual minorities in Puerto Rico. METHODS. The team conducted a secondary data analysis using a quantitative method, cross-sectional design, from a pilot study. The analysis included data from 98 Hispanic LGB+ participants aged 21-40 years. Cardiometabolic risk was evaluated through standard measures using analysis of microalbumin in urine and a Lipid Panel. RESULTS. Homogeneity of variances was confirmed through Levene's test for equality of variances ($p > .05$). Independent-samples t-tests were performed. Results showed cardiometabolic

risk[*] and high risk[**] between the participants in the following measures: systolic pressure (32%*; 7%**), diastolic pressure (20%*; 23%**), microalbumin (4.6%*), LDL-P (16.2%*; 9.1%**), LDL-C (9.1%*; 1%**), HDL-C (49.5%*; 23.2%**), triglycerides (3%*; 3%**), cholesterol (14.1%*; 1%**), HDL-P (16.2%*; 9.1%**), small DL-P (12.1%*; 2%**), LDL (5.1%*), large VLDL-P (14.3%*; 5.1%**), VLDL size (15.6%*; 10.4%**), HDL size (31.6%*; 16.3%**), & LP-IR (14.1%*; 8.1%**). In addition, results suggested no significant differences by sexual orientation (gay/lesbian vs. bisexual+). DISCUSSION. Metabolic syndrome risk and high risk were found among the sample. However, the absence of significant differences in metabolic indicators based on sexual orientation challenges previous assumptions that bisexual+ individuals have higher risks. Still, it highlights the need to consider a more comprehensive set of determinants and mediators when assessing metabolic syndrome risk among sexual minorities, especially between the Hispanic population.

31. Michelle M Martinez Montemayor, Universidad Central del Caribe-School of Medicine. **Insights into the antimetastasis effects of ergosterol peroxide in triple negative breast cancer.** Co-Authors: Adriana Aponte Ramos. Co-Authors Institutional Affiliations: Universidad Interamericana - Bayamon Campus. CTR Triple-negative breast cancer (TNBC) is a highly aggressive subtype of breast cancer (BC) characterized by the absence of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor protein (HER2) expression. TNBC accounts for ~20% of all BC, and ~27% of TNBC patients are expected to relapse with distant metastases in lungs, and liver. Ergosterol peroxide (EP) is a compound isolated from the medicinal mushroom Ganoderma lucidum, with anti-tumor anti-proliferative activity against cancer cells. In this study, the effects of EP on cancer cell metastasis to the lungs and liver of mice injected with TNBC cells are reported. Female SCID mice (n=18/group) were injected with GFP-MDA-MB-231 cells (~1x10^6). Mice were divided into: vehicle or EP, received via oral gavage 10% ethanol and 90% corn oil, or 100mg/kg BW of EP, respectively. Upon euthanasia, lungs and livers were excised and stored in liquid N2. Organs were cleaned with 1X PBS and imaged using a fluorescence stereoscope. The intensity and area of the of the metastatic foci in the organs were quantified using ImageJ. Data analysis was performed in Microsoft Excel, GraphPad Prism and R software. Results evidence a highly significant (P

32. Taylor Kalgren, Western Kentucky University. **The relationship between cognitive factors and exposure to suicide on adolescent suicide ideation.** Co-Authors: Marlee Gieselman, Lauren Morris, Amy M. Brausch. Co-Authors Institutional Affiliations: Not Listed. INBRE
Rates of suicidal thoughts and behaviors have increased in adolescents (CDC, 2023). Exposure to suicide is a well-known risk factor for these thoughts and behaviors (Nanayakkara et al., 2013; Swanson & Colman, 2013). Cognitive factors have been studied as both risk (i.e., defeat) and protective (i.e., self-efficacy) factors (Kwok et al., 2023; Pollak et al., 2021). The current study examined the relationship between cognitive factors and exposure to suicide on adolescent suicide ideation. This study included 300 high school students from the South-Central United States (M age = 15.55, SD = 1.18). Most of the sample identified as White (72%) and heterosexual (82%). Participants were asked about exposure to suicide, cognitive factors, and current suicide ideation severity. It was reported that 29% of students knew someone who died by suicide, and 25% knew someone who attempted suicide and lived. Exposure to suicide was significantly and positively associated with suicide ideation, $b = 6.64$, $p < .001$. Defeat, entrapment, and self-efficacy all significantly moderated the relationships between exposure to suicide and suicide ideation. Grit was not a significant moderator. The study reveals that low defeat, low entrapment, and high self-efficacy do not significantly impact exposure and suicide ideation. Adolescents with these traits typically show lower suicide ideation in general which may explain our findings. Considering adolescence is a period early in life, grit may not serve as a protective factor due to a lack of

fully developed long-term goals/objectives. School counselors should address cognitive factors during counseling for at-risk students.

33. Ranjita Misra, West Virginia University. **Perceptions of COVID-19 Perceived Threat, Vaccine Uptake and Health Information Source among Rural Adults with Chronic Diseases.** Co-Authors: Sweta Mahato. Co-Authors Institutional Affiliations: West Virginia University. CTR
Background: The pandemic has amplified myths and misinformation that inhibits nonpharmaceutical COVID-19 preventive measures and vaccine uptake. This study explored the source of health information, perception of COVID-19 infection and severity (or perceived threat), and vaccine uptake in rural adults with chronic diseases. Methods: A convenience sample of 2117 rural adults participated in a statewide, community-based, brief COVID-19 educational intervention delivered by trained Health Navigators (11/2022 - 12/2023). Intervention included watching brief videos of trusted healthcare professionals (HCPs) addressing COVID-19 questions and vaccine concerns, followed by survey data collection. Health information sources, perceived threat and vaccine uptake were explored in the multinomial logistic regression. Participants were grouped (1) completed basic vaccine dose and â‰¥ 1 booster, (2) basic dose only, and (3) unvaccinated or didn't complete the basic dose. Results: Two-third (65.2%) of the participants reported vaccinated/boosted, 19.5% received the basic dose and 15.3% were unvaccinated. Participants relied on HCPs, online, and social circle for health information. However, 21% indicated social media/untrustworthy sources. Compared to vaccinated/boosted individuals, those who were unvaccinated & basic dose has a lower odds ratio of perceived threat ($p < 0.001$) and relied more on social media/unreliable online sources than HCPs (p

34. Victoria Murphey, Clemson University. **Assessing an actin binding protein, thymosin beta-4, as a novel treatment for Acanthamoeba keratitis.** Co-Authors: Luis Sanchez Ferrer, Anissa Waller Del Valle, Abagail Goff, Calvin Paulsen, Timothy Brinson. Co-Authors Institutional Affiliations: Clemson University. COBRE
Acanthamoeba castellanii is an amoeba that causes Acanthamoeba keratitis (AK), a serious eye infection characterized by severe pain, corneal damage, impaired vision, and blindness. In rare cases, the retina, brain, spinal cord, and skin can be infected. The parasite exhibits two life cycle forms: amoebae and cysts. Both forms are found in the eye during infection. Current treatment for AK consists of hourly administration of broad-spectrum antimicrobial drops. No single drug can eradicate both forms of the pathogen while also being non-toxic to eye tissue. Therefore, novel treatments for AK are desperately needed. Thymosin beta-4 (TÎ²4) is a cytoplasmic G-actin sequestering protein that promotes wound healing and tissue regeneration. A topical ophthalmic formulation of TÎ²4 has been shown, in clinical trials, to promote rapid healing in patients with dry eye syndrome and neurotrophic keratopathy. Thus, we hypothesized that TÎ²4 is a viable treatment option for AK. We developed an in vitro host cell destruction assay and found that TÎ²4 inhibited the destruction of human retinal pigment epithelial-1 (RPE1) cells by the parasite. We determined that TÎ²4 hindered encystation, but not excystation, in Acanthamoeba. TÎ²4 did not reduce parasite viability or increase the proliferation of RPE1 cells. Therefore, protection of the host monolayer was not the result of parasite death or over-proliferation of host cells. We are in the process of repeating these studies with human corneal epithelial cells. Overall, our data suggest that TÎ²4 may represent a novel treatment for AK.

35. Margaret C Walsh, The Miriam Hospital. **Technology, Assessment, Data, and Analysis Core.** Co-Authors: Chris Breault, Shira Dunsiger, Sara Vargas, Nicole Nugent, Beth Bock. Co-Authors Institutional Affiliations: The Miriam Hospital, Brown University. COBRE

The Technology, Assessment, Data, and Analysis (TADA) Core supports the COBRE for Stress, Trauma, and Resilience (STAR) in leveraging novel technological, methodological, research design and analytical approaches to enrich research projects and public health impact. The TADA Core provides support for an array of innovative and state-of-the-field methods for current and future Project Leaders, the STAR faculty recruit, and Pilot Project Investigators within the STAR COBRE. Specifically, the TADA Core offers unique expertise in leveraging technology for observational, laboratory, and intervention studies critical for (1) obtaining ecologically-valid data on stress exposures and behavioral and physiological responses, (2) novel approaches to digital phenotyping, and (3) electronically-delivered adaptive interventions. Technological innovations are rapidly progressing and the TADA Core provides a centralized resource for training and exchange of expertise about emerging technological approaches. The TADA Core houses specialized equipment (e.g., eye tracker) and software (e.g., Ilumivu, ArcGIS) that will expand over time to meet the needs of STAR investigators. The TADA Core also provides support for analytic assessments including mixed quantitative and qualitative methods, data management, electronic data capture, and sophisticated statistical analysis for longitudinal, complex data. Finally, the TADA Core is developing a unique repository of data from STAR COBRE projects that will be available for secondary publications and grant applications to serve as a resource for future investigators. Our long-term goal is to provide a sustainable resource to help investigators apply innovative and integrated methodological approaches, with matched analytic strategies to the study of stress, trauma, and resilience.

36. Alia Michaelis, Wichita State University. **Characterization of Cardiomyopathic Point Mutations in the Ig3 Domain of Myopalladin.** Co-Authors: Asha Rankoth Arachchnige, Julie Tran. Co-Authors Institutional Affiliations: Not Listed. INBRE

Myopalladin (MYPN) is a recently described actin-binding protein (ABP) located at the Z of striated muscle. MYPN is believed to act as an anchor to other structural proteins such as actin, nebulin, and titin, which work together to facilitate contractile motion at the sarcomeres of muscle cells. However, its specific role in regulating the actin-cytoskeleton is largely unknown. Previous studies in the Beck lab have shown that MYPN was capable of binding and cross-linking filamentous actin directly with its Ig3 domain; thus, allowing us to narrow our domain of study to solely Ig3 to further investigate actin binding affinity. The purpose of the study is to examine point mutations in the Ig3 domain of MYPN that have been previously associated with various types of cardiomyopathies (hypertrophic, dilated, and restrictive). In this study, we explore the following properties of MYPN: the F-actin binding affinity and bundling capacity via actin co-sedimentation assays and stability via circular dichroism. Throughout the study, a total of six cardiomyopathic mutations were investigated and compared to wild-type MYPN: C1002W, R1042C, P961L, F954L, R955W, and R955Q. Thus far, the general observation is that the mutagenic constructs of MYPN bind and bundle actin less successfully than wild-type MYPN and also show less structural stability. Further studies will aim to elucidate the role of MYPN in the context of the actin-cytoskeleton its potential link to cardiomyopathy.

37. Jean Christopher Chamcheu, Southern University and A&M College Baton Rouge, and Louisiana State University School of Veterinary Medicine. **Myeloid Cell-Specific Deletion of mTOR Suppresses Psoriasiform Disease in Imiquimod-Induced Skin Inflammation in Mice.** Co-Authors: JT Folahan, ST Boateng, T Roy, S Banang-Mbeumi, JT Folahan, RC N. Chamcheu, KG Kousoulas, AL Walker, S Patial, JC Chamcheu. Co-Authors Institutional Affiliations: Southern University and A&M College Baton Rouge, Louisiana State University. INBRE

The pathophysiology of psoriasis, an autoimmune skin disorder, that affects approximately 3% of the population worldwide, is incompletely understood. In this study, we investigated the role and contribution of mTOR signaling in myeloid lineage cells in regulating the pathogenesis and the systemic

inflammation associated with psoriasis. We first established a genetic mouse model in which mTOR was specifically deleted in the myeloid lineage cells using cre-lox technology and then tested the role of myeloid-specific mTOR in psoriasis using imiquimod (IMQ)-induced mouse model of psoriasis. mTOR myeloid deficient mice (mTORflox/flox/ LysMcre+/+; mTORmyeKO) and flox-only control mice (mTORflox/flox/ LysMcre-/-; mTOR floxed) were treated with IMQ for X days and psoriasis end-points were measured at day 6 after necropsy. Interestingly, mTORmyeKO mice exhibited less pronounced psoriasiform skin lesions, associated with decreased PASI scores, epidermal thickness, suppressed hyperplasia, parakeratosis, and dermal infiltratory immune cells compared to mTORfloxed mice that showed pronounced psoriasiform disease characteristics. Furthermore, we observed significant decrease in the levels of infiltratory activated helper T-lymphocytes, dendritic cells, and macrophages in the mice skin lesions when compared to control mice skin lesions. In summary, our data shows that ablation of mTOR in myeloid lineage cells confers resistance to imiquimodinduced psoriasis-like dermatitis in mice. Genetic or pharmacological targeting of the myeloid immune cells mTOR axes may help alleviate psoriasiform disease.

38. Juli Petereit, University of Nevada, Reno. **Fostering Institutional Data Science Awareness and Capacity: A Collaborative Approach at the University of Nevada, Reno (UNR).** Co-Authors: Nicole Falk-Smith, Josh Baker. Co-Authors Institutional Affiliations: University of Nevada Reno. INBRE
Gaps persist in addressing the complexities of managing, analyzing, and ethically handling large datasets, particularly in the life and health sciences and concerning human subjects research and cybersecurity risks. To foster a comprehensive understanding of data science, ethics, and risk management, Nevada INBRE implemented the Data Science Initiative. This initiative aims to enhance institutional awareness and capacity through a multifaceted approach. Leveraging a two-year Administrative Supplement (NOT-OD-23-123), the project will pilot initiatives designed to transcend departmental silos and promote best practices in data science. Central to this endeavor is a campus-wide assessment to gauge the current state of data science awareness, knowledge, attitudes, and resources. This baseline assessment informs the development of tailored training programs and resources. Collaborating across various entities within UNR, the initiative will draw upon diverse expertise in bioinformatics, machine learning, cybersecurity, ethics, and evaluation. Objectives include growing human capital with data science competencies through trainings and conferences, as well as expanding institutional capabilities to support data-driven research through the development of data science pipelines, expanded services within the Nevada Bioinformatics (NBC) and Cybersecurity Centers, and the creation of accessible resources for researchers. Sustainability beyond the grant period is ensured through the involvement of the NBC and NV INBRE's Data Science Core. Through this collaborative and holistic approach, NV INBRE aims to cultivate a culture of ethical and informed data science practice, enriching research endeavors and advancing institutional infrastructure to meet the demands of data-driven research.

39. Kaydyn M. Carr-Turner, Millsaps College. **Photochemical Key Steps in the Synthesis of Isoindolone Piperidines As Kinase Inhibitors: Asymmetric Photochemical Cyclization.** Co-Authors: Zoe O. Elder, Tynai J. Bridges, Caroline A. McKinney, Matthew G. Donahue, Wolfgang H. Kramer. Co-Authors Institutional Affiliations: Millsaps College, The University of Southern Mississippi. INBRE
Cancer cells are the result of disruption of tightly regulated metabolic pathways. This leads to uncontrolled proliferation of cells as seen in invasive tumors. Inhibition of certain metabolic enzymes thus might provide a tool to minimize the harmful effects of excessive cell growth. Two key phosphorylating enzymes, glycogen synthase kinase-3 (GSK3) and cyclin-dependent kinases (CDKs) are the target of researchers to interfere with cancer metabolism. Valmerins are isoindolone piperidines that

have been shown to inhibit GSK3/CDK enzymes during cell proliferation. In this project, we are using a photochemical cyclization method as a key step in the synthesis of GSK3/CDK inhibitors. The syntheses are initiated from affordable building blocks and should culminate in the stereo-controlled synthesis of the target molecules. Variations in the chromophore lead to the formation of regioisomers, the control of which is important. Electron-donating and electronwithdrawing effects of the substituents might direct the cyclization to one side of the imide. Acknowledgement: This work was supported by the Mississippi INBRE, funded by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM103476.

40. Kendall Moyte, University of Wyoming. **Peptidylarginine Deiminase (PAD) Expression in the Female Hippocampus During the Estrous Cycle.** Co-Authors: Pooja Gupta, William D. Todd, Brian D. Cherrington. Co-Authors Institutional Affiliations: Not Listed. INBRE
Citrullination is the post-translational modification of arginine residues in target proteins into the non-coded amino acid citrulline and is catalyzed by peptidylarginine deiminase (PAD) enzymes. Elevated PAD catalytic activity and resulting increases in citrullinated (cit)-proteins are observed in several neurodegenerative disorders including Alzheimer's disease (AD). In a mouse model of AD, PAD2 localizes to the hippocampus where it citrullinates amyloid-Î² peptides contributing to insoluble plaques. The PAD enzymes are also highly expressed in female reproductive tissues such as uteri and mammary glands. Within these tissues, estrogen stimulates PAD expression leading to fluctuating levels across the female reproductive cycle. Interestingly, the incidence of AD is higher in women as compared to men suggesting a hormonal component to AD; however, the underlying mechanism for this sex disparity is unclear. Given this, we hypothesized that PAD expression and concomitant changes in cit-proteins in the hippocampus across the estrous cycle may contribute to the increase in AD in females. To begin testing our hypothesis, we examined PAD2 expression in the hippocampus of wild type female mice at different stages of the estrous cycle. Our results show that PAD2 expression is higher in the estrus phase of the estrous cycle when serum estrogen is elevated as compared to diestrus. Future studies will use mass spectrometry to identify the citrullinome in the hippocampus of a mouse model of AD and wild type controls. Ultimately, our work could lead to the development of new therapeutic approaches such as PAD inhibitors to address the sex disparity in AD.

41. Elizabeth Woods, University of Vermont Larner College of Medicine. **Identifying Facilitators & Barriers to Cancer Clinical Trial Enrollment in Rural Vermont.** Co-Authors: Anika Advant, Jan Carney. Co-Authors Institutional Affiliations: University of Vermont Larner College of Medicine. CTR
The NNE-CTR Community Engagement & Outreach Core has established a solid foundation for supporting students in their research. Our job is to brainstorm, initiate, guide and support research that addresses community priorities. Stressing our goal of improving health and health equity in northern New England, students are mentored by our Rural Research Navigators in communication techniques, research project design and outreach methods to achieve a bi-directional conversation with our communities. The findings are more impactful, and often lead to future collaborations. This project is one such example, and was jointly supported by the NNE-CTR, the UVM LCOM, and the Vermont Cancer Center. It is widely known that clinical trial participation is limited, despite the prevalence of cancer diagnose in the United States. It is estimated that under 5% of all patients receiving cancer care participate in clinical trials. Clinical trial enrollment and participation is further limited by geographical location, with rural residents participating at an even lower rate than their urban counterparts. This study sought to identify facilitators and barriers that impact rural Vermonter's awareness of and enrollment in cancer clinical trials (CCTs). Through structured interviews with community stakeholders (local physicians, government officials and non-profit organizations), this study identified facilitators and

barriers that affect rural Vermonter's access to and enrollment in cancer clinical trials. Results demonstrate opportunities to increase enrollment through improved patient education, community health workers and dedicated personnel, transportation and local availability of clinical trials. Future research may consider patient perspectives on clinical trial awareness and enrollment.

42. Emma Throneburg, University of Louisville. **Beyond Numbers: A Qualitative and Quantitative Investigation of Student Outcomes in a Course-based Undergraduate Research Experience (CURE) for Introductory Biology Students.** Co-Authors: Natalie Christian, Mikus Abolins-Abols, Jeffery Masters, Connor Morozumi, Rachel M. Pigg. Co-Authors Institutional Affiliations: Not Listed. INBRE
Course Based Undergraduate Research Experiences (CUREs) allow students to participate in authentic research within their undergraduate courses. This enables a broader population of students to gain the benefits that authentic research experiences provide, such as learning to think like a scientist. CUREs that are incorporated into introductory courses further increase the accessibility of these experiences to a broader population of undergraduates, and potentially increase student retention by supporting development of scientific literacy, self-efficacy, science identity, and sense of belonging at an earlier stage in an undergraduate's career. As part of the introductory biology laboratory courses for STEM majors at the University of Louisville, we designed a two-semester CURE that incorporates topics in both molecular biology and ecology. Beginning in Fall 2021, students completed the introductory biology CURE curricula and submitted survey responses to assess their concept mastery, attitudes towards biology, and demographic background. Survey data was collected three times throughout the duration of the two-semester CURE: at the beginning of the first semester, the end of the first semester, and the end of the second semester. To understand student experiences with mentorship and collaboration within the CURE more deeply, a pilot cohort of students in Spring 2024 participated in qualitative interviews. These interviews also investigated students' previous science experiences, and their identity as a scientist following completion of the course. Analyses of quantitative survey results and preliminary findings from our qualitative interviews will be presented.

43. Claudia Gonzalez, Clemson University. **Investigating Initiation of Encystation in The Intestinal Parasite Entamoeba histolytica.** Co-Authors: Cheryl Ingram-Smith. Co-Authors Institutional Affiliations: Not Listed. COBRE
Amoebiasis is a food- and water-borne intestinal parasitic infection caused by Entamoeba histolytica and results in ~100 million cases of symptomatic diseases each year, primarily in developing countries. The incidence of infection may be as high as 1 billion people each year though, as only ~10% of infections are symptomatic. E. histolytica has two cellular life stages, the trophozoite and cyst. Trophozoites are the motile amoeba form that colonizes the large intestine during infection. Cysts are smaller dormant cells with a chitinous cell wall that are shed in feces of infected individuals to disseminate the disease. The process of cyst formation, called encystation, has previously been studied in reptile pathogen Entamoeba invadens. We are now able to study this process directly in the human pathogen. Encystation in culture is triggered by glucose deprivation, and the presence of the short chain fatty acids acetate and propionate enhances the rate of initiation. The objective of this research is to investigate the genetic and metabolic reprogramming that occurs early in encystation and examine how encystation is related to other stress responses. We are particularly interested in the interplay between encystation and the heat shock response. Our results indicate that heat shock elicits upregulation of certain encystation genes and a higher heat stress results in rapid formation of a chitin cell wall, suggesting a link between certain stress responses and encystation.

44. Gerianne Olivieri-Henry, University of Puerto Rico - Medical Sciences Campus. **Characterization of the gut microbiome of Puerto Ricans with Alzheimer's disease based on their Apolipoprotein E genotype.** Co-Authors: Vanessa Sepulveda-Rivera, Carlos Herrero-Rivera, Cecilia Soler, Hiram Morales-Gonzalez, Javier Ruiz, Michel Santiago, Ana C. Sala, Filipa Godoy-Vitorino. Co-Authors Institutional Affiliations: University of Puerto Rico - Medical Sciences Campus. INBRE

Alzheimer's disease (AD) is a neurodegenerative condition characterized by a gradual decline in mental function, which culminates in death. Evidence suggests that the apolipoprotein E (ApoE) gene influences Alzheimer's risk. Allele E2 is neuroprotective, E3 is neutral, and E4 is associated with a higher genetic risk for AD. Our objective is to study the gut microbiome of Puerto Ricans with AD compared to unimpaired cognitive controls and its association with ApoE allele variants. With IRB # 2290033626 we recruited 98 participants, 50 with AD and 48 controls, who underwent clinical and cognitive assessments. Fecal samples were collected for genomic DNA extractions, followed by 16S rRNA genes (V4 region) amplification. ApoE genotyping was done at the PR-INBRE CRI genomics core, using real-time PCR TaqMan-BHQ probes. Analyses showed no significant differences in bacterial diversity and richness when comparing ApoE genotypes. However, participants with at least one E2 allele showed higher levels of Firmicutes, while those with at least one E4 allele had higher levels of Euryarchaeota. When comparing the ApoE genotypes of the AD participants, we found a significant difference in microbial richness (Faith PD pairwise p value = 0.018) between E2E3 and E2E4. Additionally, AD participants with E2E3 genotype had higher levels of Fusobacteriota and Desulfobacterota than those with at least one E4 allele. This developing study area may open the possibility for preventive microbiome-based therapies that could result in a clinical benefit for patients with and without AD.

45. Jennifer Hackett, University of Kansas. **Next Generation Sequencing at KU Genome Sequencing Core.** Co-Authors: None. COBRE

The Genome Sequencing Core (GSC) is one of three research service core labs in the NIH COBRE Center for Molecular Analysis of Disease Pathways (CMADP) at the University of Kansas (KU). The major mission of the GSC is to provide researchers with next-generation sequencing (NGS) technologies. NGS, carried out in a massively parallel fashion, has been revolutionizing bio-medical research and used in a growing list of applications. Projects supported by the GSC include de novo genome assembly, genome re-sequencing for identification of mutations and polymorphisms, transcriptome analysis (RNA-seq), and epigenomic and gene regulation studies such as ChIP-seq, Methyl-seq, and small RNA analysis. The GSC enhances the genomics infrastructure already at KU by providing a range of Illumina sequencing platforms including the NextSeq2000 and NextSeq550 (mid-sized genome re-sequencing or transcriptome projects) and the MiSeq (metagenomic or targeted amplicon sequencing projects) to researchers at KU-Lawrence and across the region. To capture the full power of NGS, we provide a range of project support, including project consultation, sample quality check, sequencing library construction, Illumina sequencing, and FASTQ generation and demultiplexing. For latest pricing, current sequencing queue, or other information, visit the Genome Sequencing Core's website: https://gsc.ku.edu/.

46. Sai Deepika Reddy Yaram, West Virginia University. **Biophysical characterization of HL-60 infected with Anaplasma spp.** Co-Authors: Soumya K Srivastava. Co-Authors Institutional Affiliations: West Virginia University.

Anaplasmosis, a disease caused by the bacterium Anaplasma phagocytophilum transmitted through tick bites, poses a significant public health concern, with increasing cases observed in recent years. Anaplasmosis cases rose to 6,729 in the U.S., higher than pre-pandemic levels in 2021. Current diagnostic methods relying on blood tests suffer from lengthy turnaround times. This study presents a novel approach utilizing dielectrophoresis (DEP) to quantify the changes observed in healthy and

Anaplasma spp. infected HL 60 cells. HL 60 cells are a human Caucasian promyelocytic leukemia cell line derived from a 36-year-old Caucasian female with acute promyelocytic leukemia at the National Cancer Institute. Healthy and Anaplasma spp. infected HL 60 cells were grown at 37oC using 5% CO2 in an incubator. Cells are suspended in a buffer media containing sucrose, dextrose, and PBS. The cell suspension is pipetted into a microchip of the 3DEP analyzer to analyze cell behavior. The cell behavior is analyzed using the dielectrophoretic crossover technique, where the cells are exposed to an alternating current (AC) field at a fixed voltage, creating a non-uniform electric field. The frequency is swept from 1 Hz to 45 KHz, and the crossover frequency where the cells have no movement, i.e., they do not move towards or away from a high electric field gradient, is noted, which further yields the dielectric properties of cytoplasm and membrane indicating the cell interior and morphological changes, respectively. Our results reveal significant differences in the dielectric properties between healthy and infected cells, as evidenced by distinct crossover frequencies in the Clausius-Mossotti plot. This distinct change in cells' bioelectric signature holds promise for developing a diagnostic platform capable of detecting Anaplasma spp. infection in humans. Leveraging the dielectrophoresis technology, i.e., label-free, non-invasive, and rapid, can improve clinical management and control of anaplasmosis.

47. Tobechukwu M. Aghadinuno, Southern University and A&M College Baton Rouge. **Garcinia Kola Nuts Extracts and Its Bioguided Kolaviron-rich Fractions Induce Skin Cancer Cell Death Involving Autophagy.** Co-Authors: Tobechukwu M. Aghadinuno, Joy T Folahan, Ekhtear Hossain, Olufunke E. Olorundare, Konstantin Kousoulas, Francis-Afred Attah, Jean Christopher Chamcheu. Co-Authors Institutional Affiliations: Louisiana State University, Southern University and A & M College, University of Ilorin. INBRE

Skin cancers including prevalent Keratinocyte carcinoma (KC) and aggressive Melanoma (MSC) pose significant morbidity and mortality threats worldwide. Current treatment often led to adverse effects or resistance, resulting in low compliance and treatment discontinuation. We addressed such challenges in studies that explore extracts and Kolaviron, derived from Garcinia Kola nuts (GKN), known for its antioxidant and anti-inflammatory properties. Current research study method involved defatting GKN powder with petroleum ether and subsequent methanol extraction, yielding Kolaviron. Further fractionation produced F3. MSC and KC cell lines were treated with F3. The anticancer effects of different extracts and F3 were assessed through MTT and colony formation assays, as well as western blotting analysis. The most susceptible cell lines were further examined to evaluate the modulation of autophagy by F3. F3 showed a significant decrease in cell proliferation and viability. The IC50 values were significantly higher in NTER1/2 normal keratinocytes compared to melanoma and nonmelanoma skin cancer cell lines. Furthermore, colony formation capacity was severely decreased in treated cells compared to control cancer cells. The observed decrease was greater than 90% in F3-treated cells. Western blot analysis showed cell cycle arrest at the G1 phase. Moreover, analysis of autophagy markers revealed conversion of LC3B-I to LC3B-II, p62 degradation, and induction of Atg-5. Findings indicate that F3 possesses potent anticancer activity associated with the induction of autophagy. This suggests the potential for further exploration and development as a promising agent for the management and control of both MSC and KC.

48. Vanessa Sepulveda, University of Puerto Rico. **Clostridium innocuum associates with cognitive impairment in the gut microbiota of Hispanics living in Puerto Rico.** Co-Authors: Gerianne Olivieri-Henry, Carlos Herrero-Rivera, Cecilia Soler Llompart, Hiram Morales-Gonzalez, Javier Ruiz, Michel Santiago, Ana C. Sala, Filipa Godoy-Vitorino. Co-Authors Institutional Affiliations: University of Puerto Rico Medical Sciences Campus. INBRE

Alzheimer's disease (AD) is a progressive neurodegenerative condition characterized initially by minor memory impairments and culminating in the total deterioration of cognitive abilities and death. In Puerto Rico, AD is the fourth leading cause of mortality, while the sixth in the United States, representing an escalating public health crisis given the aging of the population. Research establishes a connection between the gut microbiome and AD pathology, implicating mechanisms such as neuroinflammation and the accumulation of amyloid proteins in the brain. Our main objective was to determine the association of gut microbiota with cognitive decline among patients with AD and controls in Puerto Rico. With IRB # 2290033626, we recruited 100 participants, 50 with AD and 50 with controls, who underwent clinical and cognitive assessments (MoCA/CDR). Genomic DNA extractions were performed on collected fecal samples. NextGen Illumina MiSeq was used to sequence 16S rRNA genes (V4 region) and analyzed with standard pipelines for microbiome species. Analyses showed no statistically significant differences in bacterial diversity and richness between AD and controls. However, we found a substantial abundance of Clostridium innocuum in control participants showing Moderate Cognitive Impairment. Additionally, the abundance of this bacteria increased as cognitive impairment increased in Alzheimer's participants. Clostridia are anaerobic opportunistic pathogens that affect humans, causing numerous diseases. This study of the gutbrain axis (GBA) in Puerto Ricans may open the possibility for preventive microbiota-based therapies and strategies for a healthy microbiome, resulting in better outcomes for our patients with and without AD.

49. David E. Warren, University of Nebraska Medical Center. **Measuring AD-vulnerable brain systems and cognitive abilities in healthy development: cross-sectional findings from the PRANK study.** Co-Authors: None. COBRE

Individual risk for Alzheimer's disease (AD) is affected by genes, and these genetic risk factors for AD may influence brain development. If true, genetic/genomic risk factors could bias brain and cognitive development in ways that increase vulnerability to late onset AD. We are conducting a five-year study to test the hypothesis that genetic and polygenic AD risk affects neurodevelopment of brain systems most affected by AD in ways that increase vulnerability to late-onset AD. We predict that properties of AD-vulnerable brain structures (e.g., hippocampus) and AD-vulnerable brain networks (e.g., default mode network) will vary with polygenic AD risk even during youth. We have implemented our project as the Polygenic Risk of Alzheimer’s disease in Nebraska Kids (PRANK) study. We have enrolled N=230 healthy youths age 8-13 years, and we have collected cross-sectional cognitive and brain data characterizing: 1) age-related structural differences of AD-vulnerable brain regions; 2) age-related differences in functional brain networks vulnerable to AD; and 3) age-related differences in of AD-vulnerable cognitive abilities. We will discuss crosssectional findings for age-related trends in our key outcome measures as well as associations between brain structure, brain function, and cognitive abilities in our developmental sample. We will also discuss ongoing longitudinal data collection, predictions for association with outcome measures and polygenic AD risk, and targeted PRANK subprojects. Findings from the PRANK study will improve the field’s understanding of typical brain development as well as how potential developmental effects of ADPRS relate to clinical and epidemiological challenges of AD.

50. Lucas Hert, Montana State University-Billings. **Identification of Lipid Biomarkers of Alzheimer’s Disease Using a Novel Enzymatic Approach.** Co-Authors: Daniel Willems. Co-Authors Institutional Affiliations: Not Listed. INBRE

Secreted phospholipase A2 (sPLA2) non-specifically hydrolyzes the ester linkages of phospholipids at the SN2 position. Using this enzyme’s normal biochemistry, a novel digestion method was designed and implemented to stereochemically resolve structural differences in complex lipids between cognitively normal brain tissue and brain tissue affected by AD. Standardized samples of PC were digested with

sPLA2, and the lipid fragments analyzed via MS. The detected SN2:SN1 ratio was highly favorable (7.2:1). The same digestion protocol was applied to human brain tissue samples. Data acquired from this analysis showed a significant difference in the stereochemically resolved lipid profile of samples digested with sPLA2 and controls. This lipid profile may be useful as a biomarker-based diagnostic test for AD.

51. Kristine M Bragg Zizza, University of Nevada Las Vegas. **Building and Sustaining COBRE Scientific Research Cores.** Co-Authors: Linda J. Larson-Prior, Jonathan Hilpert, Judith Weber, Hannah Williams, Evan Falkenthal. Co-Authors Institutional Affiliations: Not Listed. COBRE
Scientific research core sustainability is essential for the long-term success of a COBRE. By the end of Phase 3 of the funding cycle, COBREs are expected to have secured sufficient independent funding and revenue streams to keep the research cores in operation after the COBRE award expires. Therefore, a COBRE Phase 3 program objective is the implementation of strategies to sustain research excellence. We describe features of a well-conceptualized research core and a proposed planning cycle for development and implementation. This includes discussion of the similarities and differences observed across core designs, and how to develop a successful core strategy tailored to the unique needs of that core. We further discuss strategies for core sustainability in an academic setting. Additionally, we propose an assessment method for tracking and evaluation of core sustainability readiness. Drawn from multiple sources, we identified eight areas of focus for attaining sustainability. These areas are operational efficiency and cost effectiveness, diversity of users, external collaboration, training and education programs, publication and grant records, feedback and user satisfaction, financial sustainability, and long-term strategic planning. By engaging core directors in annual analysis of their core's progress towards each of the areas, individualized core assessments can be issued in a report card style format. This process isolates and identifies areas to prioritize during the next reporting period through an efficient and straightforward process. With the right preparedness and tools in place for the selective monitoring of core operations, sustainability can be accomplished.

52. Owen Growney, Black Hills State University. **Investigation of the SpoV Peptide and Its Effects on S. pyogenes Biofilms.** Co-Authors: Michael Chaussee, Andrea Herrera. Co-Authors Institutional Affiliations: University of South Dakota. INBRE
Streptococcus pyogenes, also known as Group A Streptococcus, is a Gram positive bacteria responsible for more than 500,000 deaths worldwide each year and is the cause of countless harmful diseases. These bacteria frequently form biofilms, which are matrices of viscous extracellular DNA, peptides, and polysaccharides that contribute to a significant reduction in the effectiveness of both immune system responses as well as antibiotic treatment. These biofilms can form on newly implanted prosthetic joints as well as catheters with often catastrophic outcomes that can prove fatal if systemic infection develops. The severity of these infections or virulence of the bacteria can be attributed in part to the Streptococcal Peptide Controlling Virulence (SpoV), which is an extracellular peptide that has a direct effect on the transcript abundance of the cytotoxin Streptolysin O, and is essential for S. pyogenes to cause disease and sustain infection. The goal of this research was to investigate and develop an understanding of the effect that SpoV has on the development of S. pyogenes biofilms. Biofilms developed in the presence of SpoV had decreased biomass compared to those that were not. Analysis of enzymatic activity showed that bacterial strains producing SpoV have significantly heightened DNase activity compared to strains that do not. The discoveries made in this research have helped us to further our knowledge of SpoV as an important virulence factor that might represent an attractive target for the development of alternative therapeutic agents to inhibit or reduce the virulence of the bacteria.

53. Brisa E. Rodriguez Alcantar, University of Nevada, Las Vegas. **Associations Between Parent's Physical Activity and Children's Weekly Physical Activity in a Hispanic Sample.** Co-Authors: Tim Grigsby, Liliana Davalos, Marissa Martinez, Christopher Johansen. Co-Authors Institutional Affiliations: University of Nevada, Las Vegas. INBRE
Childhood obesity in the United States (US) has tripled in 30 years, becoming a concerning issue that requires urgent attention. One in five children in the US are obese, with Hispanic children being 1.8 times more likely to be obese than their non-Hispanic White counterparts. Studies have found that parents who engage in physical activity (PA) have more active children. This study aims to explore the relationship between Hispanic parent's PA and their child's weekly PA. Hispanic parents (n=176; Mean age= 33; 92% mothers) were recruited in Southern Nevada. A linear regression model assessed the association between parental health-focused PA and their child's weekly PA. A second linear regression model assessed the association between parental PA engagement with their child and their child's weekly PA. A third model regressed the child's PA on both parental PA variables. All models controlled for parent's age, gender, and income. Independently, weekly child PA was associated with more parental PA engagement with their child (Î²=.672, p=

54. Ishika Sharma, University of Delaware. **Selective Whole Genome Amplification Shows Potential for Sequencing Avian Malaria Pathogen Genomes.** Co-Authors: Vincenzo Ellis. Co-Authors Institutional Affiliations: University of Delaware. INBRE
Understanding the genetic makeup of pathogens is crucial for disease diagnosis, vaccine development, outbreak prediction, and implementing effective preventative measures. However, sequencing pathogen genomes in the presence of host DNA presents a significant challenge due to the abundance of host DNA compared to the relatively small amount of pathogen DNA. Traditional techniques like polymerase chain reactions (PCRs) can miss important regions of the pathogen's genome, hampering comprehensive analysis. In this study, we present a novel selective whole genome amplification approach to sequence the complete genomes of the avian malaria pathogen Plasmodium relictum, specifically genetic lineages SGS1 and GRW11, in birds. To overcome the limitation of host DNA interference, we employed the Phi29 enzyme with primers specifically designed to bind more readily to the pathogen's genetic material than to the host's. Using an isothermal amplification process, we successfully prepared the amplified product for Illumina sequencing on an Illumina MiSeq platform. Additionally, we applied this protocol to DNA extracted from the blood of a wood thrush (Hylocichla mustelina) infected with the pathogen P. unalis (lineage TUMIG03) and a negative water control. By mapping the resulting sequences to the P. relictum reference genome, we identified targeted P. relictum genomes with satisfactory coverage for SGS1, though GRW11 exhibited patchier regions with some coverage. While TUMIG03 showed limited amplification, some sequences were identified as Plasmodium but could not be mapped to the reference due to the use of the P. relictum reference genome. Our success in mapping pathogen DNA to the reference pathogen suggests that selective whole genome amplification using the Phi29 enzyme holds promise as an approach to investigate pathogen genomics, thus shedding light on their evolution. These findings have significant implications for setting up preventative measures against pathogenic diseases. By understanding the genomic characteristics and evolutionary patterns of pathogens, we can design more effective preventative strategies, contributing to the advancement of public health.

55. Kara Powder, Clemson University. **Sex as a source of shape variability in the facial skeleton.** Co-Authors: Brandon T. Sanders, Karisa Bruce, A. Allyson Brandon. Co-Authors Institutional Affiliations: South Carolina Translational Research Improving Musculoskeletal Health (SC TRIMH). COBRE
Sex is a source of phenotypic variation, as evidenced by the NIH policy of considering sex as a biological variable. We examine skeletal tissues, which display striking differences between males and females. For

instance, within the human facial skeleton, sex accounts for 13% of diversity in skull shape, generating differential disease incidence and severity and functional changes in biting. Common congenital conditions like clefting have a sex-bias, highlighting the need to examine the role of sex during development. We investigate sex-specific craniofacial variation using Lake Malawi cichlids. These fishes have evolved an unparalleled range of facial adaptations that mirror human facial variation. Further, in both cichlids and humans, the primary site of disparity between sexes is the mandible. We used geometric morphometric shape analysis to quantify differences in mandible shape from 5 cichlid species. We find that sex is a significant source of divergence across all species (p=8.1e-8), but that each species is variable in the degree of variation between males and females. This highlights how sex-determining genes can interact with genetic variation to generate phenotypic diversity, imitating patterns also observed among human populations. Ongoing experiments are exploring the developmental and molecular origins of this adult variation, for instance through estrogen signaling given its known role in bone development after sexual maturity. Together, this work provides insights into the mechanisms that can generate functional and medically-relevant phenotypic variation between the sexes. This work is supported by the South Carolina Translational Research Improving Musculoskeletal Health COBRE (SC TRIMH; P20GM121342) and NSF1942178.

56. Sara Vargas, The Miriam Hospital. **Assessing the integration of comprehensive sexual health histories at clinical practices in the Providence metropolitan area.** Co-Authors: Leslie Ramirez. Co-Authors Institutional Affiliations: The Miriam Hospital. COBRE
Trauma history may increase health-risking sexual behaviors and negatively affect sexual functioning and satisfaction. Health system encounters present an opportunity for sexual health assessment, counseling, diagnosis, and treatment; however, research suggests that comprehensive sexual health histories are not standard practice. The Centers for Disease Control and Prevention (CDC) and American Academy of Family Physicians (AAFP) have published recommendations for taking a sexual health history which include sexual behavior and history, sexual functioning, sexual pleasure, trauma history, and use of gender inclusive terminology. The goal of this study is to explore the extent to which these recommendations have been integrated into information, instructions, questions, and response options on intake paperwork collected from clinical practices in the Providence metropolitan area. For the first round of data collection (Feb-Mar 2024), we are requesting forms from a list of infectious disease (n=13), obstetrics and gynecology (obgyn; n=39), and urology (n=6) clinics generated from a Rhode Island Department of Health database. As of early March 2024, we have collected forms from 19 clinics (6 infectious disease,11 obgyn, and 2 urology). The second round (Apr-Jun 2024) will expand to internal medicine and family medicine practices. Detailed results from content analysis will be presented describing the state of sexual health assessment in this early point of clinical contact. This project is the first step in developing best practices for implementing comprehensive sexual health histories into routine standard-of-care.

57. Gopi Kolluru, LSU Health-Shreveport. **Cystathionine gamma lyase and Hydrogen sulfide signaling in aging vascular blood flow and cognitive function.** Co-Authors: Bo J. Wood, Ian Hill, Sibile Pardue, John Glawe, Xinggui Shen, Kevin S. Murnane, Chris Kevil. Co-Authors Institutional Affiliations: LSU Health Shreveport. COBRE
Aging is an independent risk factor for cardiovascular diseases. Aging alters molecular signaling including, increased ROS, ER stress, reduced autophagy, and vascular dysfunction. Aging, and associated pathologies such as neurodegeneration, and drug substance abuse such as involve progressive cognitive decline. However, the regulatory mechanisms, underlying aging vascular functions including, CSE/H2S signaling are unknown. Our research reveals how a reduction in cystathionine gamma-lyase (CSE), and

hydrogen sulfide (H2S) axis impairs endothelial function, vascular blood flow, and remodeling. Additionally, defects in vascular function can lead to cognitive impairment, and dementia (VCID) is known to participate in different dementia states with poorly defined molecular mechanisms. We will test the hypothesis that vascular CSE and H2S deficiency directly impair cognitive function due to compromised cerebral blood flow. We initially demonstrated that plasma and tissue sulfide metabolites and CSE enzyme activity significantly decrease with age. We subsequently observed the reduction in H2S metabolites blunts cerebral blood flow associated with profound cognitive impairment. This prompted us to interrogate whether decreased CSE/H2S signaling affects ischemic stroke or substance abuse models leading to reduced blood flow and cognitive impairment in an age-dependent manner. We use C57Bl6/J (WT), CSEKO, endothelial cell (ec) CSEKO, and ecCSETg mice to achieve our hypothesis. Additionally, we checked exogenous sulfide therapy or endothelial CSE overexpression mice to rectify cognitive decline coincident with reduced cerebral blood flow. These results will provide novel insights into the significance of the cell-specific role of CSE/H2S on neurovascular blood flow and cognitive function.

58. Jared Hamm, Minot State University. **Assessing Possible Influence of Anthropogenically-Derived Effluents in Lake Darling, North-Central North Dakota.** Co-Authors: Nikita Neyshtadt, Lehi Karadia, Achille Tenekeu, Joseph Collette. Co-Authors Institutional Affiliations: Minot State University. INBRE
Aquatic environments, and their respective ecosystems, are sensitive to change, making them excellent indicators of local water quality. In areas of heavy anthropogenic activity, these environments provide insight for the effects of pollution and nutrient loading on a local and regional scale. Local analysis of water quality provides context on pollutant and nutrient input, while regional-scale analysis can identify the timing and origin of nutrient fluxes, rates of nutrients moving through and being consumed in lacustrine systems, and areas of concern for remediation and rehabilitation. The decline in water quality inevitably impacts local ecosystems â€“ for example, seasonal fertilizer runoff can lead to abnormal phytoplankton blooms, which in turn can contribute to oxygen minima-related local die-offs in aquatic organisms including phytoplankton, macroinvertebrates, and fish species. Documenting the timing and magnitude of seasonal nutrient fluxes in agricultural regions is critical to understanding factors related to the health and longevity of local aquatic ecosystems and in identifying possible sources. Preliminary data (approximately 1.5 years of data of a 5-year study) are presented and some possible interpretations are explored.

59. Tyler Paul Hill, West Liberty University. **Genetic and Protein Expression Comparison of Tissues of Differing Embryonic Origin.** Co-Authors: Holly Racine, Lara Fetty, Bailee McNamara. Co-Authors Institutional Affiliations: West Liberty University. INBRE
Non-syndromic Craniosynostosis (CS) has an unknown etiology. The overproduction of thyroid hormones (THs) during pregnancy known as maternal hyperthyroidism has been cited by the CDC as a potential cause of CS. Elucidation of the mechanism for TH induced CS may allow for the creation of a novel more suitable treatment option. There are several signaling pathways involved in the differentiation and development of the tissues of the skull such as, BMP, Ihh, and Wnt. Wnt signaling has been linked to the differentiation of both embryonic mesoderm as well as neural crest cells, from which the relevant tissues of the skull originate. The goal of this study is to quantify and compare genetic and protein expression of relevant Wnt signaling molecules and their target genes within the Sagittal and Coronal sutures. Beta-Catenin is a Wnt signaling molecule that acts as a transcription factor modulating the expression of genes such as Runx2 and Twist1. These genes were selected as they are known to be involved in cranial development. Sutures were collected from an avian model of induced thyrotoxicosis and analyzed using qRT-PCR and western blotting. Results of the qRT-PCR showed a significant

downregulation in Runx2 and Twist1 expression in the coronal sutures with no change in Twist1 and a significant upregulation of Runx2 expression in the sagittal sutures. Western blot results are still pending. While further investigation into these pathways is necessary, our findings conclude that these key pathways react differently to modulation by thyroid hormones in tissues of differing embryonic origin.

60. David Johnson, University of Kansas. **Computational Chemical Biology Core: A Chemical Biology of Infectious Disease COBRE Core Laboratory.** Co-Authors: None. COBRE
The University of Kansas Computational Chemical Biology Core (CCB) provides the computational resources and expertise to enhance the productivity of researchers studying infectious diseases. The CCB is able to provide or assist with virtual screening, protein-small molecule docking, binding site prediction, protein modeling and design, prediction of protein stability changes upon mutation, fragment based probe design, as well as preparation of presentation graphics. The core utilizes the KU Community Cluster at the Advanced Computing Facility for its high-performance computing needs. The KU Community Cluster offers 458 compute nodes with a total of 8,568 compute cores, including 17 nodes that offer GPU-accelerated computing. The CCB specializes in initial hit identification of nontraditional drug targets such as proteinprotein or protein-RNA interfaces by offering high-throughput virtual screening via pocket optimization with exemplar screening at protein-protein interfaces and hotspot pharmacophore mimicry of protein-RNA interactions.

61. Emily Ekstrum, Creighton University. **Structural and Langevin-Based Dynamic Studies of the Interaction Between Two Proteins Involved in Gene-Silencing.** Co-Authors: Evan Veltri, Molly Dolan, Lynne Dieckman. Co-Authors Institutional Affiliations: Not Listed. INBRE
After DNA replication, newly synthesized DNA strands are wrapped around histone proteins to form nucleosomes during a process called replication-coupled nucleosome assembly. Two major proteins that function in replication-coupled nucleosome assembly are proliferating cellular nuclear antigen (PCNA) and chromatin assembly factor 1 (CAF-1). PCNA acts like a sliding clamp to encircle newly synthesized DNA and recruits CAF-1 to the replication fork. CAF-1 binds to PCNA and loads histone proteins onto the synthesized DNA to begin nucleosome assembly. This interaction between PCNA and CAF-1 is crucial for DNA packaging and gene regulation; however, the structural basis of this binding event is unknown. The goal of this study is to determine the structure and dynamics of the interaction between PCNA and CAF-1 using a combination of structural methods, including X-ray crystallography, small angle X-ray scattering (SAXS), and computational Langevin-based dynamics (LD) molecular simulations. We have carried out these structural studies with multiple PCNA-CAF-1 complexes, including a SUMO-modified form of PCNA. Thus far, we have generated microcrystals and P(r) curves from both SAXS and LD simulations of several PCNA-CAF-1 complexes. We are currently working to optimize the simulation-derived P(r) curves to better fit SAXS experimental P(r) curves. The comparison of the P(r) curves will validate SAXS data and support a structural ensemble determination between PCNA and CAF-1. Together, these studies will provide a comprehensive analysis of the structure and dynamics of the complexes formed between PCNA and CAF-1, and how these proteins regulate nucleosome assembly and gene silencing.

62. Morgan Bridi, West Virginia University. **Measuring and manipulating activity in stress-responsive hypothalamic nuclei to improve post-stroke outcomes.** Co-Authors: Laurel Stone, RIley Coulter. Co-Authors Institutional Affiliations: West Virginia University. COBRE
Stroke is a severe ischemic neurovascular injury, with high mortality and long-term disability for survivors. Hypothalamic-pituitary-adrenal (HPA) axis activation, which mediates the neuroendocrine stress response, is rapidly elevated following ischemic stroke, with increased corticotropin releasing

hormone (CRH) and corticosteroid (CORT) signaling. Elevated stress and HPA activity pre-ischemia is associated with stroke risk and worse stroke outcomes, while hypercortisolism in the subacute and chronic phases is both typical and deleterious. Mounting evidence suggests that targeting CRH signaling could reduce post-stroke morbidity and mortality. Central nervous system control of the activation of the HPA axis is a major contributor to CRH and glucocorticoid elevation post-stroke. The ventral hippocampus regulates CRH production and HPA activation through excitatory projections to the bed nucleus of the stria terminalis (BNST), which in turn sends inhibitory projections to CRH+ neurons in the paraventricular nucleus (PVN) of the hypothalamus. This circuit represents a viable target for both early and longer-term interventions after stroke. We hypothesized that neuronal populations upstream of HPA axis activation are progressively dysregulated after stroke due to remote hippocampal damage, and that targeting those neurons can reduce post-IS neuronal damage, attenuate corticosteroid release, and improve functional/behavioral outcomes. Our lab is currently using in vivo fiber photometry to quantify how of neuronal activity and synaptic input changes in the PVN and BNST following ischemic stroke, and investigating whether chemogenetic modulation of the PVN and BNST can improve neuronal and functional post-stroke outcomes.

63. Matthew Woolard, Louisiana State University Health Sciences Center-Shreveport. **Creating a Cost-Efficient Immunophenotyping Core Supported by COBRE to Streamline Technology Adoption and Training.** Co-Authors: Sushma Bharrhan, Ricky Wiggins Jr., Andrew D. Yurochko. Co-Authors Institutional Affiliations: Not Listed. COBRE

In 2021, we established the COBRE Center for Applied Immunology and Pathological Processes (CAIPP) Immunophenotyping core at Louisiana State University Health-Shreveport (LSUHS). This Shared Resource Laboratory provides COBRE investigators with access to state-of-the-art immunophenotyping technology. We collaborate with investigators to optimize flow cytometry experimental design, develop protocols, conduct experiments, and analyze data. So far, we have worked with 15 laboratories, including COBRE and non-COBRE investigators at LSUHS. We have completed 11 projects (involving panel designing, staining, and data analysis), and five projects are ongoing. Additionally, we improved the single-cell isolation from complex tissues for downstream analysis by encouraging investigators to use the gentleMACS dissociators at our core. Acquiring a spectral flow sorter has advanced our campus's flow cytometric capabilities. However, this led to a challenge: upfront costs for antibodies and reagents deterred investigators interested in spectral flow. To address this, our core purchased generalized antibody panels. Investigators can now acquire smaller antibody aliquots to test hypotheses. Through discussions with faculty, we have identified key panels for purchase. We have initiated the availability of these panels on campus, providing researchers with the option to begin spectral flow cytometry experiments. In addition, we recently procured a Curiox laminar wash system, eliminating the need to centrifuge the samples during the staining steps. We have had great success with Curiox as it provides better cellular viability, debris removal, and signal-noise ratio in our flow cytometry experiments with different kinds of tumors and fragile cell lines.

64. David E. Warren, UNMC. **Neuroimaging Acquisition and Analysis (NA2) Core of the Cognitive Neuroscience of Development & Aging (CoNDA) Center.** Co-Authors: Valentina Gumenyuk, David Ellis, Anna Dunaevsky. Co-Authors Institutional Affiliations: UNMC. COBRE

Cognitive neuroscience studies of human subjects increasingly rely on advanced neuroimaging and neurostimulation methods. A key aim of UNMC's CoNDA Center is to support world-class neuroimaging and neurostimulation facilities for investigators in the eastern Nebraska region. The Center's Neuroimaging Acquisition and Analysis (NA2) Core provides outstanding resources for investigators who use magnetic resonance imaging (MRI), magnetoencephalography (MEG), and/or transcranial magnetic

stimulation (TMS) in their research. CoNDA's NA2 Core provides CoNDA and other investigators with access and support for neuroimaging and neurostimulation of human subjects with field-leading MRI, MEG, and TMS instruments. The Core's main instruments include: a Siemens 3T Prisma MRI system with advanced gradients, a complete suite of neuro MRI sequences, and multiple head coils a MegIN Truix Neo MEG system with 306 channels (204 magnetometers and 102 gradiometers); and a Nexstim 5.1 Navigated Brain Stimulation TMS system with real-time stereotactic alignment of brain imaging data and Participants' physical brains. Use of CoNDA's NA2 facilities has greatly increased and diversified since the Center's initiation. In addition to supporting CoNDA Research Project Leads, Pilot Projects Awardees, and Core Voucher recipients, the NA2 supports research, often NIH-funded, led by more than a dozen principal investigators. NIH-funded projects collecting data using NA2 facilities are sponsored by NIGMS, NIA, NIMH, and NCI. Additionally, the volume of NIH R01 applications from investigators utilizing CoNDA NA2 facilities has increased substantially since receiving the award. The UNMC CoNDA's NA2 will continue to enhance neuroimaging and neurostimulation to advance cognitive neuroscience research of eastern Nebraska investigators.

65. Rebeca Sanchez, Delaware State University. **Comparing apoptosis rates in both wild type p53 cells and p53 hypomorphic HCT116 cells following treatment with Mirdametinib.** Co-Authors: Erin Perchiniak. Co-Authors Institutional Affiliations: Not Listed. INBRE

The p53 protein is the most frequently mutated gene in human cancer, and as such it has been one of the most studied tumor suppressor genes. As a tumor suppressor gene, p53 provides instructions for making a protein which is known to have numerous roles in protecting cells and regulating cell division, including the transcriptional regulation of a vast array of genes, cell cycle arrest, induction of apoptosis and other forms of cell death, as well as metabolic regulation. Germline p53 mutations result in an increased risk for multiple primary cancers throughout the lifespan of these individuals. Additionally, hundreds of spontaneous p53 mutations have been identified and have been found to promote tumorigenesis through the inactivation of the wild type p53 protein. Recent studies have reported that two different African-centric genetic p53 hypomorphs, Pro47Ser (P47S) and Tyr107His (Y107H), retain considerable p53 activity, but are defective for the transactivation of a small subset of p53 target genes and vary in spontaneous cancer formation and treatment to therapeutics. Cell lines were engineered using CRISPR to express either the P47S or Y107H p53 hypomorphs in previously published work. Our research lab is interested in understanding how cells expressing these variants respond to drug treatment compared to cells expressing wild type p53. Specifically, we are focused on the MEK inhibitor Mirdametinib, which showed increased sensitivity in the hypomorphic cells in an initial drug screen. In growth assays, we found slight differences in the doubling time of the hypomorphic cells compared to wild type, but nothing statistically significant thus far. We have completed a dose response curve with wild type cells to determine the correct dose of Mirdametinib for conducting the apoptosis studies. Our current work aims to compare the percent of apoptotic cells in the hypomorphic cell lines compared to wild type cells using a Countess 3 Automated Cell Counter. Once these assays are complete, we will conduct western blots comparing untreated and treated protein lysates from wild type and hypomorphic cells to look at the apoptotic proteins, cleaved PARP and cleaved caspase 3, as an additional method for looking at apoptosis.

66. Ronald Horswell, Pennington Biomedical Research Center, LSU System. **Modeling Effects of Public Health Policy and Viral Variants on COVID Incidence in Louisiana.** Co-Authors: San Chu, Daniel Fort, Grace Kim, Lucio Miele. Co-Authors Institutional Affiliations: Pennington Biomedical Research Center, Ochsner Health System, Louisiana Clinical and Translational Science Center. CTR

The possibility of future epidemics/pandemics leads to several important public health policy questions potentially addressable using experience with public health policy during the COVID pandemic. Among those questions: (1) Which aspects of public health policy were effective and which were not? and (2) How might more efficient public health policies be constructed? To address those questions, a new analysis approach was developed that simultaneously models infectious disease incidence, public health policy effects, effects of vaccination levels, and certain characteristics of emerging viral variants. The approach was implemented using Louisiana census tract-level incidence and vaccination data, as well as viral variant information and the durations and characteristics of COVID-related public health â€œphasesâ€• implemented in Louisiana. Among the key findings: (1) Restrictive public health policies were effective while in place, but those alone may not be sufficient to truly halt an epidemic at an acceptable economic cost; and (2) Testing strategies, for case-finding purposes, were not very effective. However, that seems to have been a result of the particular testing strategies used. Simulations based on the modeling results, in fact, suggest that a well-constructed testing strategy coupled with certain less-onerous restrictions (such as use of masks), may be a promising approach for disease control, perhaps even reducing incidence to the point where incidence falls below case-replacement levels. The modeling approach also attempts to quantify the viral variant families' relative advantages with regard to (a) size of the population inherently vulnerable to a variant, (b) transmissibility, (c) and susceptibility to vaccination.

67. Georgiana Graef and Sebastian O'Farrell, Black Hills State University. **COMT Moderates the Association Between Dispositional Gratitude and Pain Outcomes.** Co-Authors: Sabra Tompkins, Luke Whartman, Alyssa Cudney, Taryn Cook, Nathan T. Deichert. Co-Authors Institutional Affiliations: Black Hills State University. INBRE

The val158met polymorphism of the COMT gene has been linked to pain as well as variation in cognitive affective traits associated with pain, including gratitude. Although COMT and gratitude are associated with pain, less is known about whether these variables interact to influence pain. Thus, this study examined whether COMT genotype altered the relationship between gratitude and pain outcomes. Ninety-seven physical therapy patients (67% female, ages 18-90 years) completed validated self-report measures of gratitude and pain and provided buccal cell samples following a regularly scheduled therapy appointment. A majority of participants reported experiencing pain for longer than 8 weeks (84.5%). Multiple regression analyses, controlling for age, sex, BMI, and smoking status revealed a significant interaction between COMT genotype and gratitude in association with pain interference. Specifically, gratitude was negatively correlated with pain interference for individuals homozygous for valine and heterozygous individuals. Gratitude was not associated with interference for individuals homozygous for methionine. No interaction between COMT and gratitude was observed for pain severity. Our findings suggest that COMT genotype may influence the relationship between gratitude and pain outcomes. Specifically, individuals homozygous for valine, as well as heterozygous individuals, were found to benefit from higher levels of gratitude particularly in relation to pain interference. Our results suggest that genetic polymorphisms may contribute to the capacity of individuals to respond to and benefit from positive psychological states as a way to reduce pain. Funded in part by National Institutes of Health (P20GM103443).

68. Mohammad Alfrad Nobel Bhuiyan, LSU Health Shreveport. **ViViEchoformer: Predicting ejection fraction from echocardiogram videos via a video vision transformer.** Co-Authors: None. COBRE

Heart disease is the leading cause of death worldwide, and cardiac function as measured by ejection fraction (EF) is an important determinant of outcomes, making accurate measurement a critical parameter in pt evaluation. Echocardiograms are commonly used for measuring EF, but human

interpretation has limitations in terms of intra, and inter-observer (or reader) variance. Deep learning (DL) has driven a resurgence in machine learning, leading to advancements in medical applications. We introduce the ViViEchoformer DL approach, which uses a video vision transformer to directly regress the left ventricular function (LVEF) from echocardiogram videos. The model accurately captures spatial information and preserves inter-frame relationships by extracting spatiotemporal tokens from video input, allowing for accurate, fully automatic EF predictions that aid human assessment and analysis. The ViViEchoformer's prediction of ejection fraction has a mean absolute error of 6.14%, root mean squared error of 8.4%, mean squared log error of 0.04, and an R^2 of 0.55. ViViEchoformer predicted cardiomyopathy with an area under the curve of 0.83 and a classification accuracy of 87 using a standard threshold of less than 50% ejection fraction. Our video-based method provides precise left ventricular function quantification, offering a reliable alternative to human evaluation and establishing a fundamental basis for echocardiogram interpretation.

69. Ali Firooz, University of South Carolina. **Enhancing Breast Cancer Treatment: Machine Learning Predicts Medication Outcomes.** Co-Authors: Savannah M. Noblitt, Julie Martin, W. Jeffery Edenfield, Anna Blenda, Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina, Prisma Health Cancer Institute, INBRE
Purpose statement: Cancer is a leading health concern and is the second highest cause of death in the United States. In women, breast cancer has the highest incidence among cancers. The complex nature of cancer, with its diverse subtypes and heterogeneity, makes accurate diagnosis and treatment challenging. As a first step toward that an in-depth analysis, we are developing an explainable AI-based model for predicting cancer patient outcome incorporating our existing patient clinical database, covered in previous publications. Methods: A collaboration between USC College of Engineering and Computing, School of Medicine Greenville, and Prisma Health Cancer Institute was formed to aid in this task. Utilizing the data existing in our relational database, patients' treatment information (courses of treatment, medications, etc.) socio-demographic data (sex, age, etc.), and basic cancer details (diagnosis and cancer stage) was used to train, test, and validate a several models using Python and various libraries. Results: The use of more advanced machine learning models revealed some interesting relationships that can be used for explainability and reliability of the Machine Learning approaches. Finally, boosting algorithms, provided the best performance in classification of the patient’s response to medication, at the expense of model explainability. Conclusion: Our studies provide predictive models that could potentially be used to improve the diagnostic and prognostic power of data collected from patients at presentation. However, the dichotomy of black box AI approaches which perform better than explainable approaches, complicate deployment of these techniques in the domain of medicine and healthcare.

70. Hai Yao, Clemson University. **South Carolina COBRE for Translational Research Improving Musculoskeletal Health (SC-TRIMH): Core Facilities.** Co-Authors: Martine LaBerge. Co-Authors Institutional Affiliations: Clemson University. COBRE
The overall goal of SC-TRIMH is to enhance and expand biomedical research capacity at Clemson University to promote outstanding multidisciplinary, collaborative, and translational research in bone and joint diseases. The new scientific paradigm of Virtual Human Trials (VTH) for translational research is being implemented through powerful computational modeling combined with quantitative functional validation and in vivo assessment to expedite the development of new therapeutics, interventions, and devices for musculoskeletal health. Scientific cores include: 1) Multi-scale Computational Modeling (MCM) Core provides essential expertise and infrastructure in the area of multi-scale and multi-disciplinary computational modeling of bioengineering and biomedical problems, with a new addition of

Artificial Intelligence/Machine Learning (AI/ML) capacities for big data-driven modeling. This core supports SC-TRIMH investigators in their computation and simulation needs at the molecular, cellular, tissue, body, and population levels toward improving musculoskeletal health. 2) Advanced Fabrication and Testing (AFT) Core provides centralized resources for design, prototyping, testing, sensing, and instrumentation for SC-TRIMH investigators and other researchers. It utilizes advanced micro/macro fabrication and sensor technologies to validate computational models and generate, refine, and optimize devices, interventions, and therapeutics. 3) Preclinical Assessment Core (PAC) provides essential expertise, skills, and infrastructure for SC-TRIMH investigators to utilize animal models and human cadaver models to test musculoskeletal research hypotheses, validate computational models from the MCM, and assess the in vivo function of novel devices, interventions, and therapeutics.

71. Intawat Nookaew, University of Arkansas for Medical Sciences. **Refining the identity of mesenchymal cell types associated with murine bone.** Co-Authors: Jinhu Xiong ,Melda Onal, Cecile Bustamante-Gomez, Visanu Wanchai, Qiang Fu, Ha-Neui Kim, Maria Almeida, Charles A. O'Brien. Co-Authors Institutional Affiliations: Not Listed. COBRE

The transcriptomic profile derived from single cell RNA sequencing (scRNA-seq) can be used to cluster cells with similar profiles. Combining this information with known gene expression patterns can be used to define clusters of cells as specific cell types. Recent studies have used scRNA-seq to define mesenchymal cells of murine bone. However, these studies do not agree on the number of different cell types. To address this inconsistency in cell type designation, we created an atlas of murine bone-associated cells by harmonizing published datasets with in-house data. Over 100,000 mesenchymal cells were mapped to reveal 11 major clusters designated fibro-1, fibro-2, chondrocytes, articular chondrocytes, tenocytes, adipo-CAR, osteoCAR, pre-osteoblasts, osteoblasts, osteocytes, and osteo-X, the latter defined in part by Postn expression. In situ hybridization revealed that osteo-X, osteo-CAR, and pre-osteoblasts were closely associated with osteoblasts on trabecular bone, suggesting a continuum of cells spanning from osteoblast progenitors to mature osteoblasts. To determine if any of these cell populations are dependent on ongoing bone remodeling, we suppressed osteoclast formation using denosumab and examined the impact by scRNA-seq. Denosumab dramatically reduced osteoblast number, consistent with the suppression of bone remodeling. The abundance of pre-osteoblasts was also slightly reduced as was expression of its marker Spp1. In contrast, the abundance of osteo-CAR and adipo-CAR cells was not altered. In situ hybridization revealed an almost complete loss of Bglap-positive osteoblasts on trabecular bone in denosumab-treated mice. Preosteoblasts showed robust staining on trabecular bone in vehicle-treated mice, which was reduced but not abolished after denosumab. In contrast, the osteo-CAR marker Limch1 and the osteo-X marker Postn displayed little change. Thus osteoblasts, and to some extent pre-osteoblasts, are highly dependent on bone resorption and coupling factors for their existence but osteo-CAR and osteo-X cells, and their close association with the bone surface, are not.

72. Ilka Pinz, MaineHealth Institute for Research. **Loss of Rab27a causes age-induced cardiomyopathy in mice.** Co-Authors: Ashley Soucy, Abigail Kaija, Anne Harrington, Larisa Ryzhova, Calvin PH Vary, Lucy Liaw. Co-Authors Institutional Affiliations: MaineHealth Institute for Research. COBRE

Rab27a is a ubiquitously expressed, small GTPase required for endosome transport to the plasma membrane. Several human mutations in Rab27a are linked to Griscelli syndrome, a rare, autosomal dominant, fatal disease. Based on quantitative SWATH mass spectrometry analysis of Rab27a null mice (RAB27a-/-), we found significant decreases in vasculature contractile proteins, including myosin heavy chain 6. This novel finding suggests a role for Rab27a in heart function. We tested the hypothesis that global loss of Rab27a will cause cardiac contractile dysfunction in mice. RAB27a-/- and littermate wild

type (WT) control mice underwent echocardiography at 8, 16, and 21 weeks of age. Starting at 16 weeks of age stroke volume decreased in RAB27a-/- (53.7±4.1µl WT vs. 44.3±3.0µl Rab27a-/-, p

73. Eric Tirrell, Butler Hospital. **Design and Analysis Core: Promoting Best Practice in Experimental Design and Implementation.** Co-Authors: Acuff, W. Luke , Gobin, Asi (Polly), Gonsalves, Meghan, Hannah Swearingen, Barredo, Jennifer , Rich Jones, Linda Carpenter, Benjamin Greenberg. Co-Authors Institutional Affiliations: Butler Hospital TMS Clinic, Neuromodulation Research Facility, COBRE for Neuromodulation, VA Center for Neurorestoration and Neurotechnology, Brown University Warren Alpert Medical School. COBRE

The Butler Hospital Center of Biomedical Research Excellence (COBRE) Center for Neuromodulation (CCN) brings faculty and research support staff with diverse scientific expertise together under the umbrella of the Design and Analysis Core (DAC). Research methodologies represented among DAC members include magnetic resonance imaging (MRI), diffusion imaging, biostatistics, electroencephalography (EEG), and magnetic resonance spectroscopy (MRS). DAC team members also bring strong data management and computer programming skills to CCN studies, expediting the implementation of analytic, archival, and data sharing activities. The DAC fosters scientific development by offering faculty-level scientific consultation, tutorials, training, and research resources. By merging collected expertise with automated data management and processing pipelines, the DAC helps ensure implementation of state-of-the-science best practices across research groups. For example, team members help research groups implement database hierarchies utilizing common elements and hierarchies like the Brain Imaging Data Structure (BIDS) standard. By centralizing and automating many study implementation and maintenance activities, the DAC enhances the CCN's research efficiency by avoiding redundant efforts in research projects essentially limiting the extent to which research groups reinvent the wheel each time they begin a new research study or analysis project. Furthermore, lessons learned from previous research studies are easily incorporated into the DAC's library, generally improving data quality, and preventing documented missteps from recurring.

74. Muge Sak, University of Louisville. **Variations in Exon Usage Within Immune-Related Genes in Multiple Sclerosis Brain Lesions.** Co-Authors: Julia H. Chariker, Eric C. Rouchka. Co-Authors Institutional Affiliations: University of Louisville. INBRE

Immune-related genes play a significant role in the development of Multiple Sclerosis (MS) by contributing to an abnormal immune response against the CNS, leading to inflammation and demyelination. Genetic variations in these genes can influence MS susceptibility and severity. One of the mechanisms that contribute to genetic variation is alternative splicing. Alternative splicing is a regulatory process in which a single gene generates multiple protein variants by combining or omitting specific exons during mRNA processing. Our objective is to identify genes showing patterns with increased expression of inflammation in MS lesions and the alternative splicing variants of immune-related genes in normal white matter (WM) and MS active lesion (AL) tissues. Here we utilized publicly available RNA-seq data (GSE 138614) from postmortem brain tissues (Table 1). Identification of genes showing regulation patterns with MS lesion progression was performed by Short Time-series Expression Miner (STEM v1.3.13) software. Differential splicing analysis was performed using the DEXSeq in R studio (3.6.0). Overall, 441 genes showed increased expression and 2335 genes showed decreased expression patterns with the MS lesion progression. We also predicted differential transcripts in WM and AL tissues for IGHG1 (IG Heavy Constant Gamma 1), IGSF9B (IG Superfamily Member 9B), IGSF1 (IG Superfamily Member 1) and IL18 (Interleukin 18). Our results may lead to identifying genes playing a key role in the progression of inflammation in MS lesions and important variations in genes that contribute to disease progression and the discovery of possible new treatment approaches.

75. Liliana Davalos, University of Nevada, Las Vegas. **The Association Between Personal Perception of Weight Status and BMI among Latino Parents.** Co-Authors: Timothy Grigsby, Brisa Rodriguez Alcantar, Marissa Martinez, Christopher Johansen. Co-Authors Institutional Affiliations: University of Nevada, Las Vegas. INBRE
Cultural norms among Latino families favor larger-sized children, and for less acculturated families, mothers frequently identify overweight children as normal weight. Previous research has also indicated that Mexican American women have a higher prevalence of obesity compared to their White counterparts. Perceived obesity and actual body mass index (BMI) may influence intention for weight loss, and little is known about how these factors are associated among Latino parents. Greater attention to Latinos' self-perception of weight is needed to develop obesity prevention interventions to improve health outcomes. Attention to Latina mothers, in particular, provides an opportunity to understand a relatively understudied population, especially since mothers are influential in the nutritional behavior of children, and maternal BMI has been positively associated with their child's BMI. A cross-sectional survey was administered to a convenience sample of Latina mothers residing in Southern Nevada (n= 196; Mage=33). Linear regression modeling was used to determine if there was a relationship between personal perception of weight and BMI for female respondents, controlling for age and income. Preliminary analysis reveals that perception of being overweight is a strong predictor of BMI ($\hat{I}^2$= 24.011, p

76. Marcus D. French, Benedict College. **Neurodegenerative disease pathways expressed in flight muscle histolysis of the house cricket, Acheta domesticus.** Co-Authors: Sarah Dornik, Rush H. Oliver. Co-Authors Institutional Affiliations: Walter Reed NMMC. INBRE
The dorsal longitudinal flight muscles (DLMS) of the house cricket, Acheta domesticus, are specialized tissues that degenerate through hormone-regulated programmed cell death (PCD). Transcriptome analysis of mRNA from DLMs suggests intracellular pathways utilized in the break-down of flight muscles may be similar to those affected in neurodegenerative diseases in humans. Our rationale is that since flight muscles share many of the intracellular pathways of neurons, gene expression patterns that regulate the normal process of flight muscle histolysis may reflect mechanisms that are disrupted to cause or contribute to neurodegenerative disorders in humans. We have analyzed genes from DLMs of the house cricket for homology to genes involved in neurodegenerative disease in humans. Target pathways include those for Parkinson's, Huntington's and Alzheimer's diseases. Specific genes for interest are Parkin, Pink1, Huntingtin, Huntingtin Interacting Protein and Amyloid-beta Precursor Protein. Primers were designed for polymerase chain reaction (PCR) to amplify cDNA prepared from total RNA isolated from DLMs, Fat Body and brains of crickets. PCR products were verified by DNA sequencing. We currently have probes for Parkinson's and Huntington's disease pathways. We will use these probes for quantitative PCR and targeted knock-down of gene expression. Our current results reveal highly conserved components of human neurodegenerative disease are expressed in flight muscles of the house cricket and that further analysis may shed light on mechanisms shared in neurodegenerative disease.

77. Janae Phillips, University of North Dakota. **Acute kidney Injury by Hypoxia Activates the Sonic Hedgehog Pathway in Renal Progenitor Cells.** Co-Authors: Seema Somji, Sarmad Al Marsoummi, Scott Garrett. Co-Authors Institutional Affiliations: University of North Dakota.
Hypoxia is the leading cause of kidney damage with the proximal tubule being the most vulnerable site. Tubular cell regeneration, driven by kidney progenitor cells, plays a vital role in recovery, yet we lack the understanding of the response to hypoxia. The Sonic Hedgehog (SHH) pathway is essential in kidney

development and post-injury fibrosis. This study investigates the impact of hypoxic conditions on the SHH pathway in the kidney progenitors and examines the role of CD133 in modulating this pathway. The CD133+/CD24+ kidney progenitor cells (HRTPT) and the CD133-/CD24+ non-progenitor cells (HREC24T) were isolated from the immortalized human proximal tubular cell line RPTEC/TERT1. Cells were cultured under hypoxic (2.5% O2) or atmospheric conditions for 48 and 72 hours. RT-qPCR and Western blotting were used to analyze the expression of SHH, SMO, GLI1, GLI2 genes. Our data shows that the HRTPT cells have lower basal expression of SHH, GLI1, and GLI2 compared to the HREC24T cells. However, the expression of SMO is higher in the HRTPT cells compared to the HREC24T cells. Under hypoxic stress, the expression of SHH, GLI1, and GLI2 is increased and the increase in GLI1 persists for 72 hours in HRTPT cells suggesting a prolonged response to hypoxia. Knockdown of CD133 in HRTPT cells results in a decrease in GLI1 expression, implicating CD133 as a pivotal regulator within the SHH pathway. In conclusion, our study shows the activation of the SHH pathway in the HRTPT cells under hypoxia and establishes CD133's essential role in the SHH pathway.

78. Michael G. Nichols, Creighton University. **Development of a non-invasive, non-linear optical biopsy to assess changes in metabolism and collagen structure with the development of UV-induced skin cancer in SKH1 mice.** Co-Authors: Alex Chen, Kennedy A Haase, Reese A Kolar, Jackson M Laurent, Jonathan Li, Aidan J O Mara, Maimuna Nagey, Greer L Porter, Jalen K Ramos, Derek A Remitar III, Abraham J Saks, Hannah Schloman, Jinann A Shoshara, Zachary J Smith, Fiona Sun, Jacob A Sweet, Jake S Wakahiro, Laura A Hansen. Co-Authors Institutional Affiliations: Creighton University. INBRE
Changes in cellular metabolism and remodeling of the extracellular matrix (ECM) are well known diagnostic indicators of cancer. Both can be simultaneously assessed by non-linear optical imaging of metabolic cofactors and collagen. We conducted a longitudinal imaging study using the multiphoton fluorescence lifetime imaging (FLIM) of NAD(P)H in the epidermis and second harmonic generation (SHG) of collagen in the dermis to follow the development of UV-induced skin cancer in the SKH-1 mouse model. For these in vivo studies, significant differences in the bound-NADH fraction and collagen became evident after 8 weeks of chronic UV exposure (19 kJ/m2/day, 50% UVA, 50% UVB, 5 days/week) with a stronger effect observed in females compared to males. Additional in vitro experiments were conducted to determine the impact of oxygenation and HER2 expression on the optical metabolic signal. We tested the hypothesis that the NAD(P)H concentration, fraction of protein-binding, and electron transport chain (ETC) activity would change when cells were grown under hypoxic conditions. NAD(P)H Phasor FLIM clearly reflected changes associated with oxygen availability and HER2 expression. Changes in ETC utilization was also observed with a strong interaction between these two factors. These results demonstrate the diagnostic potential for non-linear optical imaging to reveal changes in metabolism and remodeling of the ECM associated with the development and progression of cancer. This research was supported by NIGMS of the NIH under Award Number 5P20GM103427. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

79. Ruth Fabian-Fine, Saint Michael's College. **The structural failure of aquaporin 4 expressing Tanycytes may be the underlying cause for neurodegeneration in Alzheimer patients.** Co-Authors: None. INBRE
During the onset of Alzheimer disease, neurons in both the locus coeruleus (LC) and hippocampus of Alzheimer Dementia patients undergo irreversible degeneration, resulting in debilitating memory loss and behavioral deficits. The progressive nature of this neurodegenerative disease that ultimately spreads to other brain areas inevitably ends in death of affected patients, which highlights the importance and urgency to identify the underlying causes for this disease. Our theory is that degeneration of neurons in both the locus coeruleus and hippocampus are caused by pathological

changes in tanycytes, a type of ependymal glial cells with characteristically long cell projections. Their location in the ventricular lining is adjacent to the LC and hippocampal formation. We propose that an important role of these aquaporin 4-like immunoreactive ependymal cells is the, aquaporin-mediated, removal of cellular waste from metabolically active neurons via cellular protrusions that project into the neuronal cytoplasm. We have demonstrated that aquaporin4/vimentin double labelled tanycytes consistently form cellular projections into adjacent hippocampal neurons. Such projections can also be observed at the ultrastructural level and are commonly dismissed as fixation artifacts, however we have demonstrated similar unambiguous glial projections in wellfixed mammalian hippocampus. We were able to show that these intraneuronal glial projections are likely important for waste clearance from healthy neurons. We postulate that the structural failure of tanycytes that are in close contact with neurons lead to the uncontrolled aquaporin4-mediated depletion of neurons.

80. Patrick Habecker, University of Nebraska-Lincoln. **Facilitating Research On Substance Use: The Longitudinal Networks Core (LNC) Service Center.** Co-Authors: Kim Tyler. Co-Authors Institutional Affiliations: University of Nebraska-Lincoln. COBRE
The Longitudinal Networks Core (LNC) facilitates research with people who use drugs (PWUD), provides expertise in hard-to-reach populations, and develops specialized mobile research software. The LNC is a service center in the Rural Drug Addiction Center (RDAR) COBRE at the University of Nebraska-Lincoln and supports the center's mission to further interdisciplinary research on substance use in the Great Plains of the US. LNC resources reduce barriers to substance use research and expanding engagement in substance use and related health disparities research in three distinct ways. 1) The LNC recruits and maintains a longitudinal cohort of people who use drugs. Participants complete surveys every 6-9 months on a range of substance use, health, and social network topics. 2) Cohort members may also volunteer to join a participant pool of PWUD from which other researchers working with the RDAR center may recruit interested participants. 3) The LNC has cutting-edge software to collect and analyze data that provide unique insights into dynamic patterns of substance use. The cornerstone of these is ODIN, a unique mobile app, designed for responsive ecological momentary assessment. In addition, a principal goal of the LNC is to help investigators who are new to substance use research develop research trajectories around substance use and develop competitive grant proposals.

81. Christopher Bender, Marshall University. **Genetic Diversity of the SARS-CoV-2 Virus Over the Course of the COVID-19 Pandemic.** Co-Authors: Julia Cardot, Peter Stoilov, Swarna Kanchan, James Denvir. Co-Authors Institutional Affiliations: West Virginia University, Marshall University. CTR
We investigated the diversity, measured by Shannon entropy, of SARS-CoV-2 protein sequences derived from over 8 million nucleotide sequences deposited in the NCBI from January 2020 until March 2024. Sequences were downloaded and filtered for those with exact dates of sample acquisition. We used Nextclade to translate nucleotide sequences to protein sequences and align the protein sequences. Entropy at each amino acid position was computed at each date, using all sequences from a 28-day window for that date using custom python scripts, and R scripts were written for visualization. The SARS-CoV-2 spike protein showed increases in average entropy across the protein which correlated with both emergence of new variants and winter months in the northern hemisphere. The diversity was low while the Delta variant predominated. Increases in diversity included the recent period from December 2023 to February 2024. The location along the protein of the diverse amino acids responsible for these spikes varied as the pandemic progressed. These results indicate that the SARS-CoV-2 virus continues to evolve, suggesting that

continued monitoring of the virus on the level of genomic sequencing may be beneficial to public health initiatives.

82. Sarah Thomas, Bradley Hospital/Alpert Medical School of Brown University. **Resting state functional connectivity associated with cognitive flexibility performance in the Adolescent Brain Cognitive Development Study.** Co-Authors: Sarah K. Ryan, Jodi Gilman. Co-Authors Institutional Affiliations: Bradley Hasbro Children's Research Center, MGH/Harvard Medical School. COBRE
Cognitive flexibility is an executive functioning skill that develops in childhood, and when impaired, has transdiagnostic implications for psychiatric disorders. To identify how intrinsic neural architecture at rest is linked to cognitive flexibility performance, we used the data-driven method of Independent Component Analysis (ICA) to investigate resting state networks (RSNs) and their whole-brain connectivity associated with levels of cognitive flexibility performance in children. We hypothesized differences by cognitive flexibility performance in RSN connectivity strength in cortico-striatal circuitry, via the executive control network, right and left frontoparietal networks (FPN), salience network, default mode network (DMN), and basal ganglia network. Participants were from the Adolescent Brain Cognitive Development (ABCD) Study who scored at the 25th, (CF-Low), 50th (CF-Average), or 75th percentiles (CF-High) on a cognitive flexibility task, were early to middle puberty, and did not exhibit significant psychopathology (n=967, 47.9% female; ages 9-10). We conducted whole-brain ICA, identifying 14 well-characterized RSNs. Groups differed in connectivity strength in the right FPN, anterior DMN, and posterior DMN. Planned comparisons indicated CF-High had stronger connectivity between right FPN and supplementary motor/anterior cingulate than CFLow. CF-High had more anti-correlated connectivity between anterior DMN and precuneus than CF-Average. CF-Low had stronger connectivity between posterior DMN and supplementary motor/anterior cingulate than CF-Average. Post-hoc correlations with reaction time by trial type demonstrated significant associations with connectivity. Our results suggest childhood cognitive flexibility performance is associated with DMN and FPN connectivity strength at rest. There may be optimal levels of connectivity associated with task performance, varying by network.

83. Tahmina Akter Anondi, Louisiana State University Shreveport. **Predicting Hospitalizations for Asthma and COPD based on PM2.5, seasonality, and COVID-19 factors.** Co-Authors: Mridula Mavuri, Devesh Sarda, Subhajit Chakrabarty. Co-Authors Institutional Affiliations: Louisiana State University Shreveport. INBRE
Hospitalizations for Asthma and COPD is a significant concern in the United States, with environmental factors such as Particulate Matter (PM) 2.5 pollution playing a crucial role. The first objective of the study was to predict hospitalization for asthma and COPD based on PM2.5 levels, using annual frequency data, at county-level in USA. The second objective was to predict hospitalization for asthma in Louisiana, based on PM2.5 levels and seasonality considerations, using monthly frequency data. The third objective was to explore the impact of COVID-19 on asthma hospitalizations in Louisiana. Our data was obtained from the National Environment Public Tracking Network by Centers for Disease Control and Louisiana Department of Health. The PM2.5 data was the annual average concentration. The asthma hospitalization data was the annual number of patients. The COPD hospitalization data was the annual numbers of patients older than 24 years of age. Our period was 2001 to 2019 for annual data, and 2010 to 2019 for monthly data. Heat-maps were created. No change-point was detected in the annual time-series. However, change-point was detected in the monthly times-series data, during the COVID-19 period. We used basic Long Short-Term Memory (LSTM), modified LSTM and Transformer, as Deep Learning (DL) techniques to model the data. The novelty of this work was to use transformer in this context. Results indicated a good accuracy of our prediction. The significance of this research is to

provide insights for capacity planning for hospitals and public health strategies, using state-of-the-art DL techniques like transformer.

84. Tara Craft, West Virginia University. **West Virginia University Experimental Stroke Core.** Co-Authors: Kate Weil, Ning Zhang, Deborah Corbin, James Simpkins, A. Courtney DeVries. Co-Authors Institutional Affiliations: West Virginia University. COBRE
The overall goal of the WVU Experimental Stroke Core (ESC) is to support translational research projects of cerebrovascular and cardiovascular investigators at WVU and WV INBRE partners by providing the instrumentation, surgical expertise, resources, and training to investigators and their staff. As such, core users have the option of receiving surgical training and access to necessary surgical equipment/space or having one of our skilled vascular surgeons perform the procedures. Available small animal experimental stroke and brain injury models include transient and permanent middle cerebral artery occlusion, photothrombotic ischemia, microembolic stroke, chronic cerebral hypoperfusion (asymmetric carotid artery stenosis and bilateral carotid artery stenosis), traumatic brain injury (closed head injury and controlled cortical impact), oxygen glucose deprivation, and hypoxia. Additional equipment and expertise are available to core users for the measurement of injury-induced changes in cerebral blood flow (laser doppler and laser speckle flowmetry), blood pressure, blood gases, and vascular function (pressure myography). Surgical equipment is also provided for pharmacological treatment of experimental mice, including stereotaxic instrumentation, syringe pump, and mouse tail vein illuminator. The ESC also offers space and equipment for tissue collection, as well as technical expertise in tissue processing including intracardiac perfusion, tissue dissection, cryosectioning, and immunohistology. Core staff work closely with users of our facility to assist with experimental design, animal protocol development, data collection, and facilitate grant applications and manuscript preparation.

85. Reydiliz Nieves-Acevedo, Inter-American University of Puerto Rico, Bayamon Campus. **New Quassinoids Isolated from the Hexane Extract of Simarouba.** Co-Authors: Claudia A. Ospina-Millan. Co-Authors Institutional Affiliations: Inter-American University of Puerto Rico, Bayamon Campus. INBRE
The Simaroubaceae family is a group of brushes and trees characterized by the presence of quassinoids. Quassinoids are complex and highly oxygenated organic molecules composed of approximately 18 to 25 carbons that are responsible for many biological activities such as antimalarial, antiviral, insecticide, and antitumor potential. In our ongoing efforts to discover new compounds with anticancer activity, we tested the antiproliferative effects of the chloroform and hexane extract of Simarouba on ovarian and breast cancer cell lines. The hexane extract showed an inhibition potential at a concentration of 24 ng/mL against breast cancer cells. However, the chemical composition is unknown. Therefore, the goal of this study is to identify new quassinoids with anticancer activity by purifying the fractions of the hexane extract using chromatographic and spectroscopic techniques. Fraction 16 was chromatographed on Silica gel with a mixture of 20% ethyl acetate in hexane. The 1H- NMR spectrum of the collections from fraction 16 showed the presence of aliphatic, allylic, oxygenated, vinylic, and aromatic protons. Subfractions 16H and 16I indicate the presence of proton signals corresponding to quassinoids with two methoxy groups. These subfractions were purified by column chromatography using 3% acetone in chloroform and analyzed by 13CNMR and 2D NMR spectroscopy to obtain more information about the structure. This preliminary data suggests that the compound isolate is a new quassinoid derivative. However, additional analysis is required to confirm the stereochemistry. Additionally, we expect to evaluate the cytotoxic activity of this compound to explore its potential as a possible cancer treatment.

86. Steven M. Poyer, University of Wyoming. **Microbial Stem Cells: Using Asymmetric Division to Enhance Bioreactor Productivity.** Co-Authors: None. INBRE

Bioreactors have become an increasingly attractive method for the production of renewable fuels, pharmaceuticals, food additives, and the management of agricultural waste. While the underlying technology continues to improve efficiency and yield, a significant hurdle to the use of bioreactors remains that product synthesis and cell proliferation are often mutually antagonistic activities, leading production to be self-limiting. An elegant solution to this problem is to control cell differentiation within a culture, allowing the roles of cell growth and product synthesis to be assigned to two different cell types. The first cell population, factory cells, would sustain constant production, utilizing all cell machinery to that end. While a second population, stem cells, would focus solely on asymmetric cell division, leading to constant replenishment of the factory cells. As many diverse organisms are used in bioreactors, our research focusses on disparate methods of leveraging asymmetric differentiation to achieve these goals.

87. Becca Olson, University of Alaska Fairbanks. **Changes in Anaerobic Cycles in the Boreal Forest.** Co-Authors: None. INBRE
As the climate continues to change, arctic and subarctic environments are being disproportionately impacted. From increased wildfire to permafrost thaw, climate change is altering boreal ecosystems in a myriad of ways, including by increasing soil moisture. Near-surface permafrost thaw can lead to increased soil moisture, creating anoxic soil environments, and increasing anaerobic microbial activity. The microbes include those involved in the methane cycle and the mercury cycle. An elevated rate of permafrost thaw unlocks previously unavailable organic matter for metabolism by microbes involved in the production of methane. Permafrost thaw also releases stored inorganic mercury that may be methylated by microbes, which has implications for the release of monomethylmercury into watersheds. Both of these processes have an impact on the environment and these cycles may be interacting with one another. Certain microbes that break down methane and those that methylate inorganic mercury both use sulfate as an electron acceptor. These microbes could be competing for sulfate, so the cycles may be changing in response to each other as well as the climate. Understanding this gap in knowledge is important because methanogenesis produces CH4, a potent greenhouse gas, and mercury-cycling microbes can produce monomethylmercury, a neurotoxin. Fish consumption is the main pathway for human mercury exposure. This is especially important in the state of Alaska, due to the large portion of native Alaskans that depend on subsistence fishing and hunting.

88. Angelie A. Carrión-Vélez, University of Puerto Rico, School of Medicine, San Juan, Puerto Rico. **Dynamics of the longitudinal changes of Human Papillomavirus infections in women living in Puerto Rico.** Co-Authors: Andrea Cortes-Nazario, Andrea Padilla-Bou, Bianka Morales-Pomalaza, Claudia Rosado-Torres, Josefina Romaguera, Filipa Godoy-Vitorino. Co-Authors Institutional Affiliations: University of Puerto Rico, Medical Sciences Campus University of Puerto Rico. INBRE
Persistent human papillomavirus (HPV) infections are the primary cause of cervical cancer. While most HPV infections are cleared naturally in young women, progression, and clearance of these remain poorly understood in older women. We recruited 71 women ages 21-70 visiting colposcopy clinics in San Juan, Puerto Rico (IRB# 1050114) for an initial visit and follow-up visit within one year if presenting Negative Intraepithelial Lesions (NILM) and within six months for High-Grade Lesions (HGSIL). These women were followed across two visits where cervical swabs were obtained for pap smears and genotyping. DNA was extracted from cervical swabs for HPV genotyping using a high-resolution SPF10 assay that amplifies 60 known HPV strains and hybridizes the SPF10 PCR product on the LiPA25, limited to 25 of the most relevant and prevalent genotypes. We compared the types and risk groups of the HPVs in the two visits and across cervical disease status. 11% of the recruited women maintained a negative HPV status, while 41.25% remained positive. Among women who were HPV positive, 36.25% became HPV negative by the

second visit. The transitions from High-Risk to High and Low-Risk genotypes, and High-Risk to High-Risk represented 12.82% of transitions. Women tend to maintain HPV infections, especially High-Risk HPV; however, 23% of women had regression of High-Risk types to HPV negative. The factors modulating the persistence and transitions of HPV dynamics are not yet understood. The alteration patterns of HPV infection detected included persistence and regression and may help guide patient follow-up.

89. Simrat Kaur Dhillon, Brown University. **Elucidating the Novel Role of Alternative Splicing of N-type Calcium Channels in Learning and Memory.** Co-Authors: Ava Cardarelli, Colin P. Call, Arturo A. Andrade. Co-Authors Institutional Affiliations: Brown University. INBRE
The hippocampus is critical for learning and memory. Particularly, pyramidal neurons of the CA1 region are crucial for memory processes. CA1 pyramidal neurons are under powerful inhibitory control of GABAergic cholecystokinin-expressing interneurons (CCK-INs). Interestingly, CCK-INs rely solely on presynaptic CaV2.2 channels to release GABA. We have previously shown that alternative splicing in the Cacna1b gene, encoding CaV2.2 channels, impacts calcium channel function. Notably, alternative splicing of the cassette exon 18a, which generates Î”18a and +18a variants with distinct functional properties and expression patterns. The +18a splice variant generates larger calcium currents and is enriched in CCK-INs compared to the Î”18a splice variants. Given these preliminary observations, this study investigates the influence of exon 18a alternative splicing on hippocampal-dependent function. To do this, we generated mice that lack the +18a-splice variant or Î”18a-only Initial findings in Î”18a-only mice show no significant differences in locomotion and exploratory behavior in the open field, or spatial working memory in the Y-maze. We did not observe significant differences in spatial navigation in the Barnes Maze. However, long-term contextual fear conditioning reveals increased freezing behavior in Î”18a-only mice, suggesting altered memory retrieval. Moreover, trace fear conditioning, which targets CA1-related behaviors, demonstrates heightened freezing responses in Î”18a mice during the trace period (p=0.015) and cue exposure (p=0.023) in the training phase. Importantly, these effects appear independent of sex. Overall, these preliminary results suggest a novel role for alternative splicing of exon 18a of Cacna1b in modulating hippocampal function. Shedding light on potential role of presynaptic mechanisms on memory formation.

90. Lyndsay Avery, Saint Michael's College. **Determining the effects of a patient mutation in moesin on T cell development.** Co-Authors: Lily Sabol. Co-Authors Institutional Affiliations: Not Listed. INBRE
Moesin is an actin-binding protein linking the cytoskeleton to the plasma membrane. Cycling between an open and closed conformation, it plays a role in cell shape change and cell migration. The importance of moesin in T cells, specifically, is exemplified by the disease Xlinked Moesin-Associated Immunodeficiency (X-MAID) caused by a single-point mutation (moesinR171W). These patients exhibit profound lymphopenia causing persistent and recurrent infections, with bone marrow transplant being the only known treatment. Based on characterization of patients and mouse models, T cells with moesinR171W have defects in migration. Because T cell differentiation relies on a functioning cytoskeleton and migration, we hypothesize that this mutation results in the inability of hematopoietic stem cells (HSCs) to properly differentiate to lymphoid progenitors, contributing to patient lymphopenia. In this study we aim to elucidate the effects of the X-MAID mutation on the differentiation of HSCs to T cell progenitors in an in vitro setting. To do this, HSCs from WT and X-MAID mouse bone marrow ,are isolated and differentiated using FLT3L and IL-7 on an OP9DL1 stromal cell line. We expect fewer T cell progenitors in the X-MAID samples suggesting that the mutation in moesin affects the differentiation process. However, in this reductionist system, it is possible that we don’t observe any significant difference in numbers. This would suggest that migration is the primary defect in XMAID T cell progenitors. The results of this study

are critical to understanding the role of moesin in T cell differentiation with clear implications for future therapeutic development.

91. Chelsea Howd, Western Kentucky University. **Examining the Association Between Boredom-Coping Substance Use Motives and Future Self-Injurious Behaviors.** Co-Authors: Anzlee Utley, Danielle Williams, Amy Brausch, Jenni Teeters. Co-Authors Institutional Affiliations: Western Kentucky University. INBRE

Suicide is now the second leading cause of death in the U.S. (CDC, 2021), with studies showing a higher risk tied to excessive alcohol and drug use (Bohnert et al., 2017). Some adults use substances to alleviate boredom (Doering et al., 2023), and understanding the link between these motives and suicidal behaviors is crucial due to the increased risk of self-injurious behaviors associated with substance misuse (Markowitz et al., 2002). This study explored how using substances to cope with boredom affects non-suicidal self-injury (NSSI) and suicidal behaviors in adults, expecting an association between boredom-coping motives and self-ratings of future NSSI and suicidal behaviors. Data were collected from 401 adults in the U.S. (mean age=23, SD=3.6) using the online survey platform Prolific. The sample was female (55%), heterosexual (60%), and 49% White. Participants completed the Substance Use Motives Measure (SUMM), which includes a boredom-coping subscale, and the Self-Injurious Thoughts and Behaviors Interview-Revised. Linear regression analyses were run and found that boredom-coping motives was significantly associated with ratings of future NSSI (B=.074, p=.015), and the association with ratings of future suicide plan (SP) approached significance (B=.026, p=.053). Boredom-coping motives was not associated with ratings of future suicide ideation (SI) or suicide attempts (SA). Boredom-coping motives was associated with ratings of future NSSI and SP, but not SI or SA. Boredom might trigger sensation-seeking behaviors as explained by the automatic positive reinforcement theory of self-injury (Nock & Prinstein, 2004). Future studies on NSSI risk should explore boredom coping motives, especially among substance users.

92. Emily Schmitt, University of Wyoming. **The Role of Exercise in Controlling Central Mediators of Circadian Rhythm.** Co-Authors: William D. Todd, Cole Wyatt. Co-Authors Institutional Affiliations: Not Listed. COBRE

Circadian disruption can lead to many deleterious health outcomes including neurological disorders, stroke, and metabolic syndrome. Despite the well-known benefits of exercise to overall health, limited studies have utilized exercise as a way to restore clock function centrally, specifically in the suprachiasmatic nucleus (SCN). Additionally, exercise has emerged as an intriguing tool that can be beneficial for diseases of the nervous system but could also help identify potential molecular targets for pharmacological approaches. Sixty-four (n=32 males, n=32 females) C57Bl/6J mice were used in this experiment. Animals were disrupted (7h advance, weekly) and exercised for 4 weeks (up to 65% aerobic capacity) to mimic chronic circadian disruption and exercise as seen in humans. At sacrifice, brains were removed, incubated in 20% sucrose at 4â€‰Â°C, and then sectioned at 40â€‰Âµm on a freezing microtome in three series for immunohistochemistry analysis of the SCN and incubated in primary c-Fos, NYP, and 5-HT antibodies. Sections were then washed, mounted, and imaged on a confocal microscope. Our preliminary results suggest that chrono-timed exercise during circadian disruption via continual light-dark cycle phase shifts results in a pattern of c-Fos expression (a marker of neuronal activation) that more closely resembles undisrupted mice compared to mice that did not exercise. We also expect our co-labeling staining for NYP and 5HT fibers to have similar results as the Fos expression, given previous research on exercise-induced entrainment. Future experiments will continue to assess the mechanisms by which exercise can restore proper function of the SCN clock under disrupted light-dark cycles.

93. Sharon Patrick, West Virginia Clinical and Translational Science Institute. **Developing a Shared Education and Training Curriculum for Real World Data Sciences in the National COVID Cohort Collaborative (N3C).** Co-Authors: Amber Abel, A. Jerrod Anzalone, Sally Hodder. Co-Authors Institutional Affiliations: West Virginia Clinical and Translational Science Institute, University of Nebraska Medical Center Great Plains-CTR. CTR

The National COVID Cohort Collaborative (N3C) presents a novel and unique opportunity to develop new educational opportunities for using real-world data (RWD). While the ongoing COVID-19 pandemic was occurring, the N3C was created as a secure data repository housing electronic health record from healthcare organizations nationwide. This data platform creates a comprehensive tool for education and training in clinical data sciences to train up-and-coming researchers and develop healthcare informatics while understanding the intricacies of RWD. Creating a shared education and training curriculum helps bridge gaps in clinical subject matter areas and will increase the number of trained researchers using RWD. The curriculum outlines the basic concepts of harmonized electronic medical records, including data acquisition from healthcare organizations. The curriculum focuses on the management of the data discussing ethical use of clinical data and ensuring the privacy of patients and the data contributing sites. Shared training and education material fosters collaboration across the N3C community making studies more reproducible. Collaboratively conducted two short courses on the use of RWD and the N3C dataset, geared toward investigators, data analysts, and statisticians. The first course had 20 attendees and the second course had 68 registrants. Shared knowledge has led to the creation of The Researcher's Guide to N3C, to create a comprehensive resource for the N3C Community. The future development of Shared Education and Training Curriculum for Real World Data Sciences will leverage knowledge from clinical data science experts and will help to train for the future.

94. Andreia Verissimo, Dartmouth College. **bioMT core facilities: advancing research at Dartmouth.** Co-Authors: Angela Kull, Zdenek Svindrych, Pat Robison, Susu He, Noor Taher, Emilie Shipman, Dean Madden. Co-Authors Institutional Affiliations: Not Listed. COBRE

The COBRE Institute for Biomolecular Targeting (bioMT) supports researchers at Dartmouth at the interface between discovery and translation, with emphasis on identification and validation of therapeutic targets for cancer, infection, and inflammation. The Molecular Tools Core (MTC) and Molecular Interactions and Imaging Core (MIIC) integrate protein biochemistry, biophysics, structural biology, and microscopy to: a) Support research projects: MTC generates high-quality proteins and other molecular tools using an integrated pipeline for easy protein expression, purification, and crystallization. We employ HTP protocols to generate tens of constructs for expression screening in multiple hosts in just a few days. The MIIC supports label-free analysis of biomolecular interactions and numerous image applications and provides expertise on a broad range of microscopy modalities to visualize biological processes at cellular and subcellular levels. b) Enhance the technology portfolio and provide training opportunities: our cores act as a hub for state-of-the-art equipment and, importantly, technical expertise in classic techniques and cutting-edge technologies. We deliver individual or group training on available instrumentation and workshops on advanced methodologies and image analysis. c) Develop education initiatives: We offer immersive hands-on wet lab training to undergraduate students enrolled in summer programs at Dartmouth (INBRE, POWERED, ASURE, ISURE) to help develop research skills that can be directly applied towards research careers and/or graduate studies in the biomedical sciences. We are currently developing survey hands-on courses on Protein Production & Analytics and Microscopy & Image analysis geared towards graduate students, to provide an overview of the technologies available at Dartmouth.

95. Gerrit Bjornstad, Mayville State University. **Utilizing Medium and Long Chain Fatty Acids to Resolve HSA Binding Characteristics in Simple Coumarin Fluorescent Lifetime Probes.** Co-Authors: Thomas Gonnella. Co-Authors Institutional Affiliations: Mayville State University. INBRE
Fatty acids (FAs) play a critical role in energy metabolism and are the main building blocks of complex lipids. Their low solubility in plasma is significantly improved upon binding to human serum albumin (HSA), the most abundant protein in the circulatory and lymphatic system. X-ray crystallographic and NMR studies have shown that HSA has up to nine FA binding sites that may be occupied by medium to long chain (C10-C18) saturated fatty acids. Comparison of the three-dimensional structures of defatted HSA and HSA-FA complexes has revealed that the binding of FA molecules to HSA causes relative rearrangements at HSA domain interfaces and conformational changes of side chains within one of the HSA subdomains. Ligand binding affinity for HSA is one of the most important factors that affects the distribution and free concentration of many ligands and this binding affinity can be modulated through simultaneous binding of FAs. The influence of FAs on ligand binding to HSA can be due to competitive binding between a ligand and an FA at the same binding site or allosteric effects from the binding of FAs. Our group has examined the effects of FAs on the binding of our ten different coumarin fluorescent lifetime probes to HSA. By fluorescence lifetime approach, a range of results were observed from simply competitively replaced of the bound probe by FA to probes remaining bound to HSA. In a couple of cases, the probes changed fluorescent lifetimes which suggests an expansion in the size of the surrounding cavity.

96. Brittany K. Taylor, Boys Town National Research Hospital. **Is your home safe? The neurodevelopmental consequences of chronic indoor radon exposure.** Co-Authors: Haley R. Pulliam, Monica Clarke-Smith, Sarah Hunter, OgheneTejiri V. Smith, Gregory E. Miller, Tony W. Wilson. Co-Authors Institutional Affiliations: Boys Town National Research Hospital, Northwestern University. COBRE
It is well established that children's brains are uniquely susceptible to the deleterious effects of exposure to numerous environmental toxins including particulate matter, lead, and other highly prevalent toxins and toxicants. Still, some ubiquitous toxins have yet to be studied for their potential impacts on neurodevelopment in youth. One such toxin is radon, a naturally occurring, radioactive gas that is known to accumulate in homes, and is the second-leading cause of lung cancer worldwide. The Environmental Protection Agency (EPA) estimates that 1 in every 15 homes across the United States will test high for radon, yet public awareness and mitigation efforts remain alarmingly low. In a series of studies supported by the Center for Pediatric Brain Health (COBRE: P20-GM144641), we elucidate the effects of chronic home radon exposure on neurodevelopment among children and adolescents living in a region of the country where at least half of all homes are expected to test over the EPA's recommended limit for radon levels. Using combinations of immune biomarkers, state-of-the-art multimodal neuroimaging, and neuropsychological testing, we demonstrate the potential mechanistic pathways through which radon modulates expected trajectories of neurodevelopment in systems critical for everyday cognitive and mental health functioning.

97. Matthew Kays, West Virginia University. **Mice exhibit impaired performance in a pairwise discrimination task after transient middle cerebral artery occlusion.** Co-Authors: Nurullah Sati, Victoria Smith, Clara Woods, Aminata Coulibaly. Co-Authors Institutional Affiliations: West Virginia University. COBRE
Stroke remains the fifth leading cause of death and a leading cause of disability in the United States. One of these disabilities is post-stroke cognitive impairments that occurs in 60% of stroke survivors and causes a significant diminishment in quality of life. Stroke recovery in mice is often characterized using simple behavior tasks. This limited approach reduces the damage to the brain to a few regions and

misses the overall view of the changes in this organ. To address this, we use a pairwise discrimination (PD) task to assess the global health of our mice brains after stroke. We hypothesize that mice stroke will lead to long term cognitive deficit underlie by damage to various areas of the brain. We expect these changes, in both cognition and brain damage to vary between male and female mice. There are no significant cognitive differences between our stroke mice and the sham animals during the acute phase of the injury (day 7-11). However, male mice exhibit a cognitive impairment in the chronic phase (weeks 2-12). We were unable to characterize the female mice due to poor survival rate (40%) compared to males (93.75%). FJC staining of male and female brains after tMCAO revealed a sex disparity in the size of infarction and regions effected by ischemia. Based on other preliminary data, we postulate this difference to be dependent on neutrophil infiltration of the brain. Therefore, we plan to ablate neutrophils before stroke and characterize the impacts on cognitive recovery in our model.

98. Reagan Kaleigh Gray, West Liberty University. **Bacillus species inhibits Methicillin-Resistant Staphylococcus aureus growth.** Co-Authors: Joseph Horzempa. Co-Authors Institutional Affiliations: West Liberty University. INBRE

Methicillin-Resistant Staphylococcus aureus (MRSA) and other antibiotic resistant strains of S. aureus present a significant risk due to limited treatment options available to combat potentially life threatening infections caused by these bacteria. Since staphylococci, including MRSA strains, can populate the microbiota of individuals, we hypothesized that antagonistic bacteria would likely also be present among these microbes. Therefore, sample swabs were collected to identify bacteria from the human microbiota that are capable of killing or inhibiting the growth of MRSA. Bacillus aerius was identified to have the most pronounced anti-MRSA activity and was selected for further analysis. Cellular extracts of B. aerius alone did apparently inhibit the growth of S. aureus so we hypothesized that a cell-to-cell interaction was likely responsible. Fluorescence microscopy showed that direct interaction between these two bacteria led to a reduction in the S. aureus population. Current efforts in the laboratory aim to determine whether laboratory Bacillus strains are also capable of mediating anti-MRSA effects. If so, recombinant fluorescent strains will be used to help elucidate the molecular mechanism of the anti-MRSA activity.

99. Shamrat Kumar Paul, Clemson University. **Exploring the diversity and function of the RTA1-like protein family in Aspergillus fumigatus.** Co-Authors: Stephen K. Dolan. Co-Authors Institutional Affiliations: Clemson University. COBRE

The ubiquitous, mold Aspergillus fumigatus (Af) is responsible for most tissue damaging, invasive pulmonary aspergillosis cases. The cumulative toll of chronic, invasive, and allergic aspergillosis results more than 500,000 deaths worldwide each year. The RTA1-like protein family is common in fungi, particularly in Af, which harbors over 20 RTA1 gene copies. These proteins have multiple transmembrane regions and are unique to fungi. RTA1 transcripts are significantly upregulated when fungi encounter several cellular stressors. While some RTA1 genes in yeast have been examined, the function of genes in filamentous fungi remains unclear. Using a combination of large-scale genome-wide analysis, coupled with gene expression data, we examined RTA1 proteins in Af. We identified over 800 in aspergilli, with 25 copies in the Af strain A1163. Despite sharing core features, these proteins exhibit significant sequence variability, implying specialized roles. Gene expression data revealed distinct regulatory networks for RTA1 proteins, suggesting responses to specific environmental cues. We generated a full deletion library of Af RTA1 mutants and screened the susceptibility of these 25 Af RTA1 mutants to various clinically relevant stressors alongside the wild type. We uncovered that multiple RTA1 genes may have a crucial role in responding to clinically relevant stressors. Treating Af infection remains challenging, with rising antifungal resistance, and a lack of new therapeutics to target this organism. Complementation of mutants of RTA1-encoding genes in Af, coupled to transcriptomics studies will provide further insight

into the biological roles and therapeutic potential of targeting these fungal-specific, stress-responsive proteins.

100. Heather Driscoll, Norwich University. **Vermont Biomedical Research Network Data Science Core Facility.** Co-Authors: Julie Dragon, Emily Curd, Nathan Herzog. Co-Authors Institutional Affiliations: University of Vermont. INBRE
The Vermont Biomedical Research Network (VBRN) Data Science Core (RRID: SCR_017686) provides informatics support and training to biomedical researchers in Vermont and Northeast Regional IDeA States. Our mission is to maintain currency with the latest tools and best practices in bioinformatics, data analysis and handling, and artificial intelligence, to be valuable collaborators as information professionals for research teams, and to support and train VBRN investigators in data science practice. Our services include genomic, transcriptomic, and proteome informatics; biostatistics; systems biology; database development; and information technology, including data storage infrastructure and high-performance computing. Working closely with the VBRN Proteomics Facility, we offer investigators experimental design consultations, data analysis, data management and publishing, and manuscript and grant support. Core personnel engage in targeted teaching and training activities associated with VBRN investigator research projects as well as introductory coding workshops and short courses for faculty and students across the network. A new internship program in the Core gives students in-depth data science training and practice. Additionally, Core members participate in regional and national projects to promote the sharing of research resources including the Association for Biomolecular Resource Facilities Core Marketplace, a resource developed and maintained by this Core and shared with ABRF. Here we highlight some recent collaborations with VBRN Primarily Undergraduate Institution (PUI) faculty and students as well as with investigators from the lead institution. The VBRN Data Science Core is funded by NIH 8P20GM103449 (NIGMS INBRE).

101. Morgane Vandendoren, University of Wyoming. **Oxytocin neuron activity and the coordination between social behavior and thermoregulation.** Co-Authors: Jason Landon, Joseph Rogers, Adam Nelson. Co-Authors Institutional Affiliations: University of Wyoming. COBRE
Huddling provides two major benefits to endotherms: thermoregulation and social reward. Regulation of body temperature is fundamental to homeostasis and has significant influence over behavior; however, the neural populations that integrate thermoregulation and sociability remain unclear. Oxytocin neurons of the paraventricular nucleus of the hypothalamus (PVNOT) modulate social behavior and have been linked to circuits associated with thermoregulation, though these roles have typically been investigated separately. The present study was conducted to simultaneously measure social and thermoregulatory biology in context of PVNOT neuronal activity. We used fiber photometry to record calcium dynamics in group-housed mice exposed to thermal challenges with solo-housed animals as controls. Group-housed female Oxytocin-IresCre mice with GCaMP8s expressed in PVNOT neurons displayed increased frequency of large Ca2+ transients during quiescent huddling behavior and when exposed to warmer ambient temperatures. In contrast, solo- housed animals had fewer high-magnitude transients during quiescent behavior; and transients were nevertheless positively correlated with ambient temperature, indicating a difference in PVNOT cell activity based on social setting. Thermal challenges (15°C - 33°C ramps) with solo animals did not evoke large transients , but consistently enhanced PVNOT cell responses in an undulating fashion. In summary, PVNOT cells showed highest responses when in social and warm contexts, suggesting that oxytocin neurons may be uniquely poised to integrate conspecific female prosocial behavior with thermoregulation.

102. Abigail Lind, University of North Dakota. **Treatment with Pevonedistat and APTO-253 downregulates the expression of ALDH3A1, and Upregulates KRT6A and SPRR2A in the As3+-Transformed UROtsa Cell Line.** Co-Authors: Aaron Mehus, Seema Somji. Co-Authors Institutional Affiliations: University of North Dakota. INBRE

There is a strong association between arsenite (As3+) exposure and development of urothelial carcinomas (UCs). Around 20% of UC tumors develop areas of squamous differentiation (SD) which is correlated to chemo and radiation resistance with unfavorable prognosis. In many cancers, there is an increase in the expression of stem cell related genes which impart uncontrollable growth characteristics. Our lab has transformed the human urothelial cell line (UROtsa) into malignant cells by exposing them to low doses of inorganic arsenic. These arsenite-transformed cells (As-T) form tumors in immune-compromised mice that display focal areas of SD enriched in the expression of keratin 6A (KRT6A) and small proline rich protein 2A (SPRR2A). They also express elevated levels of the stem cell markers SOX2, c-MYC, and ALDH3A1.We hypothesize that inhibiting the expression SOX2 and c-MYC reduces stemness and drives the expression of genes associated with SD. In this study the As-T cells were exposed to the SOX2 inhibitor Pevonedistat (PVD) either alone or in combination with the c-MYC inhibitor APTO-253 for 72 hours. The expression of ALDH3A1, KRT6A, SPRR2A was determined by RT-qPCR and Western analysis. The combined treatment of PVD with APTO-253 increased the expression of KRT6A and decreased ALDH3A1 expression, with no effect on SPRR2A expression. Thus, combined treatment with PVD with APTO-253 may reduce stemness and increase SD in As-T cells. Further studies need to be performed to assess whether this treatment can reduce proliferation and induce terminal differentiation throughout the entire tumor which may reduce their invasiveness and/or metastatic ability.

103. Hannah Higgins, Coastal Carolina University. **Synthesis of Phenyl Containing Phidianidine Analogs.** Co-Authors: Anna Tingler, Trinity Ghering, Samuel Ross, Bryan Wakefield. Co-Authors Institutional Affiliations: MUSC, CCU. INBRE

Phidianidine is isolated from the marine opisthobranch mollusk Phidiana militaris and is the first natural product known to contain a 1,2,4-oxidazole ring. Phidianidine possesses several biological functions, such as its ability to bind to u-opioid receptors and dopamine transporters. Inhibition of these targets may enable the molecule to treat central nervous system diseases. With this knowledge, other researchers synthesized analogs that replaced the alkyl chain of the molecule with a biaryl group. Some of these analogs were shown to protect against oxidative damage, which is implicated in the development and progression of Alzheimer's Disease. Based on the biaryl analog, a synthesis was devised to synthesize analogs with variation in the 1,2,4-oxidiazole ring and indole which have not yet been reported. This report focuses on the synthesis of a phidianidine analog that replaced the 1,2,4-oxidizole ring with a benzene ring. The goal is for the newly synthesized analogs to further protect against oxidative damage. The two routes devised to create the analogs were successfully verified via NMR spectroscopy. The Fisher Indole approach was low yielding and resulted in complex mixtures. The acid catalyzed Friedel-craft reaction provided better results with the furan analog, and we plan to optimize it with the phenyl containing phidianidine analog. Once the analogs are synthesized in higher yields, the compounds will be subjected to biological testing to determine their activity.

104. Elsa Shaikh, Furman University. **Benign taste experience during development impacts rodent taste learning and processing in adulthood.** Co-Authors: Veronica L Flores. Co-Authors Institutional Affiliations: Furman University. INBRE

Sensory experience modulates perception and learning of new and familiar stimuli. In taste learning, benign experience with a taste decreases the associativity of that same taste with a future conditioned taste aversion (CTA); a phenomenon known as latent inhibition. Recently, we have shown that even

familiarity with tastes other than the CS can influence later learning toward novel tastes (Flores et al., 2016). These data suggest that benign taste experiences, are in fact only seemingly benign and can modulate future taste learning. Given that benign taste experiences are ubiquitous in everyday life, it is important to consider how experiences during developmental learning might impact future taste processing. Here, we test the hypothesis that early life experience with sucrose will cause latent inhibition of future aversion learning of sucrose paired with lithium chloride. We expect that latent inhibition of learning will generalize to equally palatable concentrations of fructose and saccharin. Lastly, we test the hypothesis that latent inhibition will be correlated with higher perceptual thresholds of sucrose in adulthood. We test the above using a CTA paradigm in Long Evans Rats who experienced sucrose during different developmental periods (gestation, lactation, or weaning). A one-way ANOVA shows that early exposure to sucrose does not induce latent inhibition of CTA learning later in life, and instead leads to stronger CTA learning in adulthood. Additionally, aversions generalized to fructose and saccharin. These findings begin to characterize the impact of incidental taste experiences early in life on future taste learning in adulthood within rodents.

105. David Anthony Collins (Tony), Nemours Children's Health, Delaware Valley. **The Pediatric Research Optimizing Methods in Stakeholder Engagement (PROMISE) Research Core: Institutional supports for community-engaged research.** Co-Authors: J. J. Cutuli, D. A. Collins, J. Jung, Z. Noor, M. Garnett A.E. Kazak, M.A. Alderfer. Co-Authors Institutional Affiliations: Nemours Children's Health. COBRE
The Pediatric Research Optimizing Methods In Stakeholder Engagement (PROMISE) Core supports the Research Expanding Access to Child Health (REACH) COBRE by facilitating investigations that engage communities and investigators as equals. Communities are powerful partners in the effective, comprehensive, and equitable transformation of pediatric care. Addressing persistent disparities in child health requires an appreciation of factors across the child's social ecology such as family-level resources, beliefs, trust, provider and care system approaches, systemic disadvantages, and public policies. Communities carry forward an accumulation of the effects of and responses to these factors which have implications for health, care, and research participation. Many investigators cannot execute community engaged research because it requires advanced frameworks and tools rarely covered in training nor supported by institutional infrastructure. Trainees also often lack established connections to communities. Many junior investigators are forced to choose between community-engaged research and meeting career milestones: peer-reviewed publication and securing funding. The PROMISE Core fosters investigations in these complex areas while supporting investigators in attaining career milestones. The PROMISE Core has a multilevel infrastructure with community stakeholders. The core provides outreach, consultation, training, and technical assistance to investigators regarding effective community-engaged research. Investigators identify and build authentic relationships with community stakeholders, facilitating a context of co-participation throughout the research process. The core instills the ability for individual investigators to execute projects and maintains the norm that community-connected work is important across all research stages and at every career phase.

106. Yousaf Khan, Wichita State University. **A new vaccine platform based on the selective targeting of dendritic cells by the binding component of the anthrax toxin, protective antigen.** Co-Authors: Yousaf Khan, Srinivas Gonti, Xianglei Yan, Nancy Meyer, Vamseedhar Rayaprolu, Robert N. Brey, Karin Loré, James G. Bann. Co-Authors Institutional Affiliations: Wichita State University, Karolinska Institute, Pacific Northwest Center for Cryo-EM, Kinesis Vaccines LLC. INBRE
The anthrax toxin is an AB toxin. The B component, protective antigen (PA) is known to directly target and disrupt host immune cells as part of its pathology. In particular, PA exhibits high affinity binding to capillary morphogenesis protein 2 (CMG2), a receptor expressed on dendritic cells, macrophages, and

other antigen presenting cells. Dendritic cells are the most potent antigen presenting cells and can induce activation of T cells, crucial for a sustained immune response. Given the high affinity binding between PA and CMG2 and targeting of dendritic cells, we hypothesize that PA can be used as a vector for targeted delivery of conjugated antigens to dendritic cells. To test this hypothesis, we have generated a conjugate between PA and Spy0469, a putative 42 kDa surface protein of Streptococcus pyogenes. Since memory T-cell responses to Spy0469 are common in the human population, we surmise that activation of T-cells by the PA-Spy0469 conjugate would be stronger than Spy0469 or PA alone. We show here that the ability to bind CMG2 and formation of the heptameric structure is not perturbed with the conjugate attached to domain 4 of PA. Preliminary flow cytometry analysis is indicative of T-cell activation by the PA-Spy0469 conjugate. Although activation of CD4+ T-cells is not enhanced by the PA-Spy0469 conjugate, we find a greater activation of CD8+ T-cells, suggesting that PA is able to be cross presented.

107. Morgan Denney, West Virginia Clinical and Translational Science Institute. **Developing ad-hoc queries to extract and transform electronic health record data to fit into an existing REDCap project data model, a case study.** Co-Authors: Chloe Miller, Matthew Armistead, Rebecca Reece. Co-Authors Institutional Affiliations: West Virginia Clinical and Translational Science Institute, WVU Medicine. CTR Developing ad-hoc queries to extract and transform retrospective electronic health record (EHR) data to suit the specific needs of research projects allows minimal personnel to collect large volumes of data in a short time frame. An opioid use disorder study performed at WVU Medicine and developed by another institution required manual patient chart review. With IRB and PI permission, an alternative approach using EHR data extraction and transformation was taken to fit the data into the study's existing data model and reduce personnel time. Patients were identified using billing diagnosis codes for opioid use disorder. Hospital admissions for these patients were identified using certain infection billing codes associated with the admission, temporal criteria, and age criteria. The data model contained over 800 individual variables. Each extracted variable was transformed to meet the specific requirements of the REDCap project codebook so that minimal data consistency errors occurred. Investigators were presented with over 2,300 admissions identified by the developed algorithm. Initial collection required minimal investigator time. Ultimately, over 800 of the admissions were selected for inclusion in the study by investigators. The transformed data for those admissions were loaded into the REDCap project. EHR data extraction proved effective at identifying a large number of subjects for inclusion in the study with minimal investigator personnel time used during the initial collection. The extracted data transformation allowed the raw EHR data to fit cleanly into the REDCap project's data model.

108. Anjana N Bhat, University of Delaware. **The effects of creative and general movement on motor and cognitive skills of children with Autism Spectrum Disorder (ASD).** Co-Authors: Lombardi, K., Bertram, M., Su, W., Srinivasan, S. Co-Authors Institutional Affiliations: University of Delaware. INBRE Autism Spectrum Disorder (ASD) is a complex, neurological developmental disorder that affects Children's social communication, cognitive/executive functioning (EF), and motor skills. Past studies have reported positive effects of creative movement interventions (using music and movement, dance, play and rhythmic yoga) on the social communication and motor skills of school-age children with Autism Spectrum Disorder (ASD) (Srinivasan et al., 2015; Kaur et al., 2018); however, the key ingredients contributing to the positive outcomes were unclear. The present study compared the effects of creative movement (CM), general exercise/movement (GM), and standard-of-care interventions (i.e., seated play group) on the cognitive/executive functioning and motor skills of school-age children with ASD. Children with ASD between 6 and 14 years were included. At the pretest and posttest children completed standard motor and EF tests. During the 8-week training period, each participant received sixteen

training sessions (N=45, 15 children per group). The CM group prioritized synchronized creative movement through music, dance, and yoga-based activities, the GM group practiced whole body strengthening and endurance activities via turn taking, and the SP group focused on fine motor and communication skills without any whole-body movement. We found improvements in gross motor and cognitive/EF skills in the CM and GM group compared to the SP group. However, only the SP group improved their fine-motor skills; which was not observed in the CM or GM groups. Our findings highlight the value of creative and general movement interventions to promote motor and cognitive skills in children with ASD compared to the standard ASD interventions.

109. Manuel Delgado-Velez, University of Puerto Rico. **Downregulation of Alpha7 Nicotinic Acetylcholine Receptor by SARS-CoV-2 Spike Protein in Human Macrophages.** Co-Authors: Rolando Irizarry-Alvarez, Adriana Rodriguez-Aponte, Randy Irizarry-Alvarez, Alanis Perez-Montalvo, Sebastian Vidal-Cuevas, Bismark Madera, Sonia Corretjer-Farinacci, Negin Martin, Jerrel L. Yakel, Jose A. Lasalde-Dominicci. Co-Authors Institutional Affiliations: Not Listed. CTR
It is understood that the soluble SARS-CoV-2 spike protein circulating in the bodies of people suffering from COVID-19 interacts with the tissues of the body's organs, contributing to the pathophysiology of the infection. However, its effects on immune system cells are not well understood. In this study, we investigated the effects of the spike protein on the expression of the alpha7 nicotinic acetylcholine receptor (Î±7-nAChR) in human monocyte-derived macrophages (MDMs). Using confocal imaging and binding studies with specific antagonists against Î±7-nAChR, we determined the levels of Î±7-nAChR in MDMs after exposure to pathophysiological concentrations of spike protein typical of infected subjects. The results demonstrate that the spike protein induces downregulation of Î±7-nAChR in MDMs at all examined time points (12, 24, 36, 48, and 72 hours), and this downregulation is abrogated by preincubation with nicotine, an agonist of Î±7-nAChR. Furthermore, this downregulation is accompanied by an increase in the accumulation of intracellular clusters positive for the Î±7-nAChR antagonist, suggesting that surface Î±7-nAChRs accumulate inside the cells. This accumulation increases after 24 hours and then stabilizes. However, it does not result in an increase in Î±7-nAChR on the membrane because the downregulation persists for 72 hours or more after incubation. These results suggest that the reduction of Î±7-nAChR may contribute to the severe inflammation suffered by subjects with COVID-19, as activation of this receptor in macrophages is anti-inflammatory. Overall, the results suggest that Î±7-nAChR may emerge as a pharmacological target to mitigate inflammation in subjects with COVID-19.

110. Kathleen M. Fairfield, MaineHealth. **Engaging Community Based Organizations to Reach Vulnerable Populations for COVID-19 Testing, a RADx-UP Funded Program in Portland, Maine.** Co-Authors: Gloria Sclar, Caroline Fernandes, Andrew Volkers, Grace Price, Mike Kohut, Ann Tucker, Leslie Nicoll, Elizabeth Jacobs. Co-Authors Institutional Affiliations: Not Listed. CTR
Background: COVID-19 testing was challenging for vulnerable communities who experienced issues with both acceptability and accessibility. Partnering with CBOs was a strategy to reach structurally vulnerable community members. Methods/Approach: We partnered with three CBOs providing services for people who are unhoused, low-income/uninsured, and immigrant populations: Preble Street Learning Collaborative, Portland Community Free Clinic, and Greater Portland Health (a federally qualified health center). We conducted semi-structured interviews with vulnerable community members and key informants (reached via CBOs) to explore barriers and facilitators to COVID-19 testing. We then set up weekly testing clinics cohosted with the CBOs to improve testing. Lastly, with CBO support, we recruited a cohort of vulnerable community members and supplied at-home COVID-19 tests, following for 48-weeks to examine testing behaviors. Results: We interviewed 34 members of vulnerable populations and 27 key informants, using this information to build a model of COVID-19 testing decisions (testing

necessity and access), and to design walk-up testing and at-home testing studies. Walk-up testing clinics occurred January 2022-May 2023 (195 clinic days), with 246 tests conducted. Persons testing positive for COVID-19 were referred for follow-up and treatment. Data about exposures, demographics and reasons for testing were collected for the national RADx-UP program. We enrolled 93 participants into the home testing cohort and found that participants from all three vulnerable populations demonstrated high levels of recommended COVID-19 testing when provided with tests. Conclusion: Partnering with CBOs allowed the research team to study and serve vulnerable communities during a public health emergency, expanding representation in research.

111. Michael C. Hout, New Mexico State University. **Developing use-inspired basic research paradigms (and stimuli) for the study of medical image perception.** Co-Authors: Megan H. Papesh, Rebecca Penn, Emily Stutesman, Janelle Hernandez. Co-Authors Institutional Affiliations: University of Massachusetts, Lowell, New Mexico State University. INBRE
Medical professionals in various fields frequently rely on complex images through which they must visually scan in search of anomalies â€“ e.g., tumors, tears, or other problems â€“ that indicate the presence of disease or injury. This is an extraordinarily difficult perceptual and cognitive challenge for screeners, requiring years of experience to perfect one's skillsets. Our goals are to better understand how people perform these tasks, and to uncover training techniques that assist in turning novices more quickly into experts. Unfortunately, however, little longitudinal work exists documenting the acquisition of expertise over time. In this presentation, we will document some of our efforts to develop use-inspired basic research techniques for studying medical image perception. These include the development of a novel database of anomaly search scenes to be used in laboratory settings, the development of perceptual training paradigms to enhance target detection, and a training protocol that can be used to document novice searchers' behavior as they become efficient at a task akin to medical image search. Ongoing efforts also include pilot testing of research paradigms allowing for ambiguity in responses under conditions of uncertainty, and similarity modeling used to create custom-tailored training protocols that improve target detection by focusing on features of the stimulus commonly overlooked by the observer. Together, these advances allow basic science researchers to carefully study the acquisition of skill development over time, to contrast varying training methods, and to observe how oculomotor behavior is shaped by expertise.

112. Naveen Chintala Ramulu, Louisiana State University. **Evaluation of the immunomodulatory potential of oncolytic HSV-1(VC2) GM-CSF on Pancreatic Ductal Adenocarcinoma cells.** Co-Authors: Thota S, Stanfield BA, Begum R, Sapkota B, Pandit A, Moaven O, Kousoulas KG, Francis J. Co-Authors Institutional Affiliations: Not Listed. COBRE
Pancreatic ductal adenocarcinoma (PDAC) is a highly aggressive malignancy of the pancreas and is anticipated to be the second leading cause of cancer-associated deaths by 2030. Owing to its intrinsic immune evasive tumor microenvironment (TME), PDAC is regarded as an immunologically â€˜coldâ€™ tumor with a significant therapeutic challenge. Although FOLFIRINOX regimen with gemcitabine is administered as an adjuvant therapy, use of oncolytic virus (OV) may alternatively activate the innate immune response within the TME, potentially converting PDAC to a â€˜hotâ€™ tumor. The FDA approval of T-VEC, a modified herpes simplex virus-1 (HSV-1) for the treatment of advanced melanoma supports the preceding argument. In this study, we investigated the effect of herpes simplex virus type-1, HSV-1(VC2) overexpressing granulocyte-macrophage colony-stimulating factor (GM-CSF) in the murine KRAS, p53, and Cre (KPC), and human MIA PaCa-2 pancreatic carcinoma cells. Following a 24h infection of the KPC and MIA PaCa-2 cells with the virus, the observed cytopathic effects (CPE) included cell rounding, detachment, and aggregation as compared to the wild-type HSV-1(VC2) treated or the uninfected control

cells. The CPE effects of HSV-1(VC2) GM-CSF was proven to be a more direct and dynamic response against these cells. In the next steps, the viral titers were estimated to be 9.6E7 pfu/ml and 1.26E7 pfu/ml for HSV-1(VC2) and (VC2) GM-CSF respectively. The infection of (VC2) GM-CSF 0.1, 1.0 and 10 multiplicities of infection (MOI) in KPC and MIA PaCa-2 cells resulted in a significant regulation in the expression of inflammatory markers including cyclooxygenase -2 (COX-2), interleukin 10 (IL-10) and iNOS in contrast to the uninfected controls. This was coupled with an increase in the expression of Fas ligand (FasL) and programmed death ligand (PD-L1). Based on the evidence presented here, it is speculated that (VC2) GM-CSF induced proinflammatory profile in KPC and MIA PaCa-2 cells converts to an immunomodulatory effect characterized by the regulation of FasL and PD-L1. In addition, to propose stromal co-targeting alongside the integration of OV, we generated a cancer-associated fibroblast-like phenotype of NIH3T3 as a proof-of principle. Based on our preliminary findings, it is conceivable that a combination therapy of oHSV-1(VC2) GM-CSF and anti-stromal agent(s) may potentially overcome the challenges to PDAC therapy.

113. Malak Alradi, University of Delaware. **Exploring the Role of Visceral Fat as a Negative Regulator of Vascular Function In Obesity.** Co-Authors: Ibra Fancher. Co-Authors Institutional Affiliations: Not Listed. COBRE

Obesity promotes endothelial dysfunction, a major contributor to the development of cardiovascular disease. Work from our lab and others previously showed robust impairment of arteries embedded within visceral adipose tissue as compared to those within subcutaneous adipose tissue. Here, our research is focused on obesity-induced changes in adipose tissue gene expression, and how it may negatively or positively impact the functioning of the vascular system within the tissue. Visceral adipose tissue and subcutaneous adipose tissue were extracted from lean and diet-induced obese mice after 12-14 months on respective diets (normal chow and high fat, Western diet, respectively). RNA-seq was conducted to analyze the gene expression profiles. We identified expressed genes from SAT and VAT from lean and obese mice, changes in gene expression with obesity in SAT and VAT (up regulated and downregulated as compared to lean controls), Gene Ontology from SAT (up regulated and downregulated) and VAT (up regulated and downregulated).

114. Siam Chowdhury, Arkansas State University. **Docking Studies of Actin Cytoskeleton and Î²-Parvin Inhibitors as Antimelanoma Agents.** Co-Authors: Sanjay Adhikary. Co-Authors Institutional Affiliations: Arkansas State University. INBRE

Melanoma is one of the most lethal forms of cancer, which is recalcitrant to current treatments in most patients. A series of fused thiazole derivatives were studied for their cytotoxic properties, and several of them were found to be potent growth inhibitors of melanoma cell lines. In a subcutaneous mouse melanoma model, two potent compounds inhibited tumor growth and were non-toxic according to a comprehensive 14 blood plasma organ toxicity markers. mRNA sequencing showed actin cytoskeleton inhibitory activities via the downregulation of Î²-actin and Î³-actin proteins, which was further confirmed by immunoblotting and proteomics assays. The lead compounds also diminished formation of actin filaments as measured through lack of actin rich membrane protrusion formation in immunofluorescence. mTOR is a well-known regulator of actin cytoskeletal organization and our lead compounds might affect actin rich membrane protrusion formation through binding mTOR. Additionally, the expression of Î²-parvin, an adapter protein between the actin cytoskeleton and extracellular matrix, was increased both in genomics and proteomics studies. All these findings concluded that thiazole derivatives exhibited anti-melanoma and antimetastatic properties through inhibiting the actin cytoskeleton protein. Based on molecular docking studies, the lead compounds interacted with actin (7CC) and mTOR (7PE8) with high binding energy. To figure out the binding energy as well as for

computational docking study, AutoDock Vina, AutoDock Tools, and Discovery Studio were used as the main software. Proteins have been downloaded from the Protein Data Bank, whereas compound structures were drawn in ChemSketch for computational studies.

115. Tathagato Roy, University of Wyoming. **Sexually dimorphic immunity to Toxoplasma gondii infection.** Co-Authors: None. INBRE
Toxoplasma gondii infection outcomes are sexually dimorphic with females exhibiting higher morbidity and mortality than males during HIV/AIDS. Natural Killer (NK) cells are a major early controller Toxoplasma infection. Since CD4+ T cells are absent during HIV/AIDS and females are more susceptible to Toxoplasmic encephalitis (TE), we investigated how CD4+ T cells impacted mouse survival and NK cell responses in mice. Female CD4KO mice succumbed to T. gondii earlier than male CD4KO mice. Wild type (WT) mice similarly increased IFNg+ NK cell numbers regardless of sex and NK cell responses were intact in male CD4KO mice after infection. However, infected CD4KO female mice had 50% fewer IFNg+ NK cells than infected WT female mice and CD4KO male mice. To confirm our results, we next tested survival and NK cell responses in female and male MHCII deficient (MHCIIKO) animals. To our surprise survival, and IFNg+ NK cells were not significantly different between WT or MHCIIKO female and male mice. Additionally, the lack of T and B cells does not correlate with differential survival outcomes and NK cell responses in female and male mice. These results suggest only in female mice and not in male mice CD4 co-receptor expression is required for survival and correlates with optimal NK cell responses during acute T. gondii infection. Our findings reveal an unappreciated sexual dimorphic role of CD4 co-receptor expression in the regulation of NK cell responses to acute infection including T. gondii infection.

116. Hayden Thomas Hess, West Liberty University. **Peptidoglycan modulation by Francisella tularensis.** Co-Authors: Joseph Horzempa, Stuart Cantlay, Melanie Sal. Co-Authors Institutional Affiliations: West Liberty University, West Virginia Wesleyan College. INBRE
Peptidoglycan, a crucial component of bacterial cell walls, plays a fundamental role in maintaining cell shape, integrity, and resistance to osmotic pressure. Mycoplasmas are the only bacteria that do not produce peptidoglycan cell walls. Other peptidoglycan-producing bacteria are capable of transiently existing without a peptidoglycan as an “L-form”, but only on solid media. Preliminary observations made by our laboratory suggested that Francisella tularensis bacteria do not produce detectible levels of peptidoglycan while growing in liquid media. However, increasing salt concentration induces the production of peptidoglycan in all bacteria. In this study we confirmed and extended these observations by incubating bacteria with fluorescent D-alanine (which integrates into the peptidoglycan during synthesis). Fluorescence microscopy revealed that very few F. tularensis bacteria produce detectable peptidoglycan in low salt media, while seemingly all individual bacteria produce this layer in high salt media. Interestingly, the genome of F. tularensis encodes two distinct beta-lactamases. Here we show that both the wild-type F. tularensis LVS and beta-lactamase null mutant were both resistant to high levels of beta-lactam antibiotics in low salt liquid media. However, only the wild type and complemented mutant strains were resistant to beta-lactam antibiotics in high salt media while the beta lactamase null mutant was susceptible. These data further support the conclusion that F. tularensis does not produce, nor need, peptidoglycan in low salt liquid media. Future studies will investigate whether peptidoglycan modulation is required to avoid detection by the innate immune system.

117. Oliver-Elias Hiszczynskyj, Emporia State University. **Assessing the Protective Effects of Plant-Based Antioxidants in Neonicotinoid Treated Apis mellifera.** Co-Authors: David Claridge, Meghan Cashell, Megan Fernandez, Jacob Spidell, Joanna Gress. Co-Authors Institutional Affiliations: Emporia State University. INBRE

Over 130 commercial crops are pollinated by Apis mellifera, adding $15 billion to the U.S. economy each year. However, in 2023, beekeepers lost 48.2% of their hives due to a variety of stressors including pesticide exposure. Imidacloprid, a neonicotinoid pesticide, makes up â…• of the global insecticide market. This prevalence in both agricultural and private environments leads to high levels of exposure to forager honey bees. Exposure to this pesticide causes elevated levels of oxidative stress, which reduces the ability to break down toxins resulting in cell damage and death in the gut. This class of pesticides is also linked to gene regulation of many A. mellifera detoxification genes that metabolize toxic molecules or minimize their effects. Antioxidant compounds that are naturally present in many plant species may be able to counteract the harmful effects of this pesticide exposure by increasing the expression of the detoxification pathway. We looked at 5 classes of antioxidants from commonly pollinated plants including epigallocatechin-3-O-gallate, rosmaric acid, anthocyanins, proanthocyanins, and mint essential oils. To assess if these plant-based antioxidants contain a protective effect for neonicotinoid ROS stress in the gut, feeding trials were performed with forager bees. Each antioxidant trial consisted of feeding 20 foragers and then exposing them to imidacloprid. After 48 hours their abdomens were collected to extract RNA and to perform qPCR analysis to view the expression of the 10 detoxification pathway's genes.

118. Alejandra P. Vazquez, University of Puerto Rico, Medical Health Science Campus. **Deciphering the Impact of Running Exercises on the Gut-Brain Axis: Microbiota, Tryptophan Metabolism, and Brain Health.** Co-Authors: Nicole Rodriguez Trujillo, David Ruiz Bolivar, Patricia Morales Iglesias, Karina Marin Hernandez, Danniela Rivera Ortiz, Briana Bello Rivera, Francisco Vizcarrondo Fornaris, Filipa Godoy Vitorino, Nataliya Chorna. Co-Authors Institutional Affiliations: University of Puerto Rico Rio Piedras Campus, University of Puerto Rico School of Medicine. INBRE
The gut-brain axis, governed by microbiota and tryptophan (TRP)-derived metabolites such as serotonin, plays a crucial role in cognitive function, sociability, and emotional states. While the positive effects of running on gut and mental health are recognized, the precise role of microbiota in regulating brain TRP metabolism remains unclear. Our study aimed to investigate the impact of running exercises on gut microbiota changes and TRP metabolism along the gut-brain axis. In a study involving 20-week-old male C57BL/6J mice randomized into sedentary (SED) and running (RUN) groups, we collected feces, blood, hippocampus, and brainstem samples after an 8-week intervention, approved by IACUC #A660121. High throughput sequencing of the 16S rRNA gene assessed gut microbiota composition, while GC/MS and LC/MS-based metabolomics analyzed TRP and its metabolites. Integrative taxon-function analysis explored associations between microbial taxa, metabolic enzymes, and metabolomics data. A sociability behavioral test evaluated communication skills and sociability in response to running exercises. We identified a shift in microbiota diversity and a reduction in TRP metabolizing capabilities within the RUN group, associated with increased TRP uptake to the hippocampus and brainstem through circulation. This led to enhanced serotonin production in the brainstem and increased transport to the hippocampus, strengthening cognitive and social abilities. Additionally, the symbiotic association between Romboutsia and Akkermansia muciniphila suggested their potential probiotic function, influencing TRP transport to the brain regions. Our findings offer promise for developing novel probiotics and microbiota-based approaches in exercise-related neurological diseases, particularly focusing on mental health and overall well-being.

119. Elizabeth Steele, Ben Shertzer, West Virginia University. **Emergency Department Based Management of Tobacco Use Disorder.** Co-Authors: Bradley End, Gordon Smith. Co-Authors Institutional Affiliations: West Virginia University. CTR

Tobacco use is the leading cause of preventable death in the United States, accounting for nearly 500,000 deaths per year. 16 million additional Americans are afflicted with a disease caused by smoking such as cancer, heart disease, stroke and chronic lung disease. Despite this, nearly one quarter of West Virginians, almost double the national rate, are current cigarette smokers. West Virginia also leads the nation in rates of youth smoking, smoking during pregnancy and is second to Mississippi in rates of smokeless tobacco use. A survey instrument was developed and deployed to both patients reporting tobacco use and providers to quantify current tobacco utilization and qualify thoughts and perceptions related to tobacco use. Of 83 patient surveys completed, there were no statistical differences in reported perception primary care versus Emergency Department (ED) based treatment modalities. Of the 123 provider responses, there were concerns related to time and scope of ED based interventions, and differences in perception across the modalities of help investment, therapeutic efficacy, emotional response and causal attribution comparing tobacco use disorder to both opioid use disorder and hypertension.

120. Desiree N Thimesch, Washburn University. **Cellulose in Your Kombucha? Isolation and Identification of a Cellulose Producing Bacterium in Kombucha.** Co-Authors: Mary Tyler. Co-Authors Institutional Affiliations: Washburn University. INBRE
Kombucha is a fermented tea drink that is touted for its health benefits. Numerous bacteria and yeast ferment the sugar in the drink and produce carbonation and acidity. We investigated microbes found in small-batch, locally produced craft kombucha. While isolating the microbes, one bacterium produced a gelatin-like substance, exhibiting characteristics that are similar to the SCOBY that is formed during kombucha fermentation. Previous research has shown that some bacteria in kombucha produce cellulose. They do this to get closer to the surface of the culture to access oxygen for respiration and help them retain moisture. Bacterial cellulose has different properties than plant cellulose and is being studied for its roles in biomedicine and industry. We observed beads, a ribbon-like structure and rubbery cellulose production based on the type of growth media and addition of shaking to the culture. Multiple assays were performed to show that the substance was cellulose: a cellulase assay, cellulose fluorescent dye test, and Fourier Transform Infrared Spectroscopy. In addition, the physical characteristics of the bacteria indicate that it is likely from the species Komagataeibacter. Future directions include purifying DNA from the bacteria to obtain a sequence and investigating conditions that increase the production of the cellulose in culture.

121. Kahsi A. Pedersen, MaineHealth Institute for Research. **Mindfulness Training to Improve Mental Health of Caregivers of Children with Autism Spectrum Disorder in Rural Areas.** Co-Authors: Ellyn Touchette, Elizabeth Walker, Susan L. Santangelo. Co-Authors Institutional Affiliations: MaineHealth Institute for Research. CTR
Our grant focuses on conducting a clinical trial to evaluate the effectiveness of a mindfulness-training program delivered through a mobile app in improving the mental well-being of caregivers supporting children with Autism Spectrum Disorder (ASD), particularly in rural Maine. Caregivers of children with ASD in rural areas face unique challenges due to limited access to mental healthcare services, exacerbating stress, anxiety, and overall poor mental and physical health. Our intervention, Unwinding Anxiety, is a 30-day mobile application-based program designed to reduce stress and anxiety, with efficacy demonstrated in diverse populations. We aim to recruit 20 cohabiting caregiver couples living in rural Maine, leveraging the Glickman Lauder Center of Excellence in Autism and Developmental Disorders for recruitment. Data collection, utilizing online assessments and daily experience sampling methods, is underway and consists of five phases: baseline, intervention period (including midpoint), post-intervention, and 1-year follow-up. Preliminary data collection will inform future studies examining

dyadic effects of mindfulness training and its impact on caregiver and child outcomes. The significance of this work lies in its potential to enhance mental health in rural communities and contribute to evidence-based practices for caregiver support. Ultimately, this research aims to improve the well-being of caregivers, children with ASD, and their families, aligning with the mission of the Institutional Development Award program to address healthcare disparities in medically underserved communities like Maine.

122. Carole A. Oskeritzian, University of South Carolina School of Medicine - Columbia. **Resveratrol mitigates multipronged pathogenic mechanisms in early-phase eczema.** Co-Authors: Christopher D. Carlucci, Yvonne Hui, Hannah Gandy, Dylan Kunkel, Stacey Oxendine, Piper A. Robida, Alena P. Chumanevich, Sajish Mathew, Prakash Nagarkatti, Mitzi Nagarkatti. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine - Columbia, USC Honors College, Northwestern Oklahoma State University, University of South Carolina. COBRE
Atopic dermatitis (AD, eczema), is a chronic inflammatory skin disease characterized by recurrent itchy lesions, with a lifetime prevalence of 10 to 30% world-wide. Males and females are not equally affected by AD. Female predominance is well established, starting around puberty and persisting into adulthood. Monoclonal antibody biologics reduce disease burden but present safety concerns and side effects. Previous studies from our laboratory established that mast cells (MC), skin-resident innate immune cells, played a critical role in AD pathogenesis, becoming activated upon a single 7-day epicutaneous exposure to antigen (Ag) ovalbumin (OVA, 100 µg/ml) in a preclinical model. MC stimulation resulted in local elevation of sphingosine-1-phosphate (S1P), a sphingolipid metabolite produced by the sphingosine kinase 1 (SphK1) enzyme, and cell-attracting chemokines, initiating inflammation. Inflammation was alleviated by resveratrol (RSV), an anti-inflammatory natural compound that prevented MC activation and the production of S1P and chemokines. Mechanistically, RSV prevented in vivo activation/phosphorylation of SphK1 and of the transcription factors driving chemokine production. OVA exposure concomitantly increased skin-associated ceramides, second messengers of apoptosis. Importantly, ceramide-mediated apoptosis through endoplasmic reticulum stress was also mitigated by RSV. Ongoing preclinical, in vitro and ex vivo studies are currently conducted using house dust mite Ag to which 10% of the world population is allergic. In sum, we unraveled multipronged beneficial effects of RSV in preventing pathogenic pathways engaged at the inception of AD, reducing inflammation, perhaps paving the way to the design of next-generation AD prophylactics, a prevalent disease affecting women's health. Supported by P20GM103641.

123. San Chu, Pennington Biomedical Research Center; Louisiana State University. **Predicting Upturns in COVID19 Incidence Based on Changes in Nonamers.** Co-Authors: Ronald Horswell, Lucio Miele, Grace Kim, Daniel Fort, Jian Zhang. Co-Authors Institutional Affiliations: Pennington Biomedical Research Center, LSU Health Science Center, Ochsner Health, LSU A&M. CTR
When an epidemic is underway, only limited information is available when formulating public health policy or adopting changes to policy. The question addressed by this research is: Can viral genome sequence information feasibly be used to support formulation of public health policy? Specifically, can such information be used to predict imminent upturns in disease incidence? This research developed and compared several related approaches to predicting imminent upturns in COVID-19 incidence. The approaches all use an expanded concept of nonamers (coding regions for sequences of nine amino acids) to define several nonamer-based measures that reflect changes to the current distribution of viral subtypes. Both machine learning and statistical models were used to estimate the relationships of those nonamerbased measures to subsequent upturns in disease incidence. The expanded nonamer concept is a 27nucleotide base sequence in a genome that codes for a nine-amino acid sequence in a protein or

peptide. Weekly sequence data were obtained from NCBI and weekly incidence data were obtained from COVID-19 Data Repository by Johns Hopkins University. Three approaches estimated incidence upturn probabilities upturn from nonamer-based features: (1) logistic regression, (2) a linear support vector machine, and (3) a randomization-based method. Those methods were applied to the weekly data from 32 states. The Area Under the Receiver Operating Characteristic Curve (AUC) for logistic regression, the linear support vector machine, and the randomization approach were 80%, 58%, and 78%, respectively. The methods can be applied at different geographical levels if the viral genomic data are collected appropriately.

124. Maharshi Sharma, Western Kentucky University. **Effect of Chronic Sleep Fragmentation Upon Proinflammatory Gene Expression of Male Mice.** Co-Authors: None. INBRE

Obstructive sleep apnea (OSA) is a prevalent sleep disorder characterized by upper airway obstruction, causing sleep fragmentation. Although OSA affects both genders, it is diagnosed more commonly in males. Sleep fragmentation, a consequence of OSA, triggers acute and chronic inflammatory responses in peripheral organs and the brain. Investigating chronic sleep fragmentation (CSF) is crucial for understanding the pathophysiological mechanisms of OSA. We hypothesize that male mice subjected to CSF will exhibit increased gene expression of proinflammatory cytokines in peripheral organs and brain tissues, along with elevated serum corticosterone levels. To test this, male C57BL/6J mice were subjected to CSF for 12 hours per day using an automated sweeping bar across their cage, mimicking severe OSA sleep fragmentation. A control group experienced no CSF. Tissue samples including spleen, liver, heart, white adipose tissue (WAT), prefrontal cortex, hippocampus, and hypothalamus were collected at intervals ranging from 0 to 8 weeks. Real-time PCR measured gene expression of proinflammatory cytokines TNF-a and IL-1b, while ELISA assays determined corticosterone concentration in serum. Results indicate significant elevations in proinflammatory cytokine gene expression in all tissues except the spleen, and a notable increase in corticosterone concentration from 2-4 weeks. These findings suggest that CSF in male mice promotes an inflammatory response that is regulated by corticosterone in both peripheral tissues and brain. These data provide important and relevant characterization of the male inflammatory response to CSF. Our lab is currently evaluating the female response to CSF, which will help increase our understanding of sex-specific responses to CSF.

125. Emily Young, West Liberty University. **Increased expression of FTL_0445 confers resistance to resazomycins in Francisella tularensis.** Co-Authors: Jordan Gibson, Siena McGovern, Emma Beatty, Claire Kelly, Kendall Souder, Justin Rice, Ryan J. Percifield, Donald A. Primerano, Nicole Garrison, Deanna M. Schmitt. Co-Authors Institutional Affiliations: West Liberty University, West Virginia University, Marshall University. INBRE

Francisella tularensis, the causative agent of the potentially fatal disease tularemia, is classified as a Category A bioterrorism agent by the CDC. Aminoglycosides, fluoroquinolones, and tetracyclines can be used to treat tularemia; however, there is a high incidence of relapse and treatment failures. Furthermore, there is no tularemia vaccine licensed for use in the United States. Therefore, new antibiotics that target F. tularensis are being investigated. Resazomycins, a novel family of resazurin-based compounds, exhibit antimicrobial activity against Francisella tularensis and other Gram-negative pathogens including Neisseria gonorrhoeae. However, resazurin's mechanism of action has yet to be elucidated. To identify potential targets of resazurin (Rz), we screened for spontaneous Rz-resistance (Rzr) Ft. tularensis LVS mutants. All the Rzr mutants sequenced contained mutations within the coding regions of FTL_0421 and FTL_1504, as well as a mutation approximately 50bp upstream of the gene FTL_0445. To understand the effect this mutation has on transcription of FTL_0445, RNA was isolated from wild-type LVS and an Rzr mutant (Rzr1). Quantitative reverse transcription PCR revealed FTL_0445

was upregulated in Rzr1 compared to wild-type LVS. To determine the role of FTL_0445 in Rz resistance, an FTL_0445 null deletion mutant was generated in Rzr1 using standard molecular genetic techniques. Agar dilution assays revealed deleting FTL_0445 from Rzr1 restored sensitivity to Rz. FTL_0445 likely encodes a Rz-resistance factor. Complementation of Î”FTL_0445 and wild-type LVS with mutated copies of FTL_0445 revealed increased resistance to Rz. FTL_0445 likely alters Rz into an inactive form which can be investigated using NMR. (This research was made possible by NIH Grant P20GM103434 to the West Virginia IDeA Network for Biomedical Research Excellence and NASA West Virginia Space Grant Consortium, Grant # 80NSSC20M0055.)

126. Yutong Liu, UNMC. **CEST MRI for Neuropathology of ART and Nicotine**. Co-Authors: Gauthier, Gabriel, Bade, Aditya N, Sajja, Balasrinivasa R, Uberti, Mariano G, Gorantla, Santhi, Summerlin, Micah A. Co-Authors Institutional Affiliations: UNMC. COBRE
Antiretroviral therapy (ART) has transformed the type-one human immunodeficiency virus (HIV-1) from the deadliest modern epidemic pathogen into a manageable chronic illness. However a variety of HIV associated neurocognitive disorders still impact quality of life. As such, the elucidation of HIV-1 associated long-term neurocognitive outcomes on ART patients is imperative for the refinement of HIV immunological care. In this study, we utilized the chemical exchange saturation transfer (CEST) effects of metabolites to measure virus-associated metabolic alterations linked to neuropathological outcomes resulting from ART using magnetic resonance imaging (MRI). Humanized mice (n=14) were scanned on a 7T Bruker scanner, using CEST-MRI and MRS. Immediately after baseline scans, the mice were infected with HIV-1 and monitored for viral load. After infection was confirmed by plasma viral load (six weeks postinfection), the surviving mice were scanned again, then given daily oral gavage of either ART (n=5) or vehicle (n=5) for 28 days. The chosen treatment was TLD, a combination of tenofovir disoproxil, lamivudine, and dolutegravir. After viral loads were undetectable, the scans were reproduced a final time. When observing the CEST effect on the CTX at 3 ppm, mice showed significant differences in cortex and hippocampus. In cortex, the vehicle treated group had a decreased signal when compared to ART-treated mice (p=0.036) and early-infected mice (p=0.017). In hippocampus, the vehicle-treated group showed decreased signal when compared to ARTtreated (p=0.014), early infected (p=0.03) and baseline mice (p=0.032).

127. Bernice C Lin, University of Montana. **Balancing Act: Exploring pH Dynamics in Stem Cell Fate Regulation.** Co-Authors: Isabella R Maag, Beverly J Piggott. Co-Authors Institutional Affiliations: University of Montana. INBRE
Traditionally, cells were thought to maintain pH within a narrow range, with deviations in disease states like cancer (basic pH) or neurodegeneration (acidic pH). However, growing evidence shows that cells regulate pH not just to prevent disease but to control molecular interactions and cellular behaviors. Sodium (Na+) proton (H+) exchangers (Nhes) play a pivotal role in intracellular pH (pHi) regulation by facilitating the efflux of H+ ions in exchange for the influx Na+ ions. The extent to which cells inherently control pH to optimize molecular mechanisms remains elusive. Drosophila neuroblasts (NB), the neural stem cells of the Drosophila brain, are a powerful model to study neural stem cells in vivo thanks to their highly conserved mechanisms and precise genetic tools. While there are nine NHE (NHE1-9) proteins in humans, there are only three in Drosophila (dnhe1-3), providing a straightforward model to study the role of Nhes in neurogenesis. Using a genetically encoded pH sensor, we find that NB are more basic than their differentiated progeny. Our data suggests that Nhes regulate NB lineage pH as well as cellular division machinery. Our hypothesis posits that Nhe proteins regulate stem cell fate and proliferation by maintaining a basic pHi that supports neuroblast physiology and behavior. Further experimentation using single nuclei sequencing will identity transcriptional changes depending on pH states. Given that

mutations in human NHEs are associated with various neurodevelopmental disorders like Christianson syndrome, microcephaly, and cognitive impairment, these findings may offer valuable insights for future therapeutic interventions.

128. Qingsong Zhao, Louisiana State University Shreveport. **Utilizing Social Determinants in Obstetrics and Gynecology Virtual Cases to Enhance Clinical Reasoning: A Collaborative Initiative.** Co-Authors: Q. Zhao, M. Trutschl, M. Shah-Bruce, D. Sarda, A. Ristic, S. Ristic; S. Paudel, R.S. Mansour, D. Smith, A. Mahoney, M. Qayyum, K. Rushing, A. Fort, D. Zoorob, U. Cvek. Co-Authors Institutional Affiliations: LSU Shreveport, LSUHS Shreveport INBRE
This collaborative effort between LSU Shreveport Computer Science Department and the LSU Health System (LSUHS) Shreveport Obstetrics and Gynecology (OBGYN) Department is a direct response to the NIH initiatives on women's health within Institutional Development Award (IDeA) states. The core aim is to support NIH's Strategic Goal of Advancing Science for the Health of Women by creating an e-learning platform called e-OBGYN to enrich the foundational knowledge and clinical reasoning skills of healthcare students during their OBGYN training years. Our particular focus is addressing clinical reasoning, foundational knowledge, and social determinants of health that contribute to health disparities in this field. The project outlines four specific objectives: designing a repository of virtual cases, developing the e-learning platform, assessing student learning outcomes, and obtaining feedback from students. Accessible at no cost with internet and email access, the project aims to evaluate the impact of these virtual cases on students' clinical reasoning abilities and their awareness of health disparities. The initial phase of the project involves pre and post testing of health professions students from LSUHS to examine their knowledge of social determinants of health and their impact on healthcare in an OBGYN context before and after the eOBGYN modules. Our hypothesis suggests that the incorporation of e-OBGYN virtual cases will enhance students' comprehension of social determinants of health and health disparities within OBGYN. Ultimately, this endeavor aims to address crucial facets of medical education, cultivating awareness, and empowering future healthcare professionals to address and mitigate health disparities within OBGYN.

129. Leyre Notario Barandiaran, Dartmouth College. **Exposure to iodine, essential and non-essential trace element through seaweed consumption in humans.** Co-Authors: Vivien F. Taylor, Margaret R. Karagas. Co-Authors Institutional Affiliations: Dartmouth College. COBRE
Seaweed consumption has gained popularity due to its nutritional value and potential health benefits. However, concerns regarding the bioaccumulation of several trace elements highlight the need for comprehensive studies on exposure associated with seaweed consumption. To address this gapÂ¬ in knowledge, we carried out a feeding intervention study of three common edible seaweeds (Nori, Kombu, and Wakame) in 11 volunteers, aiming to elucidate the extent of both beneficial and harmful trace element exposure through seaweed consumption in humans. Concentrations of total arsenic, cobalt, copper, cadmium, iodine, molybdenum, selenium, and zinc were measured in urine samples before and following seaweed consumption. Elements concentrations were also measured in the seaweeds provided for the study. Descriptive analysis for each element were conducted and we used quantile g-computation approach to assess the association between the 8-element mixture and seaweed consumption. Differences in urine element concentrations and seaweed consumption were analyzed using generalized estimating equations (GEE). Urinary concentrations of iodine and total arsenic increased after seaweed consumption. When we analyze the 8-element mixture, the largest weight was observed for iodine after Kombu consumption while for total arsenic was observed after Wakame consumption. Similar results were observed when we compared the mean differences between the elements before and after seaweed consumption through the GEE. Seaweed consumption relates with

increased urinary iodine and total arsenic concentrations, particularly after Kombu and Wakame consumption.

130. Daniel Oyugi, Mississippi Valley State University. **Microtubule-Distabilization Effects of Vernonia amygdalina Fractions in Cancer Cells.** Co-Authors: Winston Anderson. Co-Authors Institutional Affiliations: Howard University. INBRE
Vernonia amaygdalina (VA), one of the medicinally-important plants of Africa is considered the most used plant in the genus Vernonia. Previously we reported the in-vitro growth inhibition and anti-proliferative activities of VA extracts on cancer cells. In the present study, we examine whether VA elicits the aforementioned effects by targeting and disrupting cellular microtubule. Using immunocytochemical and fluorescence analyses, we probed the effects of VA fractions on microtubule assembly, disassembly and apoptosis in prostate (DU-145) and breast (MCF-7) cancer cell lines. Cell viability was tested using CalceinAM Red Orange. Apoptosis was measured using Double Stain Apoptosis Detection Kit (Hoechst 33342 and Propidium Iodide (PI)). Our results indicate that organic and aqueous fractions of VA extracts abrogated the steady state-microtubule pattern into a disassembled form in DU-145. In MCF-7 cells, the fractions caused retraction, condensation and clustering of tubulin protofilaments into aggregates within the cytoplasm. Examination of cell structure and morphology revealed marked cell shrinkage, nuclear fragmentation, chromatin condensation, DNA fragmentation and formation of membrane blebs and apoptotic bodies. Further analysis of cell death by fluorescence staining indicated manifestation of condensed chromatin and nuclear fragmentation, confirming an apoptotic death, with greater quantities of apoptotic phenotypes observed in MCF-7 than in DU-145.Viability assay showed a dose-dependent reduction in viable cells, with petroleum ether and aqueous fractions exhibiting a higher reduction effect (IC50 61.02 µg/mL; 65.82 µg/mL) than methanol fraction (IC50 80.77 µg/mL) in MCF-7 cells. In DU-145 cells, methanol fraction exerted highest viability reduction (IC50 44.21Âµg/mL) than aqueous (IC50 131.7 µg/mL) and petroleum ether fractions (IC50 130.5 µg/mL). VA fractions induce microtubule disassembly in a fashion similar to Nocodazole, but different to Taxol. Taken together, these observations demonstrate that VA contains biologically active components capable of inhibiting growth and proliferation of cancer cells, exerting their properties via mechanisms that target and trigger disruption of microtubule organization, effectively causing apoptotic death. Key words: Vernonia amygdalina; anti-microtubule; apoptosis; cancer cells.

131. Ismael Mayo, Alcorn State University. **The baker's yeast (Saccharomyces cerevisiae) as a model organism to elucidate the causes of metabolic reprogramming in glycolytic tumors.** Co-Authors: Jon Ignacio Moreno, Marta Piva. Co-Authors Institutional Affiliations: Alcorn State University. INBRE
Glioblastoma multiforme (GBM) is adults' most common and devastating central nervous system cancer. GBM cells undergo metabolic reprogramming since they conduct fermentation instead of aerobic respiration. This metabolic change and mitochondrial DNA (mtDNA) depletion promote tumor formation and lead to poor prognosis and treatment resistance. The molecular mechanisms that link these events are unclear. We used baker's yeast to study the relationship between fermentation rate and mtDNA levels. We compared these parameters in a wild-type (CD) strain and two deletion mutants that lacked the CCM1 (cD) or DSS1 (Cd) genes, which are required to produce members of the electron transport chain. Therefore, the mutants cannot grow in non-fermentable substrates and must obtain energy through fermentation. The experimental strains were fresh meiotic segregants derived from the heterozygous diploid (CcDd). A polymerase chain reaction (PCR) analysis confirmed their genotypes. The fermentation rate was determined by measuring the carbon dioxide released over time per unit of yeast weight. Relative mtDNA levels were assessed by quantitative PCR. Results showed a significantly negative correlation between the mtDNA levels and fermentation. The Cd segregant, with the lowest amount of

mitochondrial genome, produced almost three times more carbon dioxide than the wild type. Still, the factor that correlates with the increased fermentation remains unclear: it may be the mtDNA levels or the inability to perform aerobic respiration, which are linked in this experimental design. Future experiments will measure the fermentation rate while decreasing the segregant's ability to conduct cellular respiration but keeping the mitochondrial genome levels steady.

132. Lexington Allen Whalen, University of South Carolina. **Quantifying Engagement in Weight Loss Studies.** Co-Authors: Lexington Whalen , Brie Turner-McGrievy, Matthew McGrievy, Carolina Delgado-Diaz, Kelly DuBois, Andrew Hester, Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina. INBRE

The mLIFE study explores the effectiveness of digital technologies in promoting weight loss, focusing on the impact of a competitive leaderboard feature. Participants were divided into two groups, with Group One having access to the leaderboard and Group Two without. To better understand participant involvement, we developed a novel engagement measurement based on user actions such as uploading food and weight data and social interactions within the app. This metric allows for the characterization of participants and provides insights into engagement patterns over time and across demographics. We compare engagement across different demographic groups and present these findings through informative figures. Additionally, we model engagement over time to identify trends and utilize the engagement metric to predict participant dropout and the amount of data each participant will contribute to the study. Our analysis reveals that the study's data is skewed towards a small number of highly engaged individuals. These findings contribute to the understanding of how digital tools and engagement metrics can enhance weight loss interventions and inform the design of future health and diet applications.

133. Chaitra Shree Udugere Shivakumara Swamy, University Of Wyoming. **Small molecules vary in their ability to protect labile Biomolecules during Desiccation.** Co-Authors: Kenny Nguyen. Co-Authors Institutional Affiliations: Not Listed. INBRE

Desiccation, the loss of intracellular water, is extremely detrimental to living cells, damaging the cell’s labile components like proteins, nucleic acids, and membranes. Despite this, there are desiccation-tolerant organisms, such as tardigrades, which have evolved to survive the loss of nearly 95% of their intracellular water. A major strategy through which desiccation-tolerant organisms mitigate damage is the enrichment of small molecules. However, there are hundreds of different metabolites implicated in desiccation tolerance, and their exact functions are poorly understood. Here, we screen several small molecules spanning various categories, including excipients, osmolytes, sugars, polymers, and polyamines, to assess their ability to prevent four different types of desiccation-induced damage: protein unfolding, protein aggregation, membrane leakage, and RNA degradation. Our results demonstrate that small molecules vary significantly in their protective capacity. Known desiccation tolerance mediators such as trehalose, sucrose, maltose, and polyamines exhibited notable efficacy in preventing various types of damage. Several small molecules were only able to prevent one type of desiccation-induced damage, highlighting the specificity of their mechanisms. Overall, this research underscores the multifaceted nature of desiccation stress, as well as the need for organisms to enrich themselves with multiple diverse protectants. Ultimately, understanding the mechanisms of these protectant molecules could offer potential avenues for developing novel strategies for the transportation and long-term storage of pharmaceuticals in arid conditions, eliminating the need for reliance on the cold chain. These advancements hold promise for addressing challenges within the pharmaceutical industry while promoting sustainability and efficiency.

134. Suzanne McCahan, Nemours Children's Health. **Nemours Biomedical Research Informatics Center (BRIC).** Co-Authors: Chris Pennington, Eileen Antico, Steve Vijayan, Cara Reedy, Lynn Allen, Brad Samuel, Mckenzie Camacho, Michael Schoenbeck, Evan Miller, Qi Zheng, Nicholas Elison, H. Tim Bunnell, Eric Hall. Co-Authors Institutional Affiliations: Not Listed. CTR

The Nemours Biomedical Research Informatics Center (BRIC) was established to enhance informatics resources by providing researchers with dedicated computing resources, application support, training, and expertise in bioinformatics and clinical data analysis while facilitating inter-institutional collaboration. BRIC leverages clinical data management, phenotypic analyses, and machine learning for comparative effectiveness and outcomes research. Notably, data are enhanced through information extracted from electronic health record (EHR) notes using natural language processing as well as links to Social Determinants of Health indices supported through address information. Additionally, BRIC provides support for bioinformatics experimental design and analyses, development of specialized software, and generalized statistical analysis. BRIC maintains a comprehensive mirror of the Nemours EHR data warehouse spanning two decades, representing 3.5 million patients, transformed into a variant of the OMOP Common Data Model. The center also maintains computational resources for big data, speech analysis, and genomics projects, along with user-defined clinical research databases. The team also maintains and manages REDCap, a secure web application for building and managing surveys and databases as well as oversight of a high-performance computing (HPC) cluster and a high-performance 2.0 PB storage system. In 2023, BRIC responded to 260+ requests, showcasing its impact. Support from grants including DE-CTR ACCEL, DEINBRE, Sickle Cell COBRE, REACH COBRE, NIH RECOVER, and PRESERVE along with participation in PEDSnet and the National COVID Cohort Collaborative (N3C) underscore BRIC's significance in advancing pediatric health research through extending core informatics services.

135. Rajani Rai, OUHSC. **Preventing endometrial cancer with sheta2: a novel conservative strategy.** Co-Authors: Rajani Rai, Debasish Kumar Dey. Co-Authors Institutional Affiliations: University of Oklahoma Health Sciences Center. INBRE

The incidence and mortality rates of endometrial cancer (EC) are continuously rising. Clinical applicability of existing standard of care (total hysterectomy and hormonal therapy) is limited in obese and young patients. Endometrial intraepithelial neoplasia (EIN) is the precursor lesions of EC. Reversing EIN to normal endometrial histology offers a promising approach to prevent EC development. Previously, we have demonstrated the anti-cancerous activity of SHetA2 (novel, small, non-toxic drug) against EC. Based on our previous findings, we hypothesized that SHetA2 will inhibit endometrial cell proliferation via cyclin D1 degradation and hamper ERÎ± mitochondrial translocation by interfering with estrogen receptor/ERÎ± and Grp75 colocalization. SHetA2 was administered orally and locally in the uterus via polymer-rod in an estrogen-induced EIN rat model established in our lab. Estrogen-induced EIN development was confirmed by significantly higher uterine weight, increased endometrial and glandular areas, as well as upregulation of proliferative markers in estrogen-supplemented animals. SHetA2 treatment significantly reversed these effects with more regression observed in animals with localized compared to oral delivery of SHetA2. Pharmacokinetic analysis by HPLC showed higher SHetA2 content in the liver when given orally compared to locally. Mechanistically, SHetA2 treatment minimized ERÎ±-Grp75 colocalization as evident by immunofluorescence imaging. Immunoblotting confirmed decreased expression of cyclin D1, and PCNA. ELISA assay confirmed reduced activity of MnSOD in the estrogen-induced EIN model. In conclusion, SHetA2-mediated suppression of ERÎ±-GRP75 colocalization and cyclinD1 levels supports our hypothesis. Overall, our study demonstrates SHetA2â€™s potential to suppress estrogen-induced EIN development. The localized delivery system retained the drug efficacy at the target tissue and reduced its off-target absorption. These results justify further translation of SHetA2 polymer rods as intrauterine

devices. Acknowledgment: The work was supported by IDeA Network of Biomedical Research Excellence (INBRE) grant.

136. Hannah Williams, University of Nevada Las Vegas. **Evaluating COBREs using the Translational Science Benefits Model.** Co-Authors: Jon Hilpert, Kristine Bragg, Evan Falkenthal. Co-Authors Institutional Affiliations: Not Listed. COBRE
Center for Translational Science Awards (CTSA) are an NIH funding mechanism for developing biomedical infrastructure that translates scientific advancements into clinical solutions, often for rural/ underrepresented populations. CTSA are difficult to evaluate due to their expansive reach, massive coordination efforts, and multitude of outcomes. The Translational Science Benefits Model (TSBM) is a framework designed to support institutional assessment of CTSA research activities/ outcomes; emerging in recent years as a framework for gathering evaluation evidence. Within the context of the Translational Research Institute (TRI), through testing on multiple funded CTSA across Arkansas, we have developed a mixed-methods approach for applying TSBM that can be useful to other evaluators interested in using TSBM within the context of CTSA evaluation. We present the results of various applications of the model, including a semistructured evaluation program for collecting data and examples of findings from different applications of the evaluation program.

137. Jae Yeon Hwang, University of Louisville. **Circular RNAs as Biomarkers in Diseases and Cancer from High throughput Sequencing Analysis.** Co-Authors: Zhenhua Shang, Juw Won Park. Co-Authors Institutional Affiliations: University of Louisville INBRE
Circular RNAs (circRNAs) are emerging as promising diagnostic and therapeutic targets in various diseases, including cancer, due to their tissue-specific expression patterns, stability, and regulatory functions. Employing advanced bioinformatics methodologies, we elucidate the diagnostic and prognostic potential of circRNAs across diverse disease contexts, particularly focusing on cancer. Through comprehensive analysis of large-scale transcriptomic datasets, including RNA-seq experiments with rRNA-depletion, we decipher disease-specific circRNA signatures and characterize their expression profiles in different pathological conditions, highlighting their potential as robust biomarkers for early detection and prognosis. Our analysis unveils distinct circRNA profiles associated with specific disease subtypes and stages, indicating their utility as non-invasive diagnostic markers with higher sensitivity and specificity compared to traditional biomarkers. Furthermore, we explore the intricate regulatory roles of circRNAs in relation to other non-coding RNAs, such as microRNAs and long non-coding RNAs, in disease pathogenesis, uncovering their involvement in key signaling pathways and molecular processes underlying disease progression. Integrative computational analyses further investigate regulatory interactions between circRNAs and other biomolecules, such as proteins, elucidating the network of disease-associated molecular mechanisms. Our comprehensive bioinformatics pipeline not only facilitates the systematic annotation and characterization of cancer-related circRNAs but also provides a valuable resource for prioritizing candidates for downstream experimental validation and functional studies, eventually facilitating personalized treatment strategies. Through bioinformatics-driven approaches, we uncover the sophisticated roles of circRNAs in cancer biology, harnessing their diagnostic and prognostic value across diverse disease contexts, and a possibility for the development of innovative precision medicine strategies to improve patient outcomes.

138. Nesreen Alsbou, University of Central Oklahoma. **Development of a Portable Microwave Imaging System for Medical Imaging and TBI Detection.** Co-Authors: Morshed Khandaker, Imad Ali, Colton Cox. Co-Authors Institutional Affiliations: UCO, OUHSC. INBRE

Microwave imaging is considered one of the emerging techniques that provides safe, cost effective, fast and noninvasive medical imaging modality compared to other conventional imaging techniques such as magnetic resonance imaging (MRI), x-ray, and computed tomography imaging (CT). The imaging in microwave imaging system is performed by mapping the interactions of microwave photons with the medium including signal reflection, attenuation, and propagation. These factors are dependent on the water or blood content of the tissue. The maps of electromagnetic properties of the tissue generated with microwave imaging can be used to generate medical images for different clinical applications such as bone degradation, tumor, and Trauma Brain Injury (TBI) detection. The microwave imaging system and the algorithm developed to reconstruct and obtain microwave images for different objects will be discussed.

139. Andrew W Brown, Arkansas Children's Research Institute and University of Arkansas for Medical Sciences. **Biostatistics Core of the Center for Childhood Obesity Prevention.** Co-Authors: Reid D. Landes, Simon Chung, Scott Stewart. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences, Arkansas Children's Research Institute and University of Arkansas for Medical Sciences. COBRE

The Biostatistics Core of the Center for Childhood Obesity Prevention (CCOP) with the Arkansas Children's Research Institute (ACRI) has a mission to provide statistically sound methodological infrastructure for the CCOP to support high quality obesity research and participate in research education and mentoring of Center investigators, particularly in the areas of study design and data analysis methods. Specifically, we provide statistical support to CCOP investigators in various aspects and stages of their research, including: statistical mentoring, education and training; development of research proposals and grant applications; statistical considerations in study design; data management, wrangling, and visualization support; gaining insights through statistical programming and analysis; navigation of ethical and regulatory issues in research; dissemination of results via reproducible workflows; support for peer-reviewed publications; and improving awareness and access to data and statistics resources. In addition, the Core serves as the foundation for an evolving institutional Biostatistics Core to support ACRI investigators broadly (i.e., not affiliated with the CCOP) as part of our sustainability plan. The Core's membership structure is built on a collaborative agreement between ACRI and the University of Arkansas for Medical Sciences' Department of Biostatistics in which faculty and staff biostatisticians within the department compose the membership of the Core. By anchoring the ACRI Core with the Department of Biostatistics, Core members maintain a connection and network of collaborators within their disciplinary department while embedding them within the context of the domain of inquiry of investigators with whom they collaborate. This provides a stronger conduit for collaboration and sustainability.

140. Angela Batson, University of Nebraska Medical Center. **Using Network Reach to Assess CTR Impact.** Co-Authors: Nishank Varshney. Co-Authors Institutional Affiliations: Great Plains IDeA-CTR. CTR

The Great Plains IDeA-CTR is a collaborative effort between seven regional institutions across the state of Nebraska. Over the eight years of its funding, the GP-CTR has shown sustained growth in its operations and membership. Yet, additional growth is necessary to change health outcomes in the region. To identify where and how the CTR can grow in the coming years, we examined the network's reach by evaluating the data from 2021-2023. The findings show the membership is growing at a robust rate with a total of 760 members and a large practice-based research network (N=89 sites), representing 7 partner institutions, 28 organizations, and 78 disciplines. We further combine this data with the current strength of the scientific community in Nebraska and neighboring states to identify gaps where prospective new members and partnerships can be scaled. Additionally, we identified the metrics related to CTR's

activities such as pilot awards, research teams, services, and events. The data from funding mechanisms and services helps identify opportunities for internal growth and external collaboration. Our network reach analysis demonstrates the significant impact the Great Plains CTR has already made and provides suggestions for engaging new members and forging novel partnerships.

141. Hamed Abdollahi, University of South Carolina. **Gene Expression Profiles Under The Influence of Kynurenic Acid During Progeny.** Co-Authors: Courtney Wright, Ana Pocivavsek, Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine, University of South Carolina. INBRE

Tryptophan metabolism plays a crucial role in sleep disorders and is also associated with various neurodegenerative diseases. Kynurenic acid, a metabolite of tryptophan, exhibits uneven distribution in different parts of rat brains. Increased production of kynurenic acid due to sleep disorders leads to its accumulation in various brain sectors. The effects of kynurenic acid have been studied during fetal, pre, and post-natal development in rats. Since genes play a significant role in sleep regulation, this study aims to identify differentially expressed genes between male and female rats exposed to increased concentration of kynurenic acid during the fetal period. The hypothesis is that kynurenic acid may influence key genes related to sleep or psychiatric disorders in young adult rats. Rattus norvegicus rats of both sexes were randomly divided into two groups. One group was fed a control dietary regimen, while the other consumed a kynurenic acid-enriched diet during pregnancy. After postnatal day 56 (young adulthood), samples were collected from the hippocampus at four different time points within a 24-hour period. Total RNA was extracted from each sample, and the Illumina RNA-seq platform was used to obtain RNA-seq data. The resulting high-throughput data underwent genomics differential gene expression analysis. After trimming the raw Illumina RNA-seq data, 28051 genes remained for further DEG analysis. By comparing gene expression at different time points (0, 6, 12, and 18) between male and female rats, a total of 303 genes were identified as differentially expressed. Among these, 138 genes showed differential expression in females across different time points, and 167 genes exhibited different expression patterns between rats consuming a control diet and those on a kynurenic acid-enriched diet.

142. Shangping Wang, Clemson University. **Viable vitreous grafts for whole porcine knee meniscus transplantation.** Co-Authors: Ge Pan, Peng Chen, Dustin Mueller, Marshall Wilson, Shuchun Sun, Zhenzhen Chen, Thomas Lee, Brooke Damon, Glenn Hepfer, Cherice Hill, Yongren Wu, Kelvin G.M. Brockbank, Hai Yao. Co-Authors Institutional Affiliations: Clemson University, Medical University of South Carolina, Tissue Testing Technologies LLC. COBRE

The shortage of suitable donor meniscus grafts from the knee impedes treatments for millions of patients. Vitrification holds potential to preserve viable biomaterials at cryogenic temperatures without the damaging effects of ice crystal formation, thanks to the strategic use of high concentrations of cryoprotectants (CPAs). However, its application is limited to small volumes (â‰¤3 ml) for musculoskeletal tissues when utilizing a distinguished CPA solution, VS55. This study identifies inadequate CPA penetration as a key obstacle in successfully vitrifying larger sizes (>3 mL). Unlike vascular tissues, these avascular tissues require prolonged CPA exposure for adequate penetration, posing challenges in balancing CPA penetration and its toxicity. To overcome this hurdle, a simulation-based optimization approach combining computational modeling with non-invasive microcomputed tomography (ÂµCT) imaging predicts CPA concentrations and distribution within tissues over time, minimizing CPA exposure for successful vitrification. The evaluation encompassed two larger volumes (4 and 10 ml). Using the optimized VS55 loading protocols, viability achieved approximately 85% in 4-ml meniscal specimens, 70% in the 10-ml entire meniscus, surpassing conventional cryopreservation (20%-40%). The addition of sucrose and trehalose has been demonstrated to facilitate the glassy forming

ability of the larger system by effectively avoiding ice crystal formation. Minimal alterations were observed in the extracellular matrix (ECM) structure and biomechanical strength of optimized vitrified tissues. These findings underscore the significant impact of optimizing the CPA loading process, resulting in remarkable viability improvements for vitrified avascular tissues of larger sizes, akin to standards expected in clinical application.

143. Tiange Feng, MaineHealth Institution for Research. **mTOR signaling in gastric X/A-like cells regulates bone metabolism.** Co-Authors: Wenzhen Yin, Weizhen Zhang, Ziru Li. Co-Authors Institutional Affiliations: Peking University Health Science Center, MaineHealth Institute for Research. COBRE Background: Gastric mechanistic target of rapamycin (mTOR) signaling is indispensable for sensing energy status and regulating peptide hormones such as ghrelin. Although the alterations in mTOR signaling within X/A-like cells affect lipid and glucose metabolism, its influence on bone metabolism remains unexplored. Methods: To delve into this question, we established a Ghrl-Cre mouse model that genetically manipulates mTOR pathway in the X/A-like cells. mTORflox/flox and TSC1flox/flox mice were bred with Ghrl-Cre mice respectively, generating Ghrl-mTOR-/- mice with mTOR signaling suppressed in X/A-like cells, and Ghrl-TSC1/- mice with mTOR signaling selectively activated. Using these mouse strains, we investigated the role of X/Alike cell mTOR signaling under baseline, ovariectomy, or calorie restriction conditions. Bone measurements were determined by micro computed tomography (micro-CT). Results: Ghrl-mTOR-/- male mice had impaired trabecular bone at 12 weeks old, progressing to cortical bone loss at 40 weeks of age. Whereas, little difference in bone parameters was observed in Ghrl-mTOR-/- female mice. Interestingly, Ghrl-mTOR-/- female mice experienced a reduction in trabecular bone mass after ovariectomy. No significant difference in bone microstructure parameters was observed in Ghrl-TSC1-/- mice, except for shorter bone length compared to control mice. Notably, male Ghrl-TSC1-/- mice were protected from trabecular and cortical bone loss when subjected to calorie restriction. Conclusions: While X/A-like cell mTOR signaling has a mild impact on bone metabolism under baseline conditions, its suppression leads to bone loss in an estrogen dependent manner. Conversely, activating mTOR signaling in X/A-like cells protects the skeleton from calorie restriction-induced bone loss.

144. Debbie Christine Lee, West Virginia University. **West Virginia Clinical and Translational Science Institute (WVCTSI) Principal Investigator's Academy: A forum to provide training to clinical trial investigators.** Co-Authors: Shelley Welch, Sarah Haymond, Meg Haller, Meghan Reeves, Judith Feinberg, Sally Hodder, Co-Authors Institutional Affiliations: West Virginia University Research Corporation, West Virginia University School of Medicine. CTR
West Virginia (WV), the only state located entirely in Appalachia, has the lowest life expectancy in the nation (74.4 years) and ranks at or near the bottom in many chronic disease categories. Participation in clinical trials has been associated with improved outcomes, yet IDeA states have fewer trials and rural residents and those of other underserved groups are underrepresented in clinical trials. To provide a forum for clinical trial investigators (early-state as well as experienced), the Principal Investigator's (PI) Academy was established in 2019 by the West Virginia Clinical and Translational Science Institute (WVCTSI). PI Academy activities include a formal curriculum for new trial investigators, quarterly discussion forums, the Idea Lab with weekly office hours. The didactic curriculum consists of seven modules ranging from topics on regulatory guidelines, setting up and implementing a study, to recruitment of diverse participants in clinical trials. The Idea Lab and Office Hours serve as a virtual forum for senior leaders and junior investigators to discuss optimization of research designs and challenges encountered in trials. To date, 49 PIs have presented their study protocols. There are currently 146 members of the PI Academy, of whom 31 have utilized the IDeA Lab. The PI Academy provides a platform for early-stage and seasoned investigators to share experiences and best practices.

145. Gangqing "Michael" Hu, West Virginia University. **The WVU Bioinformatics Core: Empowering Biomedical Research through Team Science in West Virginia.** Co-Authors: None. CTR
The vision of the West Virginia University (WVU) Bioinformatics Core is to elevate biomedical research excellence within WVU and beyond by embracing a Team Science approach. Our mission is to provide timely, high-quality services for a variety of data analyses, primarily through collaborative research endeavors. The Core collaborates closely with the WVU Genomics Core and the Marshall University Genomics and Bioinformatics Core, offering a comprehensive, statewide service that encompasses library preparation, sequencing, and data analysis. Our current suite of services includes RNA sequencing, Assay for Transposase-Accessible Chromatin using sequencing, microbiome analysis, micro-RNA analysis, DNA methylation, single-cell RNA sequencing, single-cell ATAC sequencing, and single-cell multiomics. In 2024, we are excited to expand our offerings to include spatial transcriptomics, utilizing both 10X Genomics and MERFISH technologies.

146. Sydney Green, Rhode Island College. **Determining the Active Site Environment and Mechanism for cancer derived variants of DNA Polymerase Theta.** Co-Authors: Corey Thomas, Morgan Andrews, Jamie Towle-Weicksel. Co-Authors Institutional Affiliations: Rhode Island College. INBRE
DNA is constantly being affected by a variety of endogenous and external factors. DNA damage can interrupt replication pathways leading to genomic instability and disease. Damage is mitigated through DNA repair pathways that utilize DNA Polymerases to recognize damage and work to repair it through replacing or bypassing the damaged base allowing replication to continue, promoting genomic integrity. There are some polymerases that do not accurately repair damage, often promoting DNA base mispairing. DNA Polymerase Theta (Pol Theta) is one such polymerase with little known about its role in repair. Understanding Pol Theta's mechanism for selecting and incorporating correct versus incorrect nucleotides may offer further insight into its low fidelity status. Furthermore, it may offer understanding of how DNA Polymerases promote genomic instability leading to diseases including cancer. To explore the mechanism of Pol Theta in real time we utilize a 2-aminopurine fluorescently labeled DNA substrate to monitor the microenvironment within enzyme active site through fluorescent changes during nucleotide incorporation. We hypothesize that correct nucleotide selection and incorporation are guided through subtle noncovalent interactions absent with incorrect. Additionally, we aim to observe mutagenic cancer derived pol theta variants that are unable to distinguish between correct and incorrect nucleotides. Our work suggests there are differences in fluorescent output for these variants when compared to WT Pol Theta. Through these studies we can define the network of residues important for nucleotide selection enhancing our understanding of the active site environment of Pol Theta with the goal of designing drugs to target it.

147. Edna Acosta Perez, University of Puerto Rico, Medical Science Campus. **Preparation, response, and recovery of healthcare centers in Puerto Rico after emergencies: We are stronger after all these desasters.** Co-Authors: Angellyn Santos Gonzalez, Edna Acosta Perez, Jonahan Purtle, Katyana Santiago, Damaris López Mercado, Glorisa Canino, Alexander N. Ortega. Co-Authors Institutional Affiliations: University of Puerto Rico, University of Puerto Rico Medical Science Campus, New York University, Drexel University, University of Hawaii at Manoa. CTR
Purpose: In recent years, Puerto Rico has faced a series of public health crises, including hurricanes, earthquakes, and the COVID-19 pandemic. Supported by NIH funding, our study aimed to assess the effectiveness of emergency plans at healthcare facilities in Puerto Rico. We aimed to identify successful and ineffective aspects of these plans, along with strategies employed by healthcare centers during emergencies and the challenges encountered. Method: We conducted 10 semi-structured qualitative

interviews with key informants from two community healthcare centers, resulting in a comprehensive dataset. Using a predefined category guide, interviews were transcribed and coded, ensuring agreement among judges (kappa

148. Nina K. Ayala, Women & Infants Hospital of RI / Alpert Medical School of Brown University. **Leveraging digital mindfulness training to prevent psychological birth trauma among pregnant people with low optimism.** Co-Authors: Meghan Sharp, Emily Miller, Margaret Bublitz. Co-Authors Institutional Affiliations: Miriam Hospital / Alpert Medical School of Brown University, Women & Infants Hospital of RI / Alpert Medical School of Brown University. COBRE

Traumatic birth experience is an underappreciated risk factor for development of postpartum post-traumatic stress disorder (p-PTSD), depression, and anxiety. Postpartum mental health conditions contribute significant social, medical, and economic burden, and are the leading cause of maternal death. Both TBE and postpartum mental health conditions are disproportionately experienced by minoritized populations, further widening the known gap in maternal health outcomes. We urgently need innovative, wholistic, strengths-based approaches to care for pregnant people with clear mechanisms of impact. Dispositional optimism is an resilience factor which has been associated with wide-ranging mental health benefits, including prevention and treatment of PTSD in non-pregnant populations. Mindfulness interventions show promise in improving dispositional optimism and thus may be a transdiagnostic approach to bolstering resilience and positively impacting health. The Mindfulness, Optimism, and Resilience for Perinatal Health and Equity (MORPHE) Study is an ongoing randomized clinical trial comparing use of an existing, equityfocused, perinatal mindfulness phone application (Expectful) to routine care for pregnant individuals with low baseline optimism. 100 participants will be randomized in order to assess 1) feasibility and acceptability of the digital mindfulness intervention, 2) impact of Expectful on optimism, traumatic birth experience and pPTSD, and 3) explore perspectives on the role of optimism and resilience in pregnancy experience. This is the first primary prevention trial for postpartum PTSD, and has the potential to meaningfully improve peripartum wellness. If proven efficacious, Expectful is an accessible and scalable intervention for improving perinatal outcomes and addressing birth inequities.

149. Chunkai Wang, Creighton University. **The Drug Discovery & Delivery Core in the Translational Hearing Center at Creighton University.** Co-Authors: Alekha Dash, Peter Steyger, Patrick Swanson, Satish Agrawal, Jeff E. North, Gopal Jadhav. Co-Authors Institutional Affiliations: Bellucci Translational Hearing Center, Creighton University. COBRE

The Drug Discovery & Delivery Core (DDDC) at the Creighton Translational Hearing Center has established a state-of-the-art drug discovery and development pipeline to support research projects both within and outside the Center. This core comprises four laboratories: (1) the Drug Design, Synthesis and Validation Laboratory, (ii) the ADMETox Laboratory, (iii) the Zebrafish Laboratory, and (iv) the Cell Culture and Tissue Laboratory. With substantial support from Creighton University and neighboring institutes, the DDDC accomplished the essential equipment setup and an appropriate expertise to lead the Drug discovery projects. The DDDC at Creighton employs contemporary, innovative chemical synthesis to modify chemical structures systematically to design and develop novel pharmacophore(s) ,), optimizing the efficacy and bioavailability of candidate ototherapeutic drugs while minimizing toxicity. At the DDDC we provide efficient and accurate analytical services, ensuring confidence in the structural integrity, purity, and stability of molecular syntheses. Additionally, lead compounds can undergo pre-formulation studies for enhanced characterization, paving the way for further preclinical and clinical testing. Addressing the global challenge of identifying researchers capable of supporting significant research investments, the DDDC aims to ensure its pipeline of graduate trainees, understands the

research challenges in both academia and industry, fostering opportunities for academic and industry-academic collaborations. With a proven track record in advancing drug discovery, synthesis and initiating research projects on time and within budget, we continue to broaden our expertise and invest in a knowledge-based drug discovery core at a dedicated academic medical center.

150. Subhajit Chakrabarty, Louisiana State University Shreveport**. Automatic brain stroke lesion segmentation using MRI images: a comparative analysis of backbone architectures for U-Net models.** Co-Authors: Tahmina Akter Anondi, Devesh Sarda, Mridula Mavuri, Caleb Stewart, Karen Stokes, Steven Conrad. Co-Authors Institutional Affiliations: Louisiana State University Shreveport, LSU Health Shreveport. INBRE

Accurate lesion segmentation is crucial for diagnosing, planning treatment, and monitoring brain stroke related tissue damage. The key objective of this study is to explore the impact of choice of backbone architecture on model performance in the context automatic brain stroke lesion segmentation using 3D MRI images. By backbone, we mean the encoder (or feature-extractor) part of the U-Net Convolutional Neural Network architecture. Our dataset is the ATLAS2.0. We take 600 3D MRI images (in NIFTI format) and split them into training, validation and testing. Our overall model design is based on the U-Net. Our backbone architectures are Vision Transformer, Inception, ResNet, DenseNet, HRNet, VGG16 and MobileNet. The model weights for the pre-trained backbones are derived through training on much larger datasets (non MRI, like the imagenet). We develop a new model through fine-tuning on our 3D MRI data, by adding trainable layers, after freezing the earlier layers of the best performing backbone, and performing hyper-parameter optimization. We make a comparative analysis of the choice of the backbone architectures and our new model, with Dice Similarity Coefficient as our metric. Results indicate that our new model performs well, as compared with the best among our benchmarks. This work performs a systematic analysis in the choice of backbone architecture, using a large public dataset, and also presents a new model for brain stroke lesion segmentation. Similar structured pipeline may be replicated in other contexts, for difficult 3D MRI image segmentation tasks, that are performed automatically using Deep Learning.

151. Peng Zhong, University of Nebraska Medical Center. **Hypothalamic sleep/wake neuron deficits in Alzheimer's disease.** Co-Authors: Ajay Kumar. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. COBRE

Sleep disruption is estimated to affect 30-66% of patients with Alzheimer’s disease (AD), and a major cause of institutionalization. As an important molecular hallmark of AD, the pathological tau protein is the earliest observable AD neuropathology in several sleep-wake regulating regions including the lateral hypothalamus (LH) area. Melanin-concentrating hormone (MCH) neurons are exclusively located in the LH, and regulate sleep and influence memory function. In the present studies, we tested whether the deficiencies in MCH sleep circuit underlie the sleep disturbances in the tauopathy condition of AD. We found that PS19 tauopathy mice displayed significant sleep deficits, manifested as decreased REM and non-REM sleep, and increased wakefulness. More importantly, our studies showed that the neuronal activity of MCH neurons was significantly impaired during sleep phase, in particular, rapid eye movement (REM) sleep in PS19 mice. These results suggest a critical role for MCH neurons play in sleep-wake dysregulation caused by tau pathology, and help develop circuit-based therapeutic interventions for sleep disorders and cognitive impairments in AD and other neurodegenerative tauopathies.

152. Gisela Cairo Baza, Dartmouth College. **Unraveling the mechanisms of extra divisions in eggs and polar bodies upon loss of the MOS signaling pathway.** Co-Authors: Soni Lacefield. Co-Authors Institutional Affiliations: Dartmouth College. COBRE

Mammalian oogenesis culminates in egg formation. Once the egg is fertilized by sperm, it can form a viable embryo. Oogenesis involves a complex series of events including the cell division process of meiosis. In mammals, each meiotic chromosome segregation eliminates half of the genome through the extrusion of a smaller mass known as polar body (PB), which degrades after meiosis. A key step in mammalian oogenesis occurs prior to fertilization, when the egg naturally halts during the meiotic stage of metaphase II, waiting to be fertilized by the sperm. The MOS kinase initiates a MAPK cascade and maintains metaphase II arrest through a poorly understood mechanism. Previous research shows Mos-depleted eggs break free from metaphase II arrest and some undergo aberrant divisions, occasionally causing germ cell tumors in mice. Using mouse Mos-depleted eggs, I uncovered a novel role for MOS in preventing division of the first PB extruded, which might prevent germ cell tumors. Furthermore, I have found novel phenotypes Mos-depleted eggs display that suggest MOS is not only responsible to maintain metaphase II arrest but also to prevent premature genome activation required for embryo differentiation and development. Using cutting-edge technologies, I aim to understand the mechanism of extra divisions in eggs and polar bodies upon loss of MOS. Because oogenesis is highly conserved in mammals, my work on mice will provide information on how human oogenesis is regulated.

153. Justin Parent, Bradley Hospital. **Multi-Method and Multi-Informant Youth Sleep Duration Assessment in a Partial Hospitalization Program.** Co-Authors: Kelsey Hudson, John McGeary. Co-Authors Institutional Affiliations: Bradley Hospital, Brown University. COBRE
BACKGROUND: Children with insufficient sleep are at increased risk for adverse health outcomes, including psychopathology, cardiometabolic health problems, behavior and emotional dysregulation, and delays in cognitive development. As such, assessment of youth sleep health is a vital aspect of clinical care, especially for peripubertal youth at high risk for sleep deficiencies and severe psychopathology. This study aimed to understand 1) the prevalence of insufficient sleep in children in an acute level of care and 2) how accurately youth and their caregivers' retrospective report of youth sleep duration compares to objectively assessed duration. METHOD: In a sleep research study, we enrolled 50 peripubertal youth (ages 9-12) admitted to a mental health partial hospitalization program and compared child and parent self-report total sleep time to Fitbit Charge 5-derived objective total sleep time based on activity and heart rate. RESULTS: We found that 96% of our participants did not meet sleep duration guidelines of 9-12 hours a night based on objective assessment. On average, children slept 7.47 hours a night (SD = .87), but parents reported 10.11 hours (SD = .91), and children reported 9.63 hours (SD = 1.41). Approximately 80% of parents and 60% of youth overestimated sleep by 2+ hours. DISCUSSION: These data highlight the prevalence of insufficient sleep in youth with acute mental health problems and that single-timepoint youth or caregiver report questionnaires may substantially overestimate total sleep duration. The implementation of wearable sleep measurement in clinical care can provide greater information on sleep health and inform personalized treatment.

154. Arpan Chowdhury, Louisiana State University. **Inhibiting CD2:CD58 Interaction Using Strategically Designed Cyclic Peptides.** Co-Authors: Prajesh Shrestha, Vivekanandan Subramanian, Veena Taneja, Seetharama Jois. Co-Authors Institutional Affiliations: Louisiana State University, University of Kentucky, Mayo Clinic. INBRE
Co-stimulatory molecules CD2 and CD58, when overexpressed, can increase the interaction of the T-cell receptor and the Major Histocompatibility Complex in APC by hundreds of folds, leading to excessive cytokine production in autoimmune and inflammatory diseases such as Rheumatoid Arthritis (RA). By inhibiting the CD2: CD58 nexus, we could halt the progression of RA. Our lab has previously reported a cyclic peptide, SFTI-DBF, with a dibenzofuran moiety designed by replacing the Pro-Pro residue in the Î²-turn of SFTI, resulting in sparing solubility in water. To address this solubility issue, we have now used

2,6-dimethyl Tyrosine (DMY) and PhenylGuanido (FGua) groups, resulting in complete water solubility. Analysis of the secondary structure of the peptide by circular dichroism (CD) spectra indicated that the cyclic peptides maintain a Î²-turn structure, similar to SFTI-DBF. Bioanalytical and cellular assays such as cell adhesion assays, Surface Plasmon Resonance, and Proximity Ligation Assay are used to understand and delineate these peptides' characteristics. NMR spectra has confirmed that 2,6-DMY has a single conformer, and FGua exhibits minor conformations (as shown by TOCSY and NOESY) in solution. Our future work in animal models will provide a deeper understanding and pave the way for the design of therapeutically active cyclic peptides. This research was supported by funding from the National Cancer Institute of the National Institutes of Health, Grant/Award Number: 5R01CA255176-03 (SJ and DB) and Institutional Development Award from the National Institutes of General Medical Sciences of the National Institutes of Health under the grant number P20 GM103424.

155. Janelle Beadle, University of Nebraska at Omaha. **Social Support Across the Adult Lifespan.** Co-Authors: David Warren. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. COBRE

Social support is critical to our well-being, yet many people who experience mental health issues are not able to obtain the support they need. Our willingness to seek out social support is also impacted by societal norms that may differ for men and women. Furthermore, there is evidence that older adults have smaller social networks than younger adults which may reduce older adults' capacity to obtain social support. The present study investigated the degree to which perceived social support was associated with depressive symptoms, identification with feminine or masculine attributes, and age in adults. We hypothesized that depressive symptoms and age would be associated with lower perceived social support, and greater identification with feminine attributes would be associated with higher perceived social support. The present study included an adult lifespan sample of healthy, community-dwelling adults 19 years of age and older (N=69). Participants completed the Social Support Survey Instrument, the Beck Depression Inventory, and The Bem Sex Role Inventory (BSRI-12). We conducted a linear regression investigating the relationship between social support, depressive symptoms, the degree to which individuals identified with masculine and feminine attributes, and age. The overall regression model was significant (p

156. Eric Tirrell, Butler Hospital/Brown University. **Bridging Synapses: Connecting Scientific Research and Clinical Practice in Patients Receiving Transcranial Magnetic Stimulation for Major Depressive Disorder.** Co-Authors: Linda Carpenter. Co-Authors Institutional Affiliations: Butler Hospital. COBRE

Recruitment for research studies from patients flowing through a clinical treatment service such as Transcranial Magnetic Stimulation (TMS) Therapy or Esketamine provides the ideal opportunity for biomarker investigations that help inform clinical practice. Butler Hospital researchers have been actively engaging patients undergoing TMS treatment for Major Depressive Disorder (MDD), inviting them to participate in research that don't alter their course of naturalistic clinical care. Research has included brain imaging (MRI, MRS), collection of blood specimens, recording of physiological data (EEG, heart rate variability, blood pressure), computerized cognitive assessments, app-based ecological momentary assessment (EMA) of symptoms over time, or completion of other self-report surveys. Serial assessment of symptom severity via scales were done as part of clinical routine and scores were recorded in a registry-style database to facilitate merging of treatment outcomes (response, remission) with other research outcome variables. Using this integrated approach to support clinical research can help inform the field by gathering naturalistic treatment data that reflects real-life patients and clinical practice. A registry database characterizing TMS/Esketamine patients and their outcomes is ideal for 1) evaluating durability of response and likelihood of retreatment; 2) addressing clinical questions that

have not been the subject of systematic prospective study (e.g., concurrent medications, parameter selection, targeting methods); and 3) merging clinical outcomes with imaging or other research biomarker data obtained pre- and post-TMS/Esketamine. Registry data mining can provide valuable insights about personalization of care and generate hypotheses for testing in prospective studies.

157. Maha Said Ahmed Abdeltawab Hanafi, University of Arkansas for Medical Sciences. **Discovery of Tk-850 as a novel EGFR inhibitor with efficacy in EGFR-positive lung cancer cells.** Co-Authors: Baku Acharya, Baha'a Jabali, Brendan Frett. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE

Epidermal Growth Factor Receptor (EGFR) is a driving oncogene in approximately 30% of non-small cell lung cancers (NSCLC), which has led to numerous drug discovery campaigns targeting this tyrosine kinase (EGFRTKI). Unfortunately, due to the heterogeneity of NSCLC, treatment can select for resistant mutations, which compromises efficacy of the EGFR-TKI and limits duration of effective treatment. This presents a significant challenge in drug discovery and necessitates the advancement of new EGFR-TKIs to improve efficacy of treatment. Despite the clinical development of irreversible EGFR-TKIs, off-target toxicities and resistance raise safety and efficacy concerns. Herein, we introduce Tk-850, a reversible inhibitor that can bind to EGFR and selectively target cancer cells harboring EGFR mutations. Tk-850 was screened against a kinase panel and displayed selectivity for EGFR and EGFR mutants with sub-nanomolar binding observed across various clinically relevant mutations. Tk-850 is cytotoxic to NSCLC cell lines with EGFR mutations (exon19 del, L858R/T790M) and is less active against lines harboring wildtype EGFR. Moreover, Tk-850 shows selectivity to cancer cells over normal lung fibroblasts and is less toxic to lung fibroblasts compared to osimertinib. Tk850 inhibits the phosphorylation of EGFR in a dose-dependent manner that is prominent at nanomolar concentrations in mutant lines. Further studies will be performed to test effects of Tk-850 against various EGFR mutants and to evaluate its in vivo efficacy. Tk-850 presents a novel anticancer agent that can effectively inhibit mutant EGFR and potentially overcome issues associated with irreversible inhibitors.

158. Michael G. Nichols, Creighton University. **NE-INBRE Integrated Imaging Core Facility (NIICF) at the University of Nebraska Medical Center (UNMC) and Creighton University Medical Center (CUMC).** Co-Authors: Heather Jensen-Smith. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. INBRE

The NIICF unifies resources at the Integrated Biomedical Imaging Facility (IBIF) at CUMC and nearby Advanced Microscopy Core Facility (AMCF) at UNMC. As a synergistic hub for shared research resources for biomedical imaging, the NIICF continues to advance robust researcher and Scholar training in the use of rapidly advancing imaging instrumentation and techniques at two research institutes in the NE-INBRE program, CUMC and UNMC. With an expansive biomedical research footprint in the state of Nebraska, the NIICF promotes active, inclusive research and scholarly outreach to academic institutions throughout Nebraska. By advancing research infrastructure and funding across NE-INBRE partner institutions, the NIICF accelerates discovery while illuminating rewarding biomedical career paths. Affiliated, strategically aligned instrumentation, technical and scientific expertise, training and educational resources, and outreach activities forms a nucleation point for Nebraska faculty and scholars to incorporate traditional light microscopy with super-resolution and multi-photon confocal microscopy, whole slide scanning, and mesoscopic light sheet fluorescence microscopy into their research. The NIICF provides outstanding, advanced microscopy equipment with access to a team of PhD-level team scientists qualified to acquire data, provide hands-on training for advanced instrumentation, support quantification/analyses and experimental design, all of which are especially important for developing a strong research community at PUIs throughout Nebraska and IDeA states. The NIICF is supported by the NIGMS of the NIH under

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159. S. Michal Jazwinski, Tulane University Health Sciences Center. **COBRE Mentoring Research Excellence in Aging and Regenerative Medicine (P30GM145498) Genomics, Bioinformatic, and Spatial Multiomics Integrated Cores.** Co-Authors: J. Quincy Brown, S. Kim, Md Abdul Awoal, Ahmed Moustafa, Manoswini Dash, Chenyao Xiao. Co-Authors Institutional Affiliations: Tulane University. COBRE
Our core offers Sanger sequencing (ABI SeqStudio), including DNA fragment analysis, and NextGen Seq (Illumina NextSeq 2000), including total RNAseq and mRNAseq. We employ a variety of library preparation protocols. Single cell applications (scRNAseq, snRNAseq, and multiome ATAC+gene expression snRNAseq) are also provided (10X Genomics Chromium X). RNA and DNA sizing and quality are determined (Agilent Bioanalyzer 2100 or Revvity LabChip GX Touch Nucleic Acid Analyzer). Spatial transcriptomics profiling is accomplished with the 10X Genomics Visium technology. We also offer 10X Genomics Visium for CytAssist, which allows use of customers' pre-existing slide specimens. We feature the Xenium In Situ Analyzer (10X Genomics), which allows transcriptomics on large specimens with high sensitivity and specificity, at the subcellular level. Targeted analysis with a variety of gene panels that can be customized to about 500 genes total is offered. (This will soon expand to 5,000 genes, with subpanels available.) Specimens can be re-used for H&E and immunofluorescent staining and Visium for CytAssist. We section both fresh-frozen and formalin-fixed paraffin-embedded specimens (FFPE). We work with clients closely at every step in the protocol, to assure quality and satisfaction. Our Bioinformatics Core is integrated into our experimental pipelines, offering biostatistical advice starting with experiment design and ending with standard bioinformatic and graphical output from experiments. This core also provides advanced custom bioinformatic analyses on request, as extensions of these pipelines and as stand-alone services. Our Cores have served customers throughout Louisiana and neighboring states. Visit us at: https://medicine.tulane.edu/tulane-center-aging/cobre-grant/genomics-biostatistics-bioinformatics-core.
Supported by NIH grant P30GM145498.

160. Katherine M. Sharkey, Rhode Island Hospital/The Warren Alpert Medical School of Brown University. **Developing and Implementing a Sleep Intervention for Perinatal Women in Collaboration with Direct Care Workers.** Co-Authors: Jane Hesser, Ariana Albanese, Hannah Frank, Janine Molino. Co-Authors Institutional Affiliations: The Warren Alpert Medical School of Brown University. COBRE
Disrupted and insufficient sleep is common during pregnancy and increases the risk of negative health consequences for birthing parents and their infants, including complications during delivery and higher rates of chronic illness. Although perinatal sleep disturbances may be considered expected and intractable, recent studies demonstrate that behavioral interventions are effective for preserving sleep in expectant and new parents. Efficient, scalable methods for addressing sleep disturbances in the perinatal period are critically needed to promote maternal and child health. Our aims are to develop a high-fidelity, evidencebased sleep intervention in collaboration with direct care workers who engage with perinatal women and to collect preliminary data regarding delivery of the intervention to expectant and new parents. As part of Phase 1 of the project, we are developing short, evidence-based, educational videos in English and Spanish that focus on behavioral strategies to improve perinatal sleep and that map onto modules that we created for the free, publicly-available mobile app, CBTi Coach. The videos are being produced in cooperation with direct care workers and a digital media studio with community engagement experience. Preliminary videos will be refined and revised after obtaining feedback during focus groups consisting of direct care workers and expectant and new parents. In Phase 2, direct care workers will be trained to use the videos and app and invited to utilize the intervention with clients who

report sleep problems. The project is grounded in the REAIM framework, and will assess the Reach, Effectiveness, Adoption, Implementation, and Maintenance dimensions of this model.

161. Kenny Mouzon, Benedict College. **Effects of Polycyclic Aromatic Hydrocarbons on Human Breast Cancer Cells.** Co-Authors: None. INBRE
Polycyclic aromatic hydrocarbons (PAHs) are ubiquitous and persistent environmental contaminants. Some are suspected carcinogens and may affect the reproductive systems as potential endocrine disruptors. The purpose of this experiment was to examine the effects of two PAHs, Benzo(a)Pyrene (BaP) and Fluoranthene (FLA), on cellular protein production, lactate dehydrogenase (LDH) activity, or ROS production, which could be due to altered oxidative stress. Half a million MCF-7 or MDA-MB-231 cells were cultured in a 35-mm dish. We monitored the cells under a microscope, and on day 2, we added exposure media and media containing 0.01% DMSO, BaP, or FLA (both at 1 µg/ml or 500 ng/ml). After 24 hours, the media was separated, and the conditioned media was saved in centrifuge tubes for the LDH assay using an ELISA plate reader to measure the absorbance of the samples at 490 nm. In MCF-7 cells, the protein level was decreased drastically with 1 µg/ml FLA, but we didn't see any noticeable changes in MDA-MB-231 cells. Regarding LDH release, we have observed some differences: FLA and BaP at 1 µg/ml decreased LDH in MCF-7, while in MDA-MB-231 cells, FLA at both concentrations increased LDH levels. The results showed that BAP and FLA at both concentrations increased the level of ROS production in MCF-7 cells when compared to the media and DMSO control groups. The increased level of ROS production in MCF-7 cells due to PAH exposure shows that the cells undergo oxidative stress, which may correlate with mitochondrial dysfunction.

162. Lincey Alexida Wilson, West Virginia University. **The Impact of Post-Stroke Care of Relatives and Friends on the Quality of Life of College Students in West Virginia.** Co-Authors: Alfgeir L. Kristjansson. Co-Authors Institutional Affiliations: West Virginia University. CTR
Stroke is one of the leading causes of death in the world. Stroke is the 7th leading cause of death in West Virginia. Loved ones are often burdened with the results of losing an active family member or close friend who was a provider. The research question is looking at the loved one stroke burden on actively enrolled college students in West Virginia University (WVU). This is a survey study with an estimated sampling size of 34. The purposive sampling frame for this study includes traditional and non-traditional college students enrolled in all the West Virginia University (WVU) Campuses. The inclusion criteria are a history of stroke in a loved one, family member or close friend and age 18 and over. The study administered a survey composed of an ordinal instrument made up of thirty questions, that measure the quality of life of a college student dealing with stroke in a family or friend. Quality of Life (QOL) (Stroke Version), a modified version of the QOL instrument (Family Version). A preliminary one way Analysis of Variance (ANOVA) result of a sample of 22 respondents shows that currently enrolled WVU students have a statistically significant decrease in their psychological, physical and social well-being following the impact of dealing with a loved one stroke diagnosis (P

163. Michael G. Nichols, Creighton University. **The Auditory & Vestibular Technology Core of the Dr. Richard J. Bellucci Translational Hearing Center at Creighton University.** Co-Authors: Anthony S, Stender, Sarath Vijayakumar, Molly T. McDevitt, David D. Smith. Co-Authors Institutional Affiliations: Creighton University. COBRE
The Auditory & Vestibular Technology Core (AVT) provides critical support for principal investigators and their research teams associated with the Dr. Richard J. Bellucci Translational Hearing Center of Creighton University. The AVT Core is organized as three specialized sub-cores to provide a diverse array of technological tools and research services within the areas of electrophysiology and molecular biology,

mass spectrometry, and advanced imaging. Together, the AVT core facilitates translational auditory and vestibular research across a wide range of experimental systems from single molecule analysis to whole organism models. This facility was designed to enhance research efforts by assisting investigators and foster collaboration as they pursue their interrelated research goals. Operating under a hybrid fee-for-service model, the core provides specialized services and technical support as well as individual training on advanced instrumentation while continually striving to adapt to the changing needs of this rapidly evolving field. The AVT Core Research Facility is located within the Dr. Richard J. Bellucci Translational Hearing Center of the Creighton University School of Medicine and operates a satellite facility at the University of Nebraska Medical Center. It is supported by COBRE Award GM139762 from the National Institute of General Medical Science, a component of the National Institutes of Health . The content herein is solely the responsibility of the author(s) and does not necessarily represent the official views of any supporting institution.

164. Jay DeLoriea, Coastal Carolina University. **Using a BicC Drosophila model to uncover the role of the gut microbiota in polycystic kidney disease.** Co-Authors: Gerrit A. Stuivenberg, Kait F. Al, Jeremy Burton, Chiara Gamberi. Co-Authors Institutional Affiliations: Western University, Coastal Carolina University. INBRE

Chronic kidney disease (CKD) affects 13% of the global population and causes toxin accumulation in the body due to hampered renal function. CKD patients manifest a dysregulated gut microbiota that enhances disease severity by producing toxins. Thus, remedial gut targeted therapies (i.e. probiotics) should be developed. A type of CKD, incurable autosomal dominant polycystic kidney disease (ADPKD), affects ~12.5 million people world-wide. The gut microbiota's contribution to PKD is understudied, yet could provide beneficial insight into the pathophysiology, progression, and treatment of the condition. We aimed to discover the role of the gut microbiota in PKD using an established BicC Drosophila melanogaster model of renal cyst development. Two BicC mutant genotypes with mild (BicC[Î”/YC33]) and severe (BicC[Î”/IIF34]) cystic phenotypes and control Ore[R] wildtype were generated by crossing or culturing, aged to 0-2, 8-10, and 18-20 days old and compared. The microbiota was characterized by sequencing the V4 region of the 16S rRNA gene of 5 replicates of 3 pooled flies grouped by sex, genetics, and age and analyzed by using R, DADA2, and ALDEx2. Although the microbiota of all flies was dominated by similar genera, individual taxa differentiated cystic and control groups. Specifically, cystic flies were significantly depleted in healthassociated Lacticaseibacillus (formerly Lactobacillus) and Levilactibacillus and enriched in Acetobacter and Agrilactobacillus. While preliminary, the data suggests that PKD severity and/or progression may be influenced by the gut microbiota and proposes that similar studies in humans may reveal the potential of microbiota-targeted therapies for PKD.

165. Alireza Bagheri Rajeoni, University of South Carolina. **Deep Learning For Human Vascular Analysis.** Co-Authors: Breanna Pederson, Susan Lessner, Homayoun Valafar. Co-Authors Institutional Affiliations: Not Listed. INBRE

Accurate analysis of diagnostic images, such as computed tomographic angiograms (CTAs), is pivotal for both staging and monitoring the progression of diseases within the vascular system, including conditions like peripheral arterial disease (PAD) and aneurysms. However, the manual analysis of CTA images is known for its time-consuming and labor-intensive nature. In response to this challenge, we have leveraged deep learning methodologies to automate the segmentation of the vascular system within CTA images obtained from PAD patients undergoing femoral endarterectomy surgery. Specifically, our focus was on measuring vascular calcification from the left renal artery down to the knee. Our most advanced model has demonstrated remarkable performance, achieving an 83.4% Dice accuracy in segmenting arteries from the aorta to the knee. Furthermore, our method yielded a Mean Absolute Percentage Error

(MAPE) of 9.5% when measuring calcification compared to manual scoring, with a strong correlation coefficient of 0.978. Additionally, our model has proven effective in detecting aneurysms within the vascular system, achieving an accuracy rate exceeding 90%. These results underscore the potential of deep learning techniques as rapid and precise tools for medical professionals in assessing vascular system health, thereby offering a promising avenue for enhanced patient care and management.

166. Bara Altartouri, University of Nebraska-Lincoln. **The Microscopy Core Research Facility/NCIBC Light & Electron Microscopy Core.** Co-Authors: Terri Fangman, You Zhou. Co-Authors Institutional Affiliations: University of Nebraska-Lincoln. COBRE
The Microscopy Core Research Facility (MCRF) is a unit of the Center for Biotechnology and a part of the Light and Electron Microscopy Core (LEMC) of the Center for Integrated Biomolecular Communication (NCIBC). Our missions are 1) to provide state-of-the-art imaging systems and technical support for multidisciplinary research and 2) to serve as a teaching/training center in areas of advanced microscopy for undergraduate and graduate students. The MCRF/LEMC has four advanced epifluorescence microscopes for sample screening and image stitching of large-size samples, two Nikon confocal laser scanning systems (A1R-Ti2 and A1-NiE) for image analysis using live or fixed samples, and two Hitachi electron microscopes (HT-7800 TEM and H4700 SEM) for ultrastructural or topographic analysis. We offer expert services covering a broad range of research fields and disciplines, including 1) life/food sciences (plant, animal, human, food materials, and microorganisms), 2) veterinary diagnostic analysis, 3) material sciences (such as synthetic/natural nanoparticle/fibers), and 4) biochemical engineering and bioengineering. We have established strong research collaborations with many faculty members at the University of Nebraska system. We provide imaging instrumentation and services to NCIBC members and other users from both academic and industrial communities, including 300-400 graduate students, staff and postdocs from 80-100 different laboratories/PIs (including 10-15 NCIBC members) annually. The MCRF/LEMC has also participated in teaching and training programs for >500 undergraduate students from three Nebraska universities annually for more than ten years. The core is supported by the NCBIC COBRE (P20 GM113126 and NIGMS), DOE (DESC0021101) and the Nebraska Research Initiative.

167. Elizabeth Chen, Brown University. **Health Informatics and Implementation Science Infrastructure for Clinical and Translational Research in Rhode Island.** Co-Authors: Neil Sarkar, A. Rani Elwy, Amy Princiotto, Karen Crowley, Paul Stey, Jonah Bradenday, Farahnaz Maroof, Mounika Thakkallapally, Edward Hawrot, Sharon Rounds. Co-Authors Institutional Affiliations: Brown University. CTR
The Biomedical Informatics, Bioinformatics, and Cyberinfrastructure Enhancement (BIBCE) Core for Advance Rhode Island Clinical and Translational Research (Advance RI-CTR; U54GM115677) has been offering services, resources, and training to support data- and technology-driven research for investigators in Rhode Island since 2016. Through partnerships and collaborations across the state, the BIBCE Core aims to address a range of clinical and translational research needs through: (1) informatics infrastructure to facilitate health data sharing, collection, management, and analysis, (2) consults and collaborations for providing guidance in use of health informatics best practices and implementation science methods, measures, and study designs, and (3) training and engagement in the breadth of health informatics and implementation science topics. For health informatics infrastructure, a signature effort is the Unified Research data Sharing and Access (URSA) Initiative that involves coordination of data sharing efforts in close collaboration with information services, compliance programs, and research administration offices at local health data partners. The legal, ethical, and technical infrastructure established through the URSA Initiative has enabled Advance RI-CTR researchers to securely access and use health data from: electronic health record systems at the Care New England and Lifespan health

systems; statewide health information exchange operated by the Rhode Island Quality Institute; and, statewide all-payers claims database maintained by the Rhode Island Department of Health. For training, the Implementation Science Seminar Series has featured local and national experts discussing de-implementation, implementation mechanisms, community engagement, health equity, dissemination strategies, and the spread, scale, and sustainment of evidence-based practices.

168. Hannah Gandy, University of South Carolina School of Medicine - Columbia. **Pathogenic mechanisms of eczema: regulatory roles of mast cells and resveratrol.** Co-Authors: Dylan Kunkel, Stacey Oxendine, Michael Madden, Yvonne Hui, Prakash Nagarkatti, Mitzi Nagarkatti, Carole Oskeritzian. Co-Authors Institutional Affiliations: University of South Carolina, University of South Carolina School of Medicine. COBRE

Atopic dermatitis (AD, eczema) is an inflammatory skin disease affecting approximately 20% of individuals. Mast cells (MC) initiate AD through the early release of inflammatory cell-attracting chemokines. In established AD, MC activation/degranulation occurs by binding of antigen (Ag)-specific IgE to IgE receptors(R), then crosslinked by Ag. However, we reported that skin MC were activated in prelesional AD, after one 7-day exposure to Ag ovalbumin (OVA) in a mouse model, without circulating IgE. MC activation was associated with a doubling of skin-associated sphingosine-1-phosphate (S1P), a sphingolipid metabolite that mediates MC-dependent chemokine release. Resveratrol, an anti-inflammatory natural compound, prevented MC activation, S1P and chemokine production. We initiated mechanistic studies in vitro to first measure the direct impact of a 7-day exposure to OVA on primary mouse bone marrow-derived MC (BMMC) dose-dependently. BMMC protein levels of sphingosine kinase 1 (SphK1), the enzyme producing S1P, and transcription factors Stat3 and NF-ï•«Bp65, implicated in chemokine production, were measured along with their activated forms using Western blotting. OVA (10 Î¼g/ml) elicited signaling activation in BMMC. We previously reported the occurrence of apoptosis in skin exposed to OVA, through elevation of cleaved caspase 3, the activated executioner caspase of apoptosis, via endoplasmic reticulum stress, marked by increased C/-EBP homologous protein (CHOP). OVA did not induce MC apoptosis but did trigger MC activation with augmented Stat3 phosphorylation and elevated chemokine mRNA expression. The effects of resveratrol on BMMC activation are investigated. Targeting early MC signaling activation may prevent AD progression. Supported by USC SOMC SOAR and P20GM103641.

169. Shannon Robson, University of Delaware. **Examining Dietary Approaches for Cardiovascular Health in 612 Year-old Children.** Co-Authors: Adriana Verdezoto Alvarado, Amanda Fultz, Elaine M. Urbina, Carissa Baker-Smith, Benjamin Brewer. Co-Authors Institutional Affiliations: University of Delaware, Cincinnati Children's Hospital Medical Center Cincinnati Children's, Nemours Children's House. COBRE

Poor diet quality has been identified as a leading cause of cardiovascular disease (CVD). Interventions to improve diet often focus on individual eating behaviors and less on the food environment that influences these behaviors. This ongoing study aims to examine the influence of family meal frequency on CVD risk factors (diet quality, weight status, insulin, lipids, and endothelial function). Within the context of a 6-month family-based multicomponent intervention, children are randomized to a family meal condition (FM) with a goal to have â‰¥5 family dinners per week, or a standard condition (SD) where children and parents are encouraged to meet individual daily fruit and vegetable recommendations set by the Dietary Guidelines for Americans. Both conditions also work to achieve national physical activity recommendations. To date, 31 children (9.0±1.9 years; 54.8% female; 51.6% White, body mass index (BMI) percentile of 69.2±2.5) and their parents (41.7±6.9 years; 93.5% female; 61.3% White; BMI 36.2±7.0 kg/m2) have been randomized with no demographic differences between conditions. Generalized linear mixed models have found no significant findings for diet quality, weight status, blood metrics, or

endothelial function in children. In parents, vegetable intake significantly increased in the SD group as compared to the FM group over time (b=3.0, p

170. Stephanie Ruest, Hasbro Children's Hospital at Rhode Island Hospital. **Identifying Emergency Department Providers Concern for Potential Child Abuse Using Natural Language Processing.** Co-Authors: William Rudman. Co-Authors Institutional Affiliations: Not Listed. COBRE
Background: Child abuse is often considered in young children with fractures. The frequency that emergency department providers (EDPs) raise concern for potential abuse may be underestimated by using ICD9/10 codes or child abuse pediatricians' (CAP) consultation notes. Methods: We conducted a retrospective observational study of children 0-5 years with an ED fracture diagnosis (identified by ICD9/10 codes) seen in a pediatric ED from March 2015-December 2021. Formal CAP consultation notes (consults) were documented when there was CAP abuse concern. Natural language processing (NLP) was used to identify encounters with documentation of EDP abuse concern and discussion with CAP, but no documented consultation note (discussions). Sociodemographics and fracture types for consults and discussions were compared to encounters without EDP concern. Results: EDPs raised abuse concerns in 317 of 3,089 encounters (10.3%); all were reviewed with CAP. Of these encounters, 27 (8.5%) had an abuse related ICD9/10 code. There were 199 (62.8%) consults. NLP identified 118 additional discussions (37.2%). There were statistically significant differences in encounters without EDP abuse concern versus consults versus discussions by age (p

171. Martha Rojo, University of Arkansas for Medical Sciences. **Challenges of Recruiting Hispanic Faith-Based Organization Leaders to Participate in Formative Research.** Co-Authors: Hannah Aston, Caitlin Tidwell, Johnathan Rodriguez, Janet Lopez. Co-Authors Institutional Affiliations: Not Listed. COBRE
Introduction: Technology-based strategies such as emails, text, and social media platforms have not been fully explored to recruit Hispanic faith-based leaders. We report on the challenges experienced when implementing technology-based recruitment strategies and data-collection processes in church settings. Methods: The contact information for churches and faith-based leaders were collected from publicly available websites. Various recruitment strategies were employed to contact church leaders, including emails, texts, Facebook messages, telephone calls, traditional mail, and in-person visits. Faith-based leaders were invited to complete an online survey (N=26) and an interview about their congregation and church facilities. We used descriptive statistics, means, and percentages to describe the characteristics of the churches. Results: From 3,724 emails, twelve surveys were received (0.3%). From 2,809 text messages, seven surveys were received (0.2%). From 251 Facebook messages, one survey (0.4%) was received. From 502 phone calls, one survey was received (0.2%). Mailed surveys were slightly more effective; from the 463 letters, 12 surveys were received (2.6%). A total of 33 completed surveys were received from non in-person methods. After pivoting to in-person recruitment, we have 27 completed interviews and 37 face-to-face surveys. Conclusion: Response rates suggest that digital recruitment modalities and data-collection processes are not as effective in recruiting Hispanic faith-based leaders. This could be attributed to perhaps a lack of trust in these methods. The most effective strategies remain in-person communication, the identification of key informants, and meeting with faith-based leaders. This underscores the importance of building trust and strong relationships with the community, which are crucial for successful recruitment.

172. Ying Wai Lam, The University of Vermont. **Vermont Biomedical Research Network Proteomics Facility.** Co-Authors: Bin Deng, Sydney Cohn-Guthrie. Co-Authors Institutional Affiliations: University of Vermont. INBRE

The Vermont Biomedical Research Network (VBRN) Proteomics Facility enables investigators to use an array of state-of-the-art mass spectrometry-based techniques for proteomics experiments, ranging from routine protein identification and characterization of post-translational modifications and protein interactions to large-scale quantitative proteomic analyses using stable isotopes. Since its inception in 2006, the facility has worked with over 100 internal and external users each year, contributed to a total of 200 publications, and supported more than 50 grants from various funding agencies. The facility is equipped with Orbitrap Eclipse Tribrid and Orbitrap Exploris 240 mass spectrometers and has proven expertise in training investigators in experimental design and proteomics methods while assisting with data interpretation, manuscript preparation, and grant submission. Central to our mission is our ongoing practice of developing close collaborations within the region. To address ongoing and future user needs, we are currently establishing workflows for crosslinking mass spectrometry and hydrogen-deuterium exchange mass spectrometry. Last but not least, we have helped incorporate proteomics into undergraduate curricula at a number of Vermont Colleges over the years and have recently established a robust internship program to prepare undergraduates for STEM careers. The VBRN Proteomics Facility (RRID: SCR_018667) is supported partly through NIH P20GM103449 (Vermont INBRE)

173. Drake Calhoon, Western Kentucky University. **The Effect of Sulforaphane on Chromium-Induced Toxicity in Human Lung Fibroblasts.** Co-Authors: Zain Tariq, John Pierce Wise Sr., J. Calvin Kouokam. Co-Authors Institutional Affiliations: Vanderbilt University, University of Louisville. INBRE
Lung cancer is responsible for greater than twenty percent of all cancer deaths in the United States, yet many people with the disease have never smoked. Therefore, it is imperative to understand other causes. Hexavalent chromium, [Cr(VI)], is a heavy metal and a known carcinogen. Workplace exposures are common in the welding, electroplating, and stainless steel industries. Hexavalent chromium enters the cell through anion transporters and can lead to reactive oxygen species production and inflammation. This study aims to explore the effect of sulforaphane (SFN), an isothiocyanate found in cruciferous vegetables, such as broccoli, cabbage, and Brussels sprouts, on hexavalent chromium-induced toxicity in human lung fibroblasts. Through a sulforaphane toxicity assay, the safety profile and an appropriate dose of sulforaphane were determined. Using 1Âµmol/L sulforaphane, cell viability assays revealed that sulforaphane can be used to alleviate Cr(VI)-induced reduction of cell proliferation. Additionally, CellROX and Enzyme-Linked Immunosorbent Assays demonstrated that at some concentrations of Cr(VI), sulforaphane can decrease ROS production and levels of the inflammatory cytokine, Interleukin-6. These findings demonstrate that the antioxidant and anti-inflammatory properties of sulforaphane may have the potential to treat hexavalent chromium-induced toxicity in human lung fibroblasts.

174. Shi Bai, University of Delaware. **University of Delaware Nuclear Magnetic Resonance Center.** Co-Authors: Caitlin M. Quinn. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Located in the Department of Chemistry and Biochemistry, the University of Delaware Nuclear Magnetic Resonance (NMR) Center supports the research efforts of over 400 users from 58 research groups across 4 colleges and 11 departments at UD as well as multiple academic and industrial collaborators in the region. The Center is home to nine NMR spectrometers ranging from 9.4 to 20.0 T in magnetic field strength (400-850 MHz in proton frequency), with a full range of capabilities from solution to solid state to hr-MAS NMR. The Center also houses an EPR spectrometer to be upgraded in the summer of 2024. Eight of the NMR instruments are located in the 4,650 sq ft NMR Magnet Hall in Brown Laboratory on main campus, and are connected to a helium recovery system. The Center has a satellite laboratory in the Ammon Pinizzotto Biopharmaceutical Innovation Center with a 400 MHz NMR instrument to serve faculty and students on UD's Star Campus. In this presentation, we will describe various instrumentation

capabilities, user training programs, and magnetic resonance spectroscopic services in detail. The UD NMR Center is an affiliate of DE-INBRE Centralized Shared Resources and part of the Analytical Core for UD's Design of Chemical Probes and Therapeutic Leads COBRE program.

175. Biplov Sapkota, Louisiana State University. **Understanding tumor-stromal crosstalk to identify potential therapeutic targets.** Co-Authors: B. Sapkota, N. Chintalaramulu, A. Pandit, S. Thota, R. Begum, A. Mansouri, J. Adamec, J. Francis. Co-Authors Institutional Affiliations: Louisiana State University and A&M College. COBRE
Previous studies highlight the crucial role of crosstalk between cancerous and normal cells in cancer progression and metastasis within the tumor microenvironment (TME). Conditioned Medium (CM), containing secreted factors from cancer cell cultures, can alter normal cell phenotype and behavior. Conventional 2D cultures fail to replicate the TME complexity adequately, prompting exploration of 3D models like basement membrane extract (BME) for a more physiologically relevant platform. The objective of this study is to identify an effective culture model replicating the TME while elucidating cell transformation pathways. Through this, we seek to identify targets for preventing malignant transformation and reversing already transformed cells to a normal state. Using CM from 4T1 murine triple-negative breast cancer cells, we induced transformation in NIH3T3 and RAW 264.7 normal murine fibroblasts in 2D and 3D in vitro systems. Exposure to 4T1CM upregulated key genes like Î±SMA, IL-10, CD206, and VEGF in both cell types. NIH3T3 cells treated with 4T1CM exhibited hallmarks of epithelial-mesenchymal transition (EMT), evidenced by altered EMT markers. RAW 264.7 cells exposed to 4T1CM showed elevated expression of COX-2 and PDL1, suggesting a potential immune response inhibition. Additionally, NIH3T3 cells conditioned with 4T1CM displayed increased expression of stemness markers. Our findings, supported by proteomics and KEGG pathway mapping, underscore the intricate mechanisms at play in cell transformation within the TME. Ongoing investigations aim to further elucidate additional target pathways using RNASeq, cytokine profiling, and spatial transcriptomics.

176. Laxman Mainali, Boise State University. **Cholesterol and cholesterol bilayer domains inhibit the binding of Î±A-, Î±B-, and Î±-crystallin with the model of human lens-lipid membranes.** Co-Authors: Raju Timsina, Preston Hazen, Geraline Trossi-Torres, Nawal K. Khadka, Navdeep Kalkat. Co-Authors Institutional Affiliations: Boise State University. COBRE
Î±-Crystallin (Î±ABc) is a major protein comprised of Î±A-crystallin (Î±Ac) and Î±B-crystallin (Î±Bc) that is found in the human eye lens and works as a molecular chaperone by preventing the aggregation of proteins and providing tolerance to stress. However, with age and cataract formation, the concentration of Î±ABc in the eye lens cytoplasm decreases, with a corresponding increase in the membrane-bound Î±ABc. This study uses the electron paramagnetic resonance (EPR) spin-labeling method to investigate the role of cholesterol (Chol) and Chol bilayer domains (CBDs) in the binding of Î±Ac, Î±Bc, and Î±ABc to the Chol/model of human lens-lipid (Chol/MHLL) membranes. Our results show that, with an increase in the Chol concentration in the Chol/MHLL membranes, the maximum percentage of membrane surface occupied (MMSO) by Î±Ac, Î±Bc, and Î±ABc decreases until it is completely diminished at a mixing ratio of 1.5. Furthermore, our results show that Î±Ac, Î±Bc, and Î±ABc bind differently with Chol/MHLL membranes at mixing ratios of 0 and 0.5, decreasing the mobility and increasing hydrophobicity near the membrane headgroup region, likely forming the hydrophobic barrier for the passage of polar and ionic molecules, including antioxidants (glutathione), creating an oxidative environment inside the lens, leading to the development of cataracts. However, all binding was completely diminished at a mixing ratio of 1.5, indicating that high Chol and CBDs inhibit the binding of Î±Ac, Î±Bc, and Î±ABc to membranes, preventing the formation of hydrophobic barriers and likely protecting against cataract formation.

177. Mohammad Abrar Alam, Arkansas State University. **Thiazole-fused Derivatives: Potent Î²- and Î³-Actin Inhibitors to Treat Melanoma Tumors.** Co-Authors: Sanjay Adhikary. Co-Authors Institutional Affiliations: Arkansas State University. INBRE
Melanoma, the most lethal form of skin cancer, is recalcitrant to current treatments in most patients. To find potential antimelanoma treatments, a series of fused thiazole derivatives were synthesized, and several of them were found to be potent in both in vitro and in vivo studies. Several of these compounds were significantly toxic to melanoma cell lines and inhibited tumor growth in mice. Cell migration and cell adhesion were inhibited in vitro by these chimeric molecules. Lead compounds induced a modest amount of apoptosis and significant G2/M phase mitotic cell cycle arrest. mRNA sequencing revealed actin cytoskeleton inhibitory activities via downregulation of Î²-actin and Î³-actin proteins, which was confirmed by immunoblotting and proteomics assays. Analysis of the actin cytoskeleton using fluorescence microscopy revealed that lead compounds inhibited cell spreading and the formation of actin-rich membrane protrusions by suppressing the formation of stress fibers through actin polymerization. Additionally, the expression of Î²-parvin, an adapter protein between the actin cytoskeleton and extracellular matrix, was increased both in genomics and proteomics studies. In a subcutaneous mouse melanoma model, two potent compounds inhibited tumor growth and were non-toxic according to a comprehensive 14 blood plasma organ toxicity markers.

178. Musa Azeem, University of South Carolina. **Dihedral Angle Analysis: A Novel Approach to Evaluating Protein Structure Predictions in the Absence of Experimental Data.** Co-Authors: Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina. INBRE
Proteins are the building block of life, and understanding the complex functionality of proteins in the cellular environment is essential to the advancement of modern medicine. One of the key determinants of a protein's function is its three-dimensional shape. While traditional methods to discover protein structures are slow and expensive, modern computational methods of predicting protein structures from their amino acid sequences have led to significant advances in recent years. Still, one of the key limitations of these tools is assessing the quality of their predicted structures. The classical method, Root Mean Square Deviation (RMSD), requires the experimentally determined structure of the protein to compare atomic coordinates. We propose an alternative assessment of protein structure predictions through the analysis of a protein's dihedral angles, circumventing the need for a ‘true' structure. Dihedrals alone can determine a protein's backbone structure and can be collected as a distribution across numerous proteins. For a given protein, the distribution of dihedral angles for each window of residues is queried from PDBMine. Mahalanobis distance is utilized to compute a quantified metric of the prediction's adherence to the true distribution of dihedrals for each residue. Our proposed approach is assessed for ~400 protein predictions submitted to CASP-14 for the protein 6T1Z. We compare our metric to the RMSD of each prediction and see a correlation. Our metric is able to emulate the critique of RMSD, without the requirement of an experimentally determined protein structure.

179. Mridula Mavuri, Louisiana State University Shreveport. **Predictive and Causal Modeling of Socio-economic Factors for Lung Cancer in Louisiana.** Co-Authors: Tahmina Anondi, Devesh Sarda, Subhajit Chakrabarty. Co-Authors Institutional Affiliations: Louisiana State University Shreveport. INBRE
This project aims to predict and model socio-economic factors related to lung cancer risks in Louisiana. The factors considered are smoking habits, obesity rates, poverty rates, insurance coverage, and air Particulate Matter (PM) 2.5. The data used for analysis comprises of parish-level annual cancer rates specifically for lung and bronchus tumors, collected from 2014 to 2022 and sourced from Data USA, and PM 2.5 data obtained from the National Environment Public Health Tracking Network by CDC. The rates

are age-adjusted and reported per 100,000 population. The cancer incidence rate is per 1000 population, as reported by Louisiana Tumor Registry. The utilization of deep learning models in this context allows for modeling the complex relationships among various risk factors and lung cancer incidence. The multivariate analysis will help in understanding how multiple factors interact and contribute to the overall risk profile, while LSTM and transformer models will capture temporal patterns and dependencies in the data, considering the longitudinal nature of the dataset. Preliminary analysis showed that the percentage of uninsured and obesity are significant factors. Our deep learning prediction models also performed with good accuracy. By leveraging parish-level data and focusing on a set of risk factors, this project aims to provide insights into the socio-economic dynamics of lung cancer risks in Louisiana. The findings from this analysis can potentially inform public health interventions, policy decisions, and targeted interventions aimed at reducing lung cancer prevalence and improving health outcomes in the region.

180. Nathan L. Vanderford, University of Kentucky. **The University of Kentucky Center for Cancer Metabolism: Administrative Core.** Co-Authors: Peter Zhou. Co-Authors Institutional Affiliations: University of Kentucky. COBRE

The University of Kentucky (UK) Center for Cancer Metabolism (CCM), a Center of Biomedical Research Excellence, aims to sustain a thematically focused center dedicated to defining the role of metabolism in the development and treatment of cancer and to use this novel platform to develop promising early-stage investigators with enhanced skills in an exciting new area of cancer research. The Administrative Core works to increase the scientific productivity of the center's faculty by delivering efficient administrative services. The core functions through the following three specific aims: 1) to provide overall operational management of the center; 2) to facilitate research training, mentoring and career development activities to develop earlystage investigators in cancer and metabolism and expand research in this area through pilot projects; and 3) to conduct overall planning and evaluation of CCM activities and resources. The core oversees four full projects, four pilot projects per year, two scientific cores, and ensures highly effective, well-planned teambased mentorship, including basic and clinical perspectives and external expertise, for all early-stage investigators. The core enhances the scientific productivity of the center's faculty by delivering efficient administrative services across all aspects of the center through an innovative, team-based leadership framework that supports integrated mentorship across the research continuum to enhance the career development of early-stage investigators. The University of Kentucky Center for Cancer Metabolism is funded through the NIH/NIGMS COBRE program under grant number P20 GM121327.

181. Sophie E. Craig, University of Maine. **Uncovering mechanisms of JC polyomavirus entry and signaling in primary cells.** Co-Authors: Gabriella Giftos, Michael P. Wilczek, Melissa S. Maginnis. Co-Authors Institutional Affiliations: University of Maine. COBRE

JC polyomavirus (JCPyV) infects 50-80% of the human population worldwide, establishing a lifelong, asymptomatic infection in the kidney. Under immunosuppressive conditions, the virus can spread to the brain and infect the glial cells. This results in a demyelinating neurodegenerative disease called progressive multifocal leukoencephalopathy (PML). PML is debilitating, with symptoms including motor dysfunction and cognitive impairment, and has no cure or approved treatment. Research to understand the JCPyV infectious cycle is necessary to develop antivirals. Most JCPyV research has been performed in immortalized cell lines, which has led to important advancements. However, immortalized cells are not the most accurate model for infection, and this work has not revealed the cell type-specific JCPyV infectious mechanisms that account for JCPyV pathogenesis in the kidney and brain. Primary cells better represent the phenotype of infected cells in vivo. Differences in signaling pathway activation during

infection of immortalized and primary brain cells suggest cell type-specific JCPyV mechanisms of entry and infection. Thus, mechanisms of JCPyV infection must be characterized in primary cells. Using inhibitors, siRNA knockdown, and infection assays, we have begun to elucidate the mechanisms of viral entry and signaling pathway regulation in primary kidney and brain cells. My research suggests that JCPyV infection occurs by clathrin-mediated endocytosis in primary cells, and my future research will investigate cell type-specific signaling mechanisms during infection. This work illuminates JC polyomavirus infection mechanisms in primary cells, helping to uncover potential targets for antivirals that could reduce the spread of JCPyV and the impact of PML.

182. Karen Jennings Mathis, The Miriam Hospital and Brown University. **Discrimination, Intersection of Identities, and Health Risk Behaviors in Black Adolescents.** Co-Authors: Brittany Balletto, Faith Hardy, Ernestine Jennings, Laura Stroud. Co-Authors Institutional Affiliations: The Miriam Hospital, Brown University. COBRE

Discrimination is nearly pervasive, a determinant of health for historically marginalized populations, and linked to decreased psychological, physical, and emotional functioning, negative affective states, and increased health risk behaviors. With the additional stressor of experiencing discrimination and mental health care inequities, Black youth are at increased risk for engaging in health risk behaviors. Unfortunately, most screening tools and interventions fail to account for the lived experiences of Black youth and are based on and provided primarily for White youth. This project seeks to develop, refine, and test a culturally appropriate theoretical model of the contexts (social, emotional) in which discrimination and health risk behaviors occur among Black youth while considering intersectionality. We will 1) use focus groups to explore the social and emotional contexts in which discrimination (i.e., racial, weight, gender identity/sexual orientation) and health risk behaviors (i.e., substance use, maladaptive eating) occur in Black youth ages 1417 years; 2) develop an ecological assessment protocol; and 3) evaluate the feasibility and acceptability of the ecological momentary protocol. This multi-method study will provide a culturally appropriate model of health risk behaviors in Black youth and will be used to provide insight into how to adapt screening tools and interventions for health risk behaviors in Black youth with diverse identities to be more culturally appropriate. At the conference, we will present preliminary data from recruitment and focus groups.

183. Abraham J Saks, Creighton University. **NADH Phasor FLIM Reveals Changes in Metabolism in Squamous Cell Carcinoma Cells Cultured Under Normoxic and Hypoxic Conditions.** Co-Authors: Alex Chen, Kennedy A. Haase, Reese Kolar, Jackson M. Laurent, Johnathan Li, Aidan O'Mara, Maimuna Olow Nagey, Greer L. Porter, Jalen K. Ramos, Derek A. Remitar III, Hannah Schloman, Jinann A. Shoshara, Fiona Sun, Jacob A. Sweet, Laura A. Hansen, Michael G. Nichols. Co-Authors Institutional Affiliations: Not Listed. INBRE

It has been estimated that squamous cell carcinoma (SCC) accounts for 33% of all non-melanoma skin cancer cases. Affected cells experience metabolic and structural changes. The Warburg Hypothesis describes a shift in proliferation from oxidative phosphorylation towards glycolysis in cancerous cells. The expression of human epidermal growth factor receptor 2 (HER2) explains additional metabolic alterations. SCC 74A (low HER2) and SCC 74B (high HER2) cell lines were cultured in normoxic (21% O2) and hypoxic (

184. Austen R. Anderson, University of Southern Mississippi. **The Mississippi INBRE Community Organization Proposal Awards Program: ENGAGE Community-Academic Partnerships to PROPOSE Community Driven Research.** Co-Authors: Jennifer Lemacks, Sermin Aras, Alex Flynt. Co-Authors Institutional Affiliations: University of Southern Mississippi, INBRE

Community engagement in the research process fosters community-academic relationships as critical research infrastructure for project and proposal success. The Mississippi IDeA Network of Biomedical Research Excellence (MS-INBRE) Community Engagement and Training Core supports a new service through the Community Organization Proposal Awards program. The Community Organization Proposal Awards provide funding for community organizations to lead the development of grant proposals that address Mississippi's top public health issues. Awards support the meaningful involvement of community organizations with the MS-INBRE CETC faculty and mentors from across the state. Projects focus on serving racial/ethnic minorities, rural or disadvantaged populations, or other medically underserved groups and align with one of the following three areas: socioecological and psychosocial determinants of health, multicomponent interventions, and innovative digital healthcare strategies. The Community Proposal Awards occur in two competitive phases: the ENGAGE Award and PROPOSE Award. In the ENGAGE phase, awardees participate in group training and team activities to develop their public health impact ideas into scientific research. ENGAGE awardees can subsequently apply for the PROPOSE award, which supports the final development of a grant proposal â€" with preliminary data collection if applicable â€" to be submitted to a federal funding agency. In the 2023-2024 year, the MS-INBRE CETC completed the first cycle of the ENGAGE phase and is preparing for the first PROPOSE phase and second cycle of ENGAGE awards. Lessons learned and implications will be shared with the broader audience.

185. Lyle G Best, Turtle Mountain Community College. **Fetal C-Reactive Protein rs1205 Genotype Is Not Associated with Maternal Pre-eclampsia.** Co-Authors: Shyanna larocque, Crystal Azure, Hailey Davis, Craig Poitra, Jackie Poitra, Shayden Standish, Tyler J Parisien. Co-Authors Institutional Affiliations: Turtle Mountain Community College. INBRE
Background and Purpose: Pre-eclampsia is a multifactorial obstetric complication, likely involving immune dysfunction; and annually results in approximately 60,000 maternal deaths, world-wide. We have previously identified rs1205 and two other C-reactive protein (CRP) gene variants, the maternal genotypes of which, are associated with the risk of pre-eclampsia (PE). These findings have been replicated in two non-American Indian populations. Most analyses of genetic PE risk assume that maternal genotype confers risk, whereas the fetal genotype may be determinative and the maternal genotype simply correlated with fetal genotype. Method: Relevant institutional IRBs and the Tribal Nations approved this research; and all participants provided informed, written consent. We enrolled only offspring of mothers known to be heterozygous for the rs1205 variant of CRP and experiencing either PE affected or normal pregnancies, thus eliminating the maternal genetic influence of this variant. Offspring were then genotyped using TaqMan assays to determine if fetal rs1205 genotype was associated with PE. Results were evaluated using standard chi-square and logistic regression tests. Results: Offspring of 26 of 36 normal pregnancies and 11 of 20 PE pregnancies carried the rs1205 T allele in a dominant genotype (Fisher's exact chi square p=0.192). Multivariate logistic regression analysis adjusted for maternal age, nulliparity and BMI resulted in an odds ratio of 0.433, p=0.210, 95% CI 0.117-1.603. Conclusion: Among 53 women, all heterozygous for the rs1205 allele, neither chi-square nor multivariate adjusted logistic analysis suggest an association between PE and fetal T allele dominant genotypes.

186. Haiyang Ma, Clemson University. **Advanced Radiofrequency Heating System Enhances Viability of Cryopreserved Articular Cartilage Tissues.** Co-Authors: AJ Riffe, Peng Chen, Josh Wewerka, John M. Alford, Hai Yao, Girish Srinivas, David P. Eisenberg, Shangping Wang. Co-Authors Institutional Affiliations: TDA Research, Inc., Clemson University, Medical University of South Carolina, COBRE
The limited supply and short storage time of fresh osteochondral allografts (OCAs) pose significant challenges for clinical transplantation treatments. Vitrification offers a promising solution to preserve

viable OCAs without the damages caused by ice crystal formation during cooling and warming. However, achieving rapid and uniform warming is crucial yet challenging for vitrified OCAs, particularly in larger-sized volumes. Previous research used increasing concentrations of cryoprotective agents (CPAs) up to 83% (VS83), integrated with nanowarming, but faced cytotoxicity risks and limitations in nanoparticl penetration within dense, avascular cartilage. This study introduces an electromagnetic rewarming device heating dipoles within the CPA directly, enhancing viability and tissue preservation. Porcine cartilage discs (5 mm diameter and 1.5 mm thick), loaded with VS55 solutions, underwent rewarming via a warm water bath (convection) or radio frequency (RF) alternating electric fields. RF-rewarmed tissues showed superior viability (94.2±2.8%) to convectively rewarmed tissues (55.3±3.5%), with full metabolic recovery after 4 days. In contrast, conventionally rewarmed tissues exhibited only an approximately 60% recovery in cellular metabolic function. Additionally, RF warming better preserved glycosaminoglycans (GAGs) content and overall structure within the extracellular matrix (ECM). These findings underscore the efficacy of the developed RF warming system in improving the viability and ECM compositions of articular cartilage compared to conventional warming methods, without the need of increasing CPA concentrations, thus potentially mitigating concentration-dependent CPA toxicity on biological specimens. This advanced RF warming method lays foundation for the successful vitrification of clinically relevant larger-sized OCAs and other types of tissues.

187. Ronald Horswell, Pennington Biomedical Research Center, LSU. **Effect of Anti-inflammatory Medication Background Therapy on COVID Outcomes.** Co-Authors: San Chu, Daniel Fort, Lucio Miele. Co-Authors Institutional Affiliations: Pennington Biomedical Research Center, Louisiana Clinical and Translational Science Center, Ochsner Health System, LSUHSC-New Orleans. CTR
Inflammation plays a complex and incompletely understood role in the pathogenesis of acute COVID-19 and Post-Acute Sequelae of SARS-CoV-2 infection (PASC or â€œLong COVIDâ€•). Systemic acute inflammation resulting in cytokine storm, hypercoagulability and endothelial damage is thought to be a central mechanism for severe morbidity and mortality in acute COVID-19. The research question that our analyses seek to address is: Is there an association between background chronic disease treatment with anti-inflammatory medications and outcomes from subsequently contracted COVID? To address that question, we conducted analyses using N3C data for osteoarthritis patients who did not have concomitant autoimmune disorders. Six classes of potentially anti-inflammatory medications (aspirin, celecoxib, other NSAIDS, antidepressants, steroids, and immune suppressants) were compared to a common negative control medication (benzodiazepines.) Medication effects were estimated for three COVID-related outcomes: (1) inpatient admission rate, (2) death given inpatient admission, and (3) death given COVID diagnosis. The analysis found risk-reducing effects for celecoxib, and â€œother NSAIDS,â€• but not for aspirin. For example, for the â€œdeath given COVID diagnosisâ€• outcome, estimated odds ratios include (for NSAIDs:), OR = 0.58, 95%CI = [0.40,0.84], p = 0.004; (for celecoxib:) OR = 0.33, 95%CI = [0.10,0.83], p = 0.037); and (for aspirin:) OR = 1.43, 95%CI = [1.13,1.82], p = 0.004. By definition, background medications are those used prior to acquiring COVID, which leads to certain analysis complications. The approach used to overcome those analysis challenges also is briefly overviewed.

188. Jay Mason, WV Clinical and Translational Science Institute. **WVCTSI Community Engagement Outreach Core: Fostering Research Collaborations that Improve Real-Life Conditions.** Co-Authors: Elisabeth Minnick, Jen Lukas, Bree Gustke. Co-Authors Institutional Affiliations: WV Clinical and Translational Science Institute. CTR
The Community Engagement and Outreach (CEO) Core of WVCTSI fosters collaboration among patients, providers, and community stakeholders to ensure that research aligns with the health needs of rural communities. By facilitating meaningful partnerships, the CEO Core aims to generate practical,

sustainable, and scalable strategies for health promotion. Through establishing a robust statewide infrastructure in West Virginia (WV), the CEO Core is a vital platform for community engagement, involving stakeholders as active research partners. With a clear vision of producing research outcomes that directly enhance real-life conditions, the CEO Core operates through several key initiatives and services: 1. Ambassadors for Community Health Research (ACHR) 2. West Virginia Practice-Based Research Network (WVPBRN) 3. WVCTSI Project Extension for Community Healthcare Outcomes (ECHO) 4. Community Advisory Board (CAB) 5. Support for Evidence-Informed Decision-Making 6. Connect Investigators, Clinics, and Communities 7. Study Design and Implementation 8. Technical Assistance and Training 9. Dissemination of Research Results. These initiatives and services empower communities, providers, and patients to contribute to the research process, ensuring that study findings and recommendations are relevant and impactful. Through collaborative efforts, the CEO Core strives to address the unique health challenges faced by rural populations in West Virginia, ultimately working towards improving health outcomes and fostering community well-being.

189. Onyedikachi Oti, University of Central Oklahoma. **Ex vivo and In vivo evaluation 3D-Printed PCL-HA Bone Scaffolds and Intramedullary Nail for long bone repair using Rabbit Tibia Model.** Co-Authors: Ayan Khan, Saaim Saleemi, S. Nikfarjam, A. Haleem, H. Alizereej, A. A. Moussa, Nagib Ahsan, M. Khandaker. Co-Authors Institutional Affiliations: University of Central Oklahoma, University of Oklahoma Health Science Center, Stephenson Life Sciences Research. INBRE

The clinical treatment of long bone segmental defects is a global challenge due to issues associated with the current gold standard treatment of autologous bone grafting with metallic intramedullary nail systems. While bone tissue engineering offers promise, research is required to address scaffold design and animal studies. This study aims to develop bioresorbable bone substitutes with cortical bone strength and osteoinductive properties. Our specific aim was to assess the effectivity of 3D-printed PCL-HA bone scaffolds and intramedullary nail for ex vivo and in vivo using a rabbit tibia model. Our rabbit cadaver study confirms that our manufactured targeting jig has the potential to accurately implant our developed bone scaffold and intramedullary nail and line up the screws for a rabbit tibial large bone defect repair. The most significant challenge was delivering the nail due to their small size and mechanical strength. Higher mechanical stability was achieved for the purpose of higher weight-bearing capability and matching the scaffold and nail compressive and shear strength 200 MPa and 130 MPa with the same cortical bone. We are currently doing in vivo study to match the mechanical stability of our designed systems while enhancing osteogenic capability with BMSCs and PCL-HA scaffolds using rabbit model. We will also conduct toxicity analyses from the collected blood, liver, and kidney samples from the in vivo study.

190. Bradley Webb, West Virginia University. **Lysosomal amino acid homeostasis in retinal health and disease.** Co-Authors: Donald Dariano. Co-Authors Institutional Affiliations: West Virginia University. COBRE

Autophagy is a conserved catabolic process that plays a crucial role in maintaining retinal health and ensuring intracellular homeostasis across various eye structures. Dysregulated autophagy is implicated in the onset of several disparate ocular diseases, including cataracts, glaucoma, retinitis pigmentosa, and agerelated macular degeneration, highlighting its importance in ocular health. The molecular mechanisms regulating autophagy are essential for understanding the initiation and pathogenesis of blinding diseases but remain incompletely understood. Mutation and deletion of the endolysosomal cationic amino acid transporter solute carrier family 7 member 14 (SLC7A14) causes late onset retinitis pigmentosa (RP) in vertebrates through an undefined mechanism. The goal of this study was to generate and characterize a SLC7A14 knockout mouse model for use in mechanistic studies. We generated a

SLC7A14 knockout (KO) mice to investigate SLC7A14 expression in retinal cells through immunohistochemistry (IHC) and assess its impact on retinal function via electroretinography (ERG). IHC analysis reveals that SLC7A14 is primarily expressed in retinal interneurons, which is concordant with published single cell RNA sequencing data. Consistent with a phenotype of late-onset vision loss, there were no significant differences between the ERG recordings of WT and KO mice at two-months of age. However, nine-month-old mice displayed a decrease in interneuron response during dark-adapted, high-intensity flashes but no significant difference in photoreceptor response. Together, these findings suggest a late-onset, progressive reduction in retinal interneuron function in SLC7A14-KO mice. Further research will test the hypothesis that SLC7A14 links lysosomal amino acid homeostasis to autophagic

191. Katherine Motyl, MaineHealth Institute for Research. **Osteoclastic beta-adrenergic receptors support bone formation.** Co-Authors: Rebecca Peters, Ryan Neilson, Tyler Roy, Deborah Barlow, Dorothy Hu, Roland Baron, Karen Houseknecht, Christine Lary, Katherine Motyl. Co-Authors Institutional Affiliations: Not Listed. COBRE
Perimenopausal administration of beta blockers is a promising preventative osteoporosis therapy, currently being investigated in a clinical trial (NCT04905277). However, the effects of beta blocker targets, betaadrenergic receptors (betaARs), in bone resorbing osteoclasts have been understudied. We have found direct effects of both cardio-selective and non-selective beta-blockers on human and mouse osteoclastmediated bone resorption in vitro. To test the physiologic role for betaARs in osteoclasts, we generated mice with osteoclast-lineage specific deletions of beta1- and beta2-adrenergic receptors. BetaAR agonist isoproterenol-induced bone loss was not prevented by beta1AR deletion, but bone resorption from the beta2-favoring agonist salbutamol was attenuated in the absence of beta2AR in osteoclasts. Interestingly, deletion of either receptor in osteoclast lineage cells resulted in impaired bone acquisition in growing mice, with a more striking negative effect on bone in the absence of beta1AR. Thus, while beta2AR may be necessary for bone loss from beta-agonists, blockade of either receptor in osteoclasts may indirectly influence bone formation in mice. Consistent with this hypothesis, a pilot clinical study demonstrated reduced bone formation with 20-week beta-blocker administration in perimenopausal women. This work will lead to the identification of novel factors that maintain bone homeostasis through balanced bone formation and bone resorption, and inform future clinical strategies to optimize the net positive effects of beta-blockers on bone.

192. Kayla Analese Smith, Langston University. **Impairments in Cerebral Autoregulation and Cerebrovascular Reactivity in Cancer Survivorship.** Co-Authors: Britton Scheuermann, Shannon Parr, Stephen Hammond, Carl Ade. Co-Authors Institutional Affiliations: Kansas State University. INBRE
Roughly 46% of cancer survivors report cognitive dysfunction across many types of cancer, which has been associated with anti-cancer therapy and often results in reduced quality of life. Pre-clinical studies have suggested that the underlying factors of cognitive decline likely involve cerebrovascular dysfunction. We aimed to characterize local cerebrovascular regulatory functions (cerebrovascular reactivity and cerebral autoregulation) and central large artery stiffness (aortic arch stiffness) in cancer survivors, within 1-5 years of completing treatment compared to age- and sex-matched healthy controls. Aortic arch pulse wave velocity (aaPWV) was determined using Doppler ultrasound scans of the aortic valve and the descending aortic arch. Cerebrovascular reactivity was assessed as the change in middle cerebral artery velocity relative to the change in end-tidal carbon dioxide during a modified rebreathing protocol. Cerebral autoregulation was determined using Mx, a moving correlation coefficient between finger plethysmography-derived arterial blood pressure and cerebral blood velocity of the middle cerebral artery. Higher Mx values indicate poorer cerebral autoregulation. 11 women were recruited (5 healthy controls and 6 cancer survivors who had received treatment). Mx values were higher in cancer

survivors. Both cerebrovascular regulatory functions were impaired in cancer survivors compared to healthy controls and decreases in cerebral autoregulation were associated with increases in aortic stiffness. The present findings highlight the importance of monitoring cerebral and global vascular function in cancer survivors who are at high risk for cognitive decline.

193. Leah A. Rose, Coastal Carolina University. **The impact of yeast strain on millet beer.** Co-Authors: Drew Budner. Co-Authors Institutional Affiliations: Coastal Carolina University. INBRE
Gluten free beer has gained popularity among consumers with a gluten intolerance such as celiac disease, or those seeking an alternative beer option. Traditional beer contains grains that contain gluten such as barley, wheat, or rye all in which play a crucial role in the brewing process. The gluten free grain, millet, has gained popularity throughout the recent years due to its unique flavor and being 100% gluten free. As a vital component of the brewing process, yeast plays a crucial role in shaping the final product. The sensory characteristics of millet beer, such as aroma, flavor, and mouthfeel, are significantly influenced by the choice of yeast strain. Certain strains may impart fruity, or spicy contributing to the complexity and diversity of the beverage. Moreover, yeast metabolism during fermentation can directly affect the production of volatile compounds, which further shape the sensory attributes of millet beer. Samples are taken the day of brewing, 7 days into fermentation, and 14 days into fermentation. Samples taken are characterized by taking the pH, total titratable acidity, and color. The data collected shows that millet can achieve fermentation within approximately 7 days. This provides evidence that a gluten free beer not only meets consumer expectations but also adheres to the strict gluten-free regulation.

194. Fata Moradali, University of Louisville. **Cyclic di-AMP Regulation of Lipopolysaccharide Structure and Function in Periodontal Pathogens.** Co-Authors: Shirin Ghods. Co-Authors Institutional Affiliations: Not Listed. COBRE
A highly active biosynthesis of lipopolysaccharide (LPS) components from Gram-negative bacteria is associated with disease progression in periodontitis, an infectious polymicrobial-driven inflammatory disease of the tissues supporting the teeth. Additionally, studies have identified the expression of components of c-di-AMP signaling within the diseased periodontal pocket. Our findings demonstrate that biosynthesis and modification of lipopolysaccharide (LPS) is regulated by cyclic di-3', 5'-adenylic acid (c-diAMP) second messenger signaling in Porphyromonas gingivalis, a key bacterium in the onset and development of periodontitis. Our data show that c-di-AMP signaling is an essential and predominant nucleotide-based second messenger signaling in a variety of periodontal pathogens, suggesting the significant role of this signaling system in the pathoadaptation of periodontal pathogens. Specifically, we have identified some of the key components constituting the genetic basis of c-di-AMP signaling pathway in P. gingivalis, including the c-di-AMP synthase gene (dacpg; PGN_0523), the c-di-AMP phosphodiesterase gene (pdepg; PGN_0521), and the predicted regulatory gene cdaR (PGN_1486), all of which are required for regulation of LPS structure and function. Here, we report a community-based study of how c-di-AMP regulation of P. gingivalis LPS structure and function plays a role in the context of microbe-microbe and hostmicrobe interactions. Notably, the deletion of cdaR resulted in a lack of, or shortened, LPS polysaccharide, giving the P. gingivalis colonies a rough or non-smooth appearance, while significantly reducing the potential for polymicrobial interactions. Overall, our data indicate that c-di-AMP regulation of the LPS profile, and the LPS-driven persistence mechanisms of the pathogen play a significant role in the pathoadaptation, modulation of immune responses, and promotion of persistence in the human host.

195. Kieran P Rajagopal Switzer, University of Hawaii at Hilo. **LC/MS^2 Analysis of Mamaki (Pipturus Albidus) using Feature Based Molecular Networking.** Co-Authors: Mazen Hamad, Justin Reinike. Co-Authors Institutional Affiliations: Not Listed. INBRE
The feature based molecular networking platform GNPS (Global Natural Products Social Molecular Networking) has become one of the most powerful tools for visualizing non-targeted Mass Spectrometry data. GNPS compares submitted spectra against a massive spectral network, and uses an algorithm to sort the submitted spectra into a related subgroup of the molecular network made from compounds with similar functional groups and characteristics. The submitted spectra are further identified as either a specific known compound in that group, or a simulated compound with similar properties. In this project, we are studying Mamaki (Pipturus Albidus), a plant used in traditional medicine across the Hawaiian islands. Despite some early research suggesting it's anticancer, antiviral, and other medicinal properties, there's been little research describing it's molecular profile. Through the GNPS molecular network, compounds in Mamaki extracts can be automatically separated based on separation time, ionization energies, and mobility; and will automatically be sorted into their respective molecular families. GNPS automatically describes how compounds found in Mamaki matched with known spectra in the molecular network; and can propose theoretical compound structures based on data in the network. The reliability of each result is ranked in a â€œLibrary classâ€• going from gold (most reliable), to silver, and bronze (least reliable). Data has been processed for eight standards expected to be found in Mamaki. Work is currently underway to use the same procedure to analyze extracts of Mamaki. By analyzing these results, we can identify compounds in Mamaki which may be responsible for it's purported health benefits.

196. Alejandro L. Hernandez Padilla, University of Puerto Rico Cayey Campus. **An intact microbiome is essential for tolerance development induced by diet modification in Drosophila melanogaster.** Co-Authors: Enrique Rodriguez Borrero, Omaris Rosario Luquis. Co-Authors Institutional Affiliations: University of Puerto Rico Cayey Campus. INBRE
Alcohol use disorder (AUD) is a worldwide major health problem. Repeated alcohol consumption leads to the development of tolerance, expressed as a reduced response to a normally consumed dose of alcohol. Environmental factors, such as diet, could play a role in alcohol tolerance and can influence the gut microbiota composition. Therefore, the diet could impact the microbiota metabolic product that interacts with the nervous system leading to an undiscovered mechanism that could modulate the alcohol response. Drosophila melanogaster is a powerful model to study both the gut microbiome and AUD. Studies have demonstrated that gut bacteria affect many components of their physiology and behavior. Our goal was to investigate how a High-Fat Diet (HFD), a High-Protein Diet (HPD), and gut disruption affects the development of alcohol tolerance. The flies were placed for 7 days (n=12 flies per vial/6 vials) in a HFD or HPD to make changes in the resistance, sedation, and tolerance. The diet was supplemented with a mixture of antibiotics. Then, they were exposed to 50% ethanol vapor to observe the sedation and their recovery time. Our findings show that HPD increases the sedation time and lower recovery time, while adding an antibiotics cocktail decreases the sedation time. HFD flies have a faster recovery time than flies in a HFD with antibiotics. This data demonstrates that diet and microbiota are key factors in alcohol tolerance development. Future experiments are aimed to sequence the microbiota and find which taxa are involved in the tolerance development.

197. Julia Ward, Roger Williams University. **Negative Curvature THz Fiber based Biosensor Development for Analysis of Blood Constituents.** Co-Authors: Riley Como, Ethan Neidt, Ethan Howard, Ahmet E. Akosman. Co-Authors Institutional Affiliations: Roger Williams University. INBRE

Terahertz (THz) radiation has recently gained significant attention owing to its potential in sensing, detection and communications applications. The unique interactions of THz signals with materials, particularly their strong absorption by water, have sparked interest in employing THz technology for cancer detection and biosensing applications. Among recent advancements, hollow-core negative curvature fiber topologies have emerged as a promising candidate for low-loss electromagnetic wave transmission and refractive-indexbased sensing. This study aims to explore unique fiber geometries for optimized total loss and sensitivity, enabling improved broadband THz biosensing capabilities. Utilizing a finite element method based electromagnetic solver, comprehensive numerical analyses were executed to design and evaluate performance of elliptical and circular 5-tube negative curvature fiber geometries tailored for THz radiation, featuring tube thicknesses of 0.15 mm and core radius of 3 mm. To assess refractive-index-based sensing, individual blood constituents were introduced into the fiber core region. Blood components including water, plasma, hemoglobin, RBCs, and WBCs were numerically examined as fiber core analytes. Uniform relative sensitivities exceeding 90% for all blood constituents are achieved for a broadband frequency interval of 0.5 THz centered at the targeted frequency of 1 THz. To evaluate the feasibility of fabricating these hollow core fiber designs, they were manufactured using an SLA Resin 3D Printer. Various printing parameters were optimized to create consistent prints. In conclusion, unique fiber designs were developed to investigate their biosensing potential in blood constituents through THz radiation. The findings of this study pave the way for advancements in THz biosensing technology.

198. Allison D Abney, University of Arkansas for Medical Sciences. **Duchenne Muscular Dystrophy musculoskeletal impairment involves distinct cellular population shifts within bone.** Co-Authors: Abney AD, Nookaew I, Sato AY. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE

Duchenne muscular dystrophy (DMD) is caused by dystrophin loss-of-function mutations, resulting in skeletal muscle and bone deterioration. DMD individuals exhibit high fracture rates with 80% fracturing at 18yrs. Currently, muscle and bone in DMD are treated independently; and thus, the DMD impact on bone and its cellular populations remains unclear. Towards this end, 4mo mice lacking dystrophin (MDX) and wildtype (WT) mice (N=11-15), underwent monthly in vivo muscle function testing and dual-energy x-ray absorptiometry imaging for 4months. In muscle, MDX exhibited dysfunction, detected by decreased strength and contraction energy with increased contraction relaxation time (4mo: 75-300Hz; 5-8mo: 25-300Hz). Lean body mass, an index of muscle mass, was also increased from 4-8mo, without changes in body weight, a DMD hallmark due to fibrotic infiltration. Wet weight of isolated hindlimb muscles (TA, quadriceps, soleus) was also markedly increased in MDX. For bone, low bone mass was detected monthly from 4-8mo in MDX mice, corresponding with increases in bone resorption marker CTX and decreases in bone formation marker P1NP, detected as early as 4mo. scRNA-seq was performed on pooled cellular populations (N=1) isolated from 5mo WT and MDX bones (N=2) after serial liberase digestions and microbead depletion for hematopoietic and endothelial (CD45, CD117, CD31) cells. MDX exhibited increases in adipoq-CAR (+39%) and osteo-CAR (+41%) cells with decreases in pre-osteoblastic (-62%) and osteoblastic (-55%) cells. These findings show that DMD impairment of muscle and bone occurs simultaneously in vivo and suggests that the loss of pre-osteoblastic/osteoblastic cells is a component of DMD skeletal pathophysiology.

199. Yancy Ferrer Acosta, UPR-Medical Sciences Campus. **Elucidating 4R cembranoid's anti-tumorigenic mechanism in non-small cell lung carcinoma.** Co-Authors: José G. Cirino Simonet, José L. Torres Irizarry, Ivette Suárez, Ariana Acevedo, Nadezhda Sabeva. Co-Authors Institutional Affiliations: Universidad Central del Caribe-School of Medicine, Bayamón, Puerto Rico, University of Puerto Rico, Medical Sciences Campus, San Juan, Puerto Rico, Anatomy and Neurobiology Department. INBRE

Non-small cell lung carcinomas (NSCLC) represent the majority of lung cancer cases, characterized by a 5year survival rate of 26% due to limited responsiveness to conventional therapies. Consequently, there's an imperative for non-toxic treatment alternatives. Our research identified (1S,2E,4R,6R,-7E,11E)-2,7,11cembratriene-4,6-diol (4R), derived from Nicotiana tabacum, as a non-toxic compound with antitumorigenic properties specifically targeting NSCLC cells. This study aims to elucidate 4R's molecular impact on NSCLC progression. We found that 4R inhibits the activity of the alpha 7 nicotinic acetylcholine receptor (Î±7nAChR), which is overexpressed in NSCLC and promotes tumor growth. Through Western blot analysis, we observed significant overexpression of Î±7nAChR in NSCLC cell lines compared to normal lung cells. Further investigation revealed that 4R upregulates LYNX-1 expression, a negative modulator of Î±7nAChR, upon treatment. Colony formation assays demonstrated 4R's ability to dose-dependently reduce NSCLC cell proliferation. Additionally, Western blot analysis indicated that 4R induces apoptosis in NSCLC cells by decreasing the expression of pro-survival proteins and activating caspase-3. These findings suggest that 4R inhibits NSCLC progression by affecting cell proliferation, colony formation, and promoting apoptosis through Î±7nAChR inhibition via LYNX-1 modulation. Further studies will validate these observations, potentially positioning 4R as a novel, non-toxic adjuvant therapy for NSCLC.

200. Lauren Lessard, University of Alaska - Anchorage. **My Best Alaskan Life: Youth-Driven Community Based Research to Address Sexual and Reproductive Health.** Co-Authors: Allex Mahanna. Co-Authors Institutional Affiliations: University of Alaska - Anchorage. INBRE
Introduction: Alaskan youth lead the nation in gonorrhea and chlamydia infection rates. Contraceptives are inconsistently used, with 46% of youth not using condoms during their last sexual intercourse and 15% not using any pregnancy prevention method. Alaskan youth also experience disproportionately high rates of suicidality and hopelessness, and poor mental health is related to high risk sexual behaviors. The My Best Alaskan Life (MBAL) digital tool is a preventive approach to support young adult health practices, designed by and for Alaskan youth. Methods: This youth-driven community-based participatory research co-adapted the reproductive life plan (RLP), an evidence-based protocol supporting individuals to identify and pursue their reproductive intentions. MBAL builds on the RLP with a motivational interviewing framework to prevent risky health behaviors through goal setting for mental, social, and sexual health. Youth (ages 14-20) and researchers developed the Alaskan-specific tool for educational and clinical settings in a 2021 pilot study, using the Youth Participatory Action Research curriculum. Three interactive modules offer a decision-making guide where youth write out responses to questions and are provided relevant resources. Results: We will detail the adaptation of these initial materials for an older age demographic (18-26). The Community Advisory Board (during 6 meetings), the Youth Advisory Group (during 4 meetings), and 25 youth focus group participants interactively revised the existing modules, and developed two new modules: Healthy Relationships & Substance Use. The Community Advisory Board is a community/research coalition. The Youth Advisory Group consists of youth from urban and rural communities, with diverse sexual orientations, gender identities, socioeconomic backgrounds, racial backgrounds, and tribal relationships. Following the interactive revisions, researchers incorporated evidence-based materials and practices to further support future participants, including harm reduction, Indigenous resilience, identity exploration, reflective journaling, and coping skills. Conclusions: This presentation will explore benefits of using the RLP in supporting youth sexual and mental health decision making. We will also provide an overview of MBAL’s culturally-specific modules and evidence-supported materials. Finally, we will offer insights on effective community and youth engagement in co-designing interventions, presenting strategies that researchers can use in their own co-developed youth-driven preventive interventions.

201. Md Mozaharul Mottalib, University of Delaware. **Subtyping COVID-19 infected children with risk of obesity using longitudinal BMI percentile classification patterns and associations with social determinants of health.** Co-Authors: None. INBRE

The study aims to identify patient subtypes with the diagnosis of COVID-19 based on the trajectory of longitudinal body mass index (BMI) percentile values before and after COVID-19 infection and associate social determinants of health (SDoH) with the characteristics of the subtypes. Children with positive test results for coronavirus disease (n=11474, 53% male, mean [SD] age 5.57 [3.29] years, 54% white) were included in the cohort. The retrospective study assessed BMI measurements from at most six months before the disease diagnosis to a maximum of six months. Using the longitudinal BMI measurements, we identify distinct subtypes among the children and explore the associations with SDoH factors within subtypes. We identified five distinct BMI clusters in 11,474 children with COVID-19, labeled 'Always normal', 'Always overweight', 'Progressive obesity', 'Progressive overweight', and 'Regressive overweight'. We noted that physiological factors like gender and age group, alongside social determinants of health such as education, income, daily commuting, and employment status, have a significant impact on children's obesity status.

202. Christopher Wardell, University of Arkansas for Medical Sciences. **Skellytour: Automated Skeleton Segmentation from Whole-Body CT Images.** Co-Authors: Daniel Mann, Michael Rutherford, Phillip Farmer, Joshua Eichhorn, Fathima Fijula Palot Manzil. Co-Authors Institutional Affiliations: Not Listed. COBRE

Purpose: To construct machine-learning segmentation models to accurately label bones in whole-body CT images. Materials and Methods: 90 whole-body CT scans were manually segmented using 60 labels and subsegmented into cortical and trabecular bone. Segmentations were verified by board-certified radiology and nuclear medicine physicians. The impacts of isotropy, resolution, multiple labeling schemes, and postprocessing were assessed. Models were benchmarked against 364 samples from three datasets and compared against an alternative segmentation model. Performance was assessed using Dice scores (DSC), normalized surface distance (NSD), and manual inspection. Results: Our model performed consistently across all three datasets (DSC: 0.935, 0.936, 0.953, NSD: 0.993, 0.999, 0.999), outperforming the alternative in two datasets (DSC: 0.890, 0.927, 0.990, NSD: 0.962, 1.000, 1.000). Subsegmentation was similarly accurate (DSC: 0.953, NSD: 0.995). Skellytour produced finely detailed segmentations, even in low density bones. Conclusion: Skellytour is a highly accurate and generalizable bone segmentation and subsegmentation solution for CT data which is available as a Python package via GitHub (https://github.com/cpwardell/Skellytour). Key Results: Skellytour can segment CT scans with up to 60 labels, including surgically implanted hardware, and can subsegment bones into cortical and trabecular bone. Consistent high performance was achieved across three disparate datasets (DSC: 0.935, 0.936, 0.953, NSD: 0.993, 0.999, 0.999). Skellytour segmentations were quantitatively better with qualitatively higher resolution than a comparable method and can segment low-density bone. Summary Statement: Skellytour provides open source, generalizable bone segmentation and subsegmentation models for CT data that perform consistently across a range of datasets, including low-density bone.

203. Arohi Singhal, Clemson University. **Unravelling Cryptococcus neoformans Metabolic Adaptations: Implications for Therapeutic Targets.** Co-Authors: None. COBRE

Cryptococcus neoformans, a leading cause of fungal meningitis causing over 200,000 deaths annually, exhibits complex metabolic pathways crucial for its survival and virulence. Its ability to adapt to different nutrient environments and resist host defenses is highlighted through the study of arginine and carnitine biosynthesis pathways. The arginine biosynthesis pathway, involving enzymes such as glutamate Nacetyltransferase (Arg7, CNAG_01238), acetylornithine transaminase (Arg8, CNAG_05134),

and arginosuccinate synthase (Arg1, CNAG_00930), is essential for growth and immune resistance. Carnitine biosynthesis, essential for mitochondrial acetyl/acyl transport, involves four key enzymatic steps. Deletion mutants in genes for the first, third, and fourth steps impact melanin production, a critical factor for oxidative stress resistance. Gly1 (CNAG_02851) potentially encoding the second step enzyme, hypothesized to be hydroxytrimethyllysine aldolase (HTMLA), based on its similarity to Candida albicans' Orf19.6305. Understanding these pathways offers insights into fungal adaptability and virulence, presenting potential targets for antifungal drug development to combat cryptococcal infections more effectively.

204. Nilay Saha, University of Wyoming. **Enhanced Carbohydrate and Sterol Detection in Bee and Rat Brain Tissues through On-Tissue Derivatization via MALDI/MALDESI Mass Spectrometry.** Co-Authors: Nilay Saha, Andrew Goodenough, Taylor Hatcher, Michael Dillon, Franco Basile. Co-Authors Institutional Affiliations: University of Wyoming. INBRE
The utilization of mass imaging techniques, such as MALDI-MS imaging, has proven to be an invaluable tool in obtaining spatiotemporal dynamics of various biological molecules. Through this method, the distribution of a wide range of compounds can be obtained. However, certain molecules, such as sterols and carbohydrates, present a significant challenge in terms of ionization, rendering it difficult to attain spatial information through MALDI-MS imaging alone. To overcome this limitation, on-tissue derivatization of sterols and carbohydrates can be a powerful technique for identifying the spatial distribution of these molecules. In the initial phase of method development, bee sections were separated using MTBE/MeOH/H2O solvent. The aqueous layer was treated for carbohydrate derivatization with Girard P reagent. For sterol derivatization, the organic layer was treated with cholesterol oxidase and Girard P at a 1:1:1 ratio. MALDI-MS analysis was done using the Sciex 5800 MALDI-ToF/ToF-MS system. Similarly, On tissue derivatization involved spraying cholesterol oxidase and Girard P reagent via HTX-TM sprayer. This enhanced carbohydrate signals in bee aqueous extracts from head, thorax, and abdomen sections. A notable difference in spectra was observed between Girard P-derivatized and underivatized bee samples. A prominent signal at m/z 314.1, corresponding to a monosaccharide ([M + GP]+ ion) with the formula C6H12O6, was detected. Successful sterol derivatization was achieved in bee and rat brain samples using a two-step reaction: oxidation by cholesterol oxidase followed by Girard P reaction, resulting in a strong signal at m/z 530.4, likely indicating 24-methylenecholesterol and at m/z 518.4 likely corresponding to 5-CHOLESTEN-3Î²-OL.

205. Angeline Claudia Atheby, Delaware State University. **A dopaminergic release agonist confers neuroprotection against a Drosophila model of sporadic Parkinson’s disease.** Co-Authors: Katarzyna Rosikon, Hakim Lawal. Co-Authors Institutional Affiliations: Not Listed. COBRE
Parkinson’s disease (PD) is the second most common neurodegenerative disease. Decades of research have established key environmental and genetic factors as contributors to its etiology although the precise cause of most PD cases remains unknown. Moreover, despite the advances in our understanding of the possible causes of PD, a viable treatment remains elusive. Rotenone, a potent laboratory model for sporadic PD has been used to uncover important insights into the etiology of the disease. We are testing the neuroprotective capability of the small molecule dacarbazine (which we identified in a previous pharmacological screen) and its structural derivative, 5-Amino-4-imidazolecarboxamide (AICA) against Rotenone induced neuronal toxicity. Both dacarbazine and AICA have been reported previously to increase synaptic activity in a manner that is dependent on vesicular monoamine release. In this project, we investigated whether both compounds are capable of conferring organismal and/or neuroprotection against rotenone toxicity. We report that dacarbazine confers a small but reproducible protection against organismal toxicity induced by rotenone exposure in both male and female

Drosophila. These results are all the more remarkable given that dacarbazine is a chemotherapeutic drug with a toxic potential of its own. Crucially, we report for the first time, that consistent with its published role as a VMAT-dependent drug, AICA protects dopamine (DA) neurons against rotenone-induced neuronal toxicity in an assay in which we combined both a pesticide (rotenone) and age as risk factors for PD. Together, these findings identify an promising new anti-PD compound and highlight the feasibility of the physiological enhancement of DA release in vivo as a viable strategy for developing therapeutics against Parkinson's disease.

206. Devesh Sarda, Louisiana State University Shreveport. **Automatic Cognitive Classification of Brain MRI.** Co-Authors: Tahmina Akter Anondi, Mridula Mavuri, Subhajit Chakrabarty. Co-Authors Institutional Affiliations: Louisiana State University Shreveport. INBRE
Cognitive classification in this study refers to the severity of Alzheimer's Disease (AD) ranging from Cognitively Normal to mild Alzheimer's Disease. This study aims to utilize the clinical data alongside the brain MRIs to train a model to accurately classify brain MRIs into the differing levels of Alzheimer's Disease. Our datasets are ADNI and OASIS, comprehensive datasets from studies that include consistent clinical data such as neurological exams, cognitive assessments, diagnosis summaries, etc., and brain MRIs. There are various sequences of brain MRIs such as MPRAGE, FLAIR, images with skull and skull stripped, etc. Our Deep Learning Methodology is to utilize various evaluated AD models proven to have high accuracy in the classification of brain MRIs. We use the ResNet CNN-based architecture and a transformer-based transfer learning model, and our loss function is sparse categorical entropy for the multiclass classification. Results indicated high model accuracy for the 3D modality in the multiclass classification of the brain MRIs on the AD scale. The significance of this work is to help neurosurgeons and neurological doctors hasten their timeliness of the diagnosis and prognosis using brain MRIs to determine and help patients with cognitive disabilities due to AD.

207. Emily Elizabeth Curd, University of Vermont. **A genomic exploration of malignant melanoma found in the Brown Bullhead (Ameiurus nebulosus) of Lake Memphremagog.** Co-Authors: Emily Curd, James Lubkowitz, Kirsten Tracy, Stacia Richard, Scott Tighe, Mohammad Molla, Vicki Blazer, Tom Jones, Pete Emerson, Matthew Bodnar, Mark J Henderson, Julie Dragon. Co-Authors Institutional Affiliations: University of Vermont, VT Cooperative Fish & Wildlife Research Unit, USGS Eastern Ecological Science Center, Vermont Fish and Wildlife. INBRE
Malignant melanoma occurs in 30% of the Brown Bullhead (Ameiurus nebulosus) fish population in Lake Memphremagog, a 40 square mile lake shared by Vermont (USA) and Quebec (Canada). Despite the broad geographic distribution of Brown Bullhead, the prevalence and pathology of melanistic growths are unique to this population. Histopathology characteristics of the lesions suggest tumorigenesis is associated with genetic and environmental factors. Preliminary comparative expression analysis confirms that tumor tissue samples have differential gene expression and pathway enrichment consistent with melanoma, however these sequences lack mutational signatures for UV damage or exposure to a known mutagenic agent. We are currently applying a population genomics approach to explore a possible genetic and epigenetic predisposition for tumorigeneses. We assembled and annotated eight high quality Bullhead genomes four geographically distinct and lesion-free populations across Vermont. Using these references, we generated low coverage genomes from brain tissue of 92 Lake Memphremagog Brown Bullhead individuals (46 healthy and 46 afflicted) collected from eight sites across the lake. For four afflicted fish, we generated low coverage genomes for the tumor tissue as well. Here we will present population genomics results, including population variant analysis, germline vs somatic variation in tumor matched individuals, and methylation differences between populations, as well as between healthy and normal fish.

208. James Kenyon, University of Nevada - Reno. **T32 Institutional Predoctoral Training Grants - The UNR Experience.** Co-Authors: N. Mohammad, T.H. McKim, J.E. Baker. Co-Authors Institutional Affiliations: University of Nevada - Reno. INBRE
The NIH supports the development and training of biomedical researchers through Research Education (R25) and Training Grant (T34 - undergraduate, T32 - Ph.D.) mechanisms. IDeA states hold only 105 of 1980 active T32s with 45 of these in KY, RI, and SC. We set out to leverage the research infrastructure developed by IDeA funding to obtain a predoctoral (Ph.D.) NIGMS T32. Training grants fund trainee stipends (â€œfunds to defray living expenses during trainingâ€• $27,144/trainee/year), training-related expenses (TRE, $4,400/trainee/year), trainee travel ($300/trainee/year), and 60% of trainee tuition and fees. Few, if any, funds are available to support faculty or administrative costs, the F&A rate is 8%. Thus, the incentive and resources to develop and support a T32 must come from the institution. We found that PIs of active training grants were willing to share their proposals and we modeled our program on funded T32s. Each year, we will select five trainees from the first-year students to receive two years of stipend support plus mentoring and program support until Ph.D. completion. The five-year budget is $1,412,061 total costs (F&A=$91,710). The proposal is challenging: 22 interacting and overlapping components including a 25-page Training Program Plan linking all pieces plus required plans to increase diversity, training in responsible conduct of research, and rigor and reproducibility. Required data tables (running over 100 pages) characterize the participating faculty, past and current trainees, research funding, and publications. Locating, collecting, curating, and formatting these data are challenging. Our January 2023 proposal is under consideration for 1 July 2024.

209. Oxana Gorbatenko, Black Hills State University. **Core Facility Service: Optimization of Influenza A whole genome sequencing for clinical samples on Illumina platforms.** Co-Authors: Cynthia Anderson. Co-Authors Institutional Affiliations: Not Listed. INBRE
Influenza A is human respiratory virus responsible for seasonal epidemics. Influenza surveillance is a crucial tool for tracking virus evolution and vaccine development. Increased access to Next generation Sequencing (NGS) technology often comes with a need for optimized library preparation protocols and data analysis pipelines to produce reliable and robust data, especially for clinical specimens with low viral load. Due to coverage issues and mis-priming identified during NGS sequencing of Influenza using published and commercial protocols, optimization of the protocols used by our Core was necessary. We believe insights gained during this optimization experiment will be valuable to the Influenza research community. Samples belonging to two subtypes of Influenza A (H1N1 and H3N2) were used to optimize a whole genome library preparation protocol for NGS sequencing on Illumina platform using primers traditionally used for the amplification and sequencing of Influenza genome fragments to address coverage issues due to mispriming, as well as optimize amplicon coverage among the eight viral RNA genome fragments. A customized workflow using tools available in CLC Bio's Genomic Workbench v.23.0.5 was used for data analysis and to assess the effect of protocol modifications on library performance.

210. Richard Roberts, University of Delaware. **Hsp90β Facilitates Cell Death During Acute Cardiac Ischemia/Reperfusion Injury.** Co-Authors: Jamie Pottman, Dexter Matthews, Catelyn Charette, Chloe Ko, Stacy Mahiga, Chi Keung Lam. Co-Authors Institutional Affiliations: University of Delaware. INBRE
Myocardial infarction (MI), which caused 110,000 deaths in America in 2020, occurs following a complete blockage (ischemia) in one or more of the coronary arteries. Additionally, clearing the blockage (reperfusion) causes massive cell death, resulting in permanent tissue damage in the heart. Preventing cell death in IR injury is key to improving patient outcome in this disease. Molecular chaperones have

emerged as promising targets in IR injury due to their pro-survival functions. However, the role of Hsp90Î², the most abundant and constitutively active chaperone, in IR injury has not been fully elucidated. Therefore, we generated a cardiacspecific Hsp90Î² conditional knockout (cKO) mouse model to address it. To our surprise, current preliminary results suggest that cardiac-specific Hsp90Î² ablation reduces myocardial damage during IR injury, as Hsp90Î² cKO mice showed reduced infarct size compared to control. Opening of the mitochondrial permeability transition pore (mPTP) is the major driver of necrotic cell death during early reperfusion. Isolated mitochondria from the hearts of Hsp90Î² cKO mice show decreased sensitivity to mPTP opening during calcium overload, suggesting that it may be one of the cardioprotective mechanisms mediated by Hsp90Î² ablation. The Hsp90Î² cKO hearts also display an anti-apoptotic shift of the BAX/BCL2 apoptotic rheostat, suggesting the heart will be more resistant to apoptotic cell death during late reperfusion phase as well. Findings from this study will help us understand the role of Hsp90Î² in cell death activation during IR injury. In the future, we plan to investigate the underlying protective mechanisms mediated by Hsp90Î² ablation.

211. Xintao Wu, University of Arkansas. **Data Science Core of Arkansas Integrative Metabolic Research Center.** Co-Authors: Prateek Verma. Co-Authors Institutional Affiliations: University of Arkansas. COBRE This poster covers an overview of the data science core of Arkansas Integrative Metabolic Center (AIMRC) including personnel, equipment, software tools, computing resources, research projects, collaboration, and education training activities. AIMRC is an NIH-designated Center of Biomedical Research Excellence (COBRE) established in April 2021 at the University of Arkansas with Phase I funding from NIGMS (P20GM139768). Research conducted within the AIMRC largely focuses on understanding changes in metabolism at the tissue and cellular level, and how these changes impact disease, aging, and tissue repair. The data science core specializes in artificial intelligence-based approaches to elucidate relationships between large imaging, bioenergetics, genomic, and proteomic data sets. The data science core collaborates with the imaging and spectroscopy core, the bioenergetics core, and project leaders in the AIMRC. Specifically, it aims to provide 1) foundational training for those getting started with high-performance computing and Arkansas Research Platform (ARP), 2) training for Python programming, basic data mining, and machine learning, 3) training and support for using open-source deep learning based biomedical imaging resources (e.g., ZeroCostDL4Mic and Bioimage Model Zoo), and 4) customized solutions for deep learning based and large foundational models based biomedical imaging analysis, multi-omics data integration and analysis, and quantitative analysis pipelines for large data sets.

212. Sthephanie Estrada Mojica, University of Puerto Rico Cayey. **Selectivity, anti-resistance, and antimetastasis effect of oregano, graviola and cinnamon nanosuspensions in lung carcinoma.** Co-Authors: Grace Torres, Keishmarie Ortiz, Laurie Santos, Alejandra Diaz, Yamixa Delgado, Yancy Ferrer. Co-Authors Institutional Affiliations: University of Puerto Rico Cayey, San Juan Bautista School of Medicine, Ponce Health Science University, University of Puerto Rico-Medical Sciences Campus. INBRE Translational studies of phytochemicals have led to the discovery of many therapeutics available on the market. Furthermore, over-the-counter supplements are the most accessible phytochemical-based medications for the general population. However, many of these supplements are not uniformly prepared with an effective dose, e.g., against cancer. For this study, we hypothesize that aqueous nanosuspension (NS) of graviola, oregano and cinnamon leaves/barks, where the phytochemicals are coated and stabilized by the primary metabolites, have the potential of diminishing chemoresistance and metastasis in cancer. Thus, we developed three phyto-NS to be tested on the deadliest cancer type: non-small cell lung carcinoma (NSCLC). The three phyto-NS showed strong cytotoxicity in a concentration dependent manner after 24h of incubation. The IC50 values results of graviola, oregano and cinnamon

NS on the NSCLC lines A549 and H1975 were 0.31, 0.38 and 0.46 mg/mL, and 0.27, 0.074, 0.65 mg/mL, respectively. The IC50 values results of graviola, oregano and cinnamon NS on normal lung cell lines NL20 and MRC5 were 0.17, 0.19, 0.50 mg/mL, and 0.51, 0.34, 0.75 mg/mL, respectively. After the calculation of the therapeutic indexes, oregano and cinnamon NS were the most selective against H1975 and A549 cells, respectively. Then, we determined the expression of chemoresistance- (PDL1; STAT3), and metastasis-related (EGFR) genes on the NSCLC A549 cells exposed to these phyto-NS using RT-qPCR. Results showed that graviola, cinnamon, and oregano NS downregulated EGFR and PDL1, EGFR, and EGFR, respectively. These results elucidate the bioactivity of plant extracts establishing a foundation for using phytochemicals against NSCLC.

213. Dagmara Motriuk-Smith, University of Wyoming. **Identifying amino acid sequence features of a protein hub that organizes bacterial cytoplasm.** Co-Authors: Brooke Johnson, Hannah Swan, Tanner Roberts, Breelyn Semon, Samantha Patterson, Rachel Kaiser, Maddie Sites, Ellie Groves, Tess Palen, Ainsley Hokanson, Rachel Heffley, Cody McClarnon, Dagmara Motriuk-Smith, Joshua Holmes, Grant Bowman. Co-Authors Institutional Affiliations: University of Wyoming in Casper, Western Wyoming Community College, University of Wyoming in Laramie. INBRE
Despite being the simplest known forms of life, bacterial cells are highly organized. Many species segregate the cytoplasm into biochemically distinct zones through the formation of membraneless microcompartments. In Caulobacter crescentus, a protein called PopZ self-assembles into large structures that span the width of the cell poles, forming microcompartments that selectively partition dozens of different client proteins apart from the main cytoplasm. At least ten client proteins gain selective entry by interacting directly with a highly conserved, partially helical 26 amino acid domain in PopZ's N-terminus. Here, we describe a genetic screen for identifying amino acid sequence features within PopZ that are responsible for these interactions. We built a comprehensive mutant library that includes all possible point mutations across PopZ's N-terminal hub domain. Three teams of undergraduate students at Western Wyoming, UW Casper, and UW Laramie institutions have thus far screened over (286+JH) library entries and identified more than (49+JH) loss-of-function mutants. The data is providing information on the structural and biochemical nature of the binding interface, and whether different client proteins utilize unique, partially overlapping, or the same set of binding sites on PopZ. As we continue the screen, additional sequence information will reveal increasingly rich views of the structure and function of this molecular hub and how it contributes to complex subcellular organization in bacteria.

214. Katya Mack, KU. **Gene-by-environment interactions and body size in mice from the Americas.** Co-Authors: Megan Phifer-Rixey. Co-Authors Institutional Affiliations: Drexel University. COBRE
Understanding the genetic variation that underlies differences in survival and reproduction is essential to the study of biology and human disease. A classic example of adaptation in a complex trait is body mass variation in association with latitude. In the Americas, house mice (Mus musculus domesticus) show a number of phenotypic differences consistent with climate adaptation, including heritable changes in body size and aspects of metabolism. Using new wild-derived strains of mice from divergent climates, we examine gene-by-environment interactions affecting body size and gene expression. We demonstrate that expression divergence is extensive between populations and across environmental treatments. Finally, we utilize allelespecific to characterize gene regulatory divergence between populations and examine the genetic architecture of gene-by-environment interactions. Altogether, these results contribute to our understanding of the genetics of adaptation and metabolism.

215. Yanbao Yu, University of Delaware. **A novel E3technology deepens the biological impact of mass spectrometry-based proteomics.** Co-Authors: None. COBRE

MS-based proteomics experiments often have high economic and technical barriers to broad biomedical scientists, which not only result in costly supplies but also create difficulties to standardization and the reluctance to adopt new techniques. Here, we present a novel efficient, effective, and economical approach (named E3technology), for proteomics sample processing. We developed a novel membrane, which could be used as a robust and low-cost medium to generate LCMS-friendly samples in a rapid and reliable fashion. Using different formats of E3technology, we explored a variety of sample types, including bacterial and mammalian cells, fungi, mouse kidney tissue, and human saliva, in varied complexity, quantity, volume, and size. We benchmarked their performance against several established approaches, and our data suggest that E3technology provides equivalent or better performance in terms of proteome-wide identification and quantitation. Moreover, we developed an enhanced yet simplified single vessel approach, E4technology, which opens new avenues for low-input or low-cell proteomics analysis. To further demonstrate their practical applicability, we applied the E3 and E4 technologies to investigate RNA-binding proteins derived from affinity purification, and to profile the intact bacterial cell proteome. Overall, our data suggest that these technologies are highly reliable, widely applicable, easily scalable, and much affordable and feasible to non-expert proteomics laboratories. They represent a breakthrough innovation in biomedical science, and we anticipate their widespread adoption by the proteomics community.

216. Julia Palmer, University of Idaho. **Exploring Akt-mediated lysyl oxidase production during tenogenesis in mesenchymal stem cells.** Co-Authors: Collin Marcus. Co-Authors Institutional Affiliations: Not Listed. INBRE

Tendon injuries are common and often result in altered mechanical properties, which affect quality of life. In developing tendons, the collagen molecules within the collagen fibrils are crosslinked by lysyl oxidase (LOX), an enzyme produced by cells, to form a strong collagen network. The amount of these crosslinks determines the mechanical properties of the tendon. A major challenge is the limited information on how LOX production is regulated by cells. To address this, our recent work found that LOX production may be increased by mesenchymal stem cells (MSC) when treated with transforming growth factor (TGF)Î²2, but the cell signaling pathways involved in this regulation are unknown. TGFÎ² cell signaling may include the Akt pathway, and our prior work showed that Akt may regulate stem cell differentiation toward the tendon lineage (tenogenesis). Akt is a kinase that, once activated (phosphorylated), can have downstream effects on cell growth, protein synthesis, and apoptosis. Though previous studies have indicated that Akt signaling and TGFÎ² impact tendon, there remains a gap in knowledge on how Akt regulates the production of LOX by MSCs. Therefore, the objective of this study was to determine how TGFÎ²-induced LOX production by MSCs is regulated by Akt signaling. To test this, we treated MSCs with a chemical inhibitor of Akt (MK-2206) and evaluated LOX protein production. These findings enhance our understanding of how the Akt pathway plays a role in tendon formation, which will improve tendon tissue engineering and treatments to restore tendon function.

217. May-Tal Sauerbrun-Cutler, Alpert Medical School of Brown University. **Identification of Breast Cancer Cohorts in the Rhode Island All Payers Claims Database.** Co-Authors: Elizabeth S Chen, Jason D. Wright, Katina Robison, Karen Crowley, Ling Chen, Farahnaz Maroof, Neil Sarkar, Allegra Rollo, Christopher Schmid, Zexuan Yu. Co-Authors Institutional Affiliations: Brown University, Columbia University Medical School, Tufts Medicine, The Warren Alpert Medical School of Brown University, Dartmouth University. CTR

Fertility is of high concern for cancer survivors, and utilization of fertility preservation (FP) services is reported to be low at approximately 3%, making it critical to study ways to increase access to this service. Utilization of FP is challenging to identify on a statewide level and most data are provided from single institutions. Our study utilized the Rhode Island All Payers Claims Database (RI APCD) to identify reproductive age incident breast cancer (BC) patients for future analysis of FP utilization in RI. Three cohort identification algorithms were created with different inclusion and exclusion criteria, because as more BC patients are initiating treatment with chemotherapy, previous algorithms based on proximity to surgery, which was previously the first treatment for BC are no longer accurate. First, BC patients age 14-43 were selected based on ICD-9/10 codes from 2011-2022. The algorithms then varied to exclude those with no surgery or radiation (12 months) + chemotherapy (two months or three months) post BC diagnosis, no continuous insurance coverage for six months post diagnosis, and no chemotherapy within various time intervals from diagnosis or post surgery (nine months post surgery, six months post diagnosis, or nine months post diagnosis). Two of the algorithms yielded similar number of incident BC patients, while one algorithm yielded lower numbers because it may exclude patients who received neoadjuvant chemotherapy and no surgery within one year. Future work linking to cancer registry data could identify which algorithm is more accurate for identifying incident BC cases from statewide claim data.

218. Nalini Santanam, Marshall University SOM. **Testing Elagolix Inhibited Pain Mechanism.** Co-Authors: Jadyn Simon, Courtney Lulek, Vinitha Joseph, Taylor Kennedy, Angela Redmond, Co-Authors Institutional Affiliations: Not Listed. INBRE
Elagolix is an FDA-approved drug to treat moderate-to-severe pain associated with endometriosis. Elagolix is a competitive gonadotropin-releasing hormone (GnRH) antagonist and binds to the pituitary glands' GnRH receptors, suppressing estrogen production. No other pain-relieving mechanism of elagolix is known. This IACUC-approved study aimed to determine if elagolix decreases formalin-induced pain in a mouse model. 67 weeks old female C57bl mice (n=5/group) were injected with either (i) vehicle, (ii) 50 Î¼mol of fractalkine receptor antagonist (FRA), (iii) 15 mg/ml elagolix, or (iv) or 50 Î¼mol of FRA + 15 mg/kg elagolix, intraperitoneally in an injection volume of 10 ml/kg, 30 minutes before implanter injection of 10 Î¼L of 2.5% formalin into the right hindpaw. Following formalin administration, mice were assessed for 60 minutes for acute (Phase I: 0-15 minutes) and inflammatory (Phase II: 15-60 minutes) pain responses. The composite pain scores were calculated across each phase of the formalin test and represented the combined area under the curve. At 50 ï•-mol dose, FRA alone reduced inflammatory pain (Phase II) compared to the formalin-alone group (p=0.0079). In contrast, elagolix alone (15mg/kg) or in combination with 50 ï•-mol of FRA lowered the pain but did not reach significance. Interestingly, FRA and elagolix alone treatment inhibited the circulating levels of the transmembrane chemokines CXCL16 and CX3CL1, known to be activated in inflammatory diseases such as atherosclerosis and cancer. The significance of these findings in diseases such as endometriosis remains to be explored.

219. Adam Sczepanski, University of North Dakota. **Hypoxia upregulates progenitor markers in kidney proximal tubular cells.** Co-Authors: Seema Somji, Sarmad Al Marsoummi, Scott Garrett. Co-Authors Institutional Affiliations: University of North Dakota. INBRE
Hypoxia is a reduction of oxygen supply to the cells and is a major cause of acute kidney injury. In the kidney, proximal tubules are the most affected sites by hypoxia due to their high metabolic demands; at the same time, they are the site where most of the kidney regeneration and repair takes place by unique cells that have a regenerative capacity and are known as kidney progenitors. This study aims to determine the effect of hypoxia on the expression of critical markers of kidney progenitors. We used the immortalized human proximal tubular cell line (RPTEC/TERT1), which was sorted using flow cytometry

into two distinct cell populations: CD133+/CD24+ Human Renal Tubular Precursor TERT (HRTPT) cells with progenitor characteristics and Human Renal Epithelial Cell 24 TERT (HREC24T) with non-progenitor characteristics. Cells were cultured under hypoxic conditions (2.5% oxygen) for 48 and 72 hours as a model of acute kidney injury. RT-qPCR and Western blot were used to analyze mRNA and protein levels of CD133, CD24, PAX2, and SOX9, respectively. Our results showed that hypoxia significantly increased the progenitor markers CD133 and CD24 protein levels in HRTPT cells but significantly reduced CD24 protein levels in HREC24T nonprogenitor cells. In contrast, CD133, CD24, and PAX2 mRNA levels were significantly downregulated in all cell lines. In conclusion, our study demonstrates that hypoxia increases the expression of progenitor markers, in particular, CD133, through post-transcriptional stabilization and reduction of degradation of CD133 protein in HRTPT kidney progenitor cells.

220. Baku Acharya, University of Arkansas for Medical Sciences. **Novel 9H-pyrimido[4,5-b]indole as dual RET/TRK inhibitors: Design, synthesis, and in vitro evaluation.** Co-Authors: Debasmita Saha, Noemi Garcia Garcia, Katie R Ryan, Brendan Frett. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE

Aberrant expression of tyrosine kinases has been implicated in tumorigenesis and metastasis and their inhibition as an anticancer treatment has been widely explored. Both rearranged during transfection (RET) and tropomyosin receptor kinases (TRK) have been known to be aberrantly expressed in various cancers including lung and thyroid. Both tyrosine kinases present promising opportunities as drug targets, evident by the existence of several FDA approved kinase inhibitors for these targets. Despite the approval of various multi-kinase and selective inhibitors for treatment of cancers with abnormal RET or TRK expression, the persistent challenge lies in the emergence of resistance during treatment. It is, therefore, important that new scaffolds are generated to circumvent the challenges associated with resistance. Additionally, dual inhibition of both kinases is particularly useful when both targets are known to be involved in cancer progression. For instance, crosstalk between RET and TRK in neuroblastoma has been reported and dual inhibition of the kinases present an excellent treatment option. Therefore, we have identified novel 9H-pyrimido[4,5-b]indole dual RET/TRK inhibitors that are capable of decreasing phosphorylation of both RET and TRK. The inhibitors decreased cell viability via G1 cell cycle arrest in cells driven by RET and TRK oncogenes without effecting cells with wildtype RET or TRK.

221. Edna Acosta Perez, University of Puerto Rico Medical Science Campus. **Advancing Health Equity: Building Strong Community-Academic Partnerships in Hispanic and Latino Communities of Puerto Rico.** Co-Authors: Carlamarie Noboa, Yari Valle-Moro, Yashira Marie Sanchez Colon, Mayra Roubert Rivera, Christine Miranda-Di-az, Valeria M. Schleier Albino, Enid Garcia. Co-Authors Institutional Affiliations: University of Puerto Rico Medical Science Campus, Ponce Health Sciences University, Universidad Central del Caribe. CTR

The Community Outreach and Engagement Core endeavors to bolster population health, trust, and research participation among Hispanic communities in Puerto Rico (PR) through fostering meaningful Community Academic Partnerships, establishing a Community Health Research Council (CHRC) and coordinating capacity-building activities. In 2021-2022, our focus centered on organizing community forums and reinstating a Practice-Based Research Network infrastructure (GROW) to enhance community participation in research and foster collaboration among healthcare providers and researchers. Employing a rigorous mixed methodology, we integrated various data sources, including community-level epidemiological data, readiness assessments, and an analysis of available resources and capacity. We apply established frameworks such as the Colorado State University's Tri-ethnic Center Model and the Delphi Technique to guide our methodology. Community forums efforts engaged 223

participants from 51 municipalities, predominantly females (79%) aged 25-67 in PR. Collaboration with the CHRC resulted in stable group of 12-21 members supporting the alignment of research with community health needs, including data enhancement, addressing care disparities, and fostering over 10 Community-Academic Partnerships. GROW network comprises over 90 collaborators and facilitating capacity-building activities to promote new collaborations and recruit for Alliance-supported studies. These results underscore the importance of proactive community engagement and collaborative efforts in addressing primary health needs within Hispanic/Latino communities. By leveraging strategic partnerships and inclusive practices, we've aligned research initiatives with pressing health priorities, including data enhancement and addressing care disparities. It is essential to continue mobilizing resources for community engagement and capacity building, emphasizing mentorship, education, and effective dissemination strategies to advance collective efforts and promote health equity and well-being in these communities.

222. Sarah A Rice, University of Alaska Fairbanks. **Development of methodology for measuring physiologically relevant protein and ribosomal synthesis rates in atrophy-resistant hibernating mammals.** Co-Authors: AV Goropashnaya, MH Sugiura, BF Miller, EE Dupont-Versteegden. Co-Authors Institutional Affiliations: University of Alaska Fairbanks, Oklahoma Medical Research Foundation, University of Kentucky. COBRE

Finding novel mechanisms to combat muscle atrophy holds immense therapeutic value. Hibernating arctic ground squirrels (AGS) are resistant to muscle atrophy despite prolonged inactivity and fasting. Both slow and fast protein and ribosomal fractional synthesis rates (FSR) constitute physiologically relevant FSR. Capturing physiologically relevant FSR is challenging in AGS due to their radical changes in metabolism during hibernation, oscillating between torpor and interbout arousal. Methods to measure physiologically relevant protein and ribosomal FSR have not been validated in these animals, but may help us understand how AGS muscle is resistant to muscle atrophy. The goal of this study was to develop a method to measure protein and ribosomal FSR in hibernating AGS. We used deuterium oxide (D2O) to establish feasibility of measuring protein and ribosomal FSR in hibernating (n=12) and summer (n=8) AGS quadriceps and liver across multiple time-points. Samples were analyzed by GC-MS. FSR of protein was determined by the rate of deuterium-labeled alanine incorporation into protein, while ribosomal FSR was determined by the rate of incorporation of deuterium-labeled ribonucleic acids into total RNA. Preliminary data validate that protein and ribosomal FSR can be accurately measured in torpor, interbout arousal and summer across different tissues. Further, torpid FSRs were extremely low compared to interbout arousal (estimated 0-5%), verifying that the vast majority of protein and ribosomal synthesis occurs during interbout arousal of hibernation. Lastly, hibernation to summer comparisons were highly dependent on FSR normalization and highly variable, indicating technical issues need to be resolved for future D2O studies.

223. Selbi Ilmuradova, Montana State University Billings. **Advancing Alzheimer's Disease Treatment: Assessing Drug Regimens with Living 3D-Printed Neuronal Networks for Rapid Near-In Vivo, Analysis.** Co-Authors: Willems, Daniel L. Co-Authors Institutional Affiliations: Montana State University Billings. INBRE

A nonfunctional Eppendorf pipetting robot is currently being converted into a complete 3D bioprinter capable of maintaining an environmental growth chamber and producing complex, multi-cell type, living networks of neuronal cells including those from brain regions critically impacted by Alzheimer's disease, such as the entorhinal cortex and hippocampus. By utilizing open-source neuronal models from the NIH 3D Print Exchange, this project aims to replicate the complex human brain physiology and the specific neural circuitries first targeted by Alzheimer's. Precise control of environmental conditions will accurately

mimic human brain physiology, facilitating direct assessment of potential drug therapies on bioprinted neural models. Integration of advanced imaging and analytical technologies will allow real-time monitoring of metabolite analysis, this project promises to offer extraordinarily rapid insights into neuronal behavior and drug efficiency at a far lower cost compared to traditional methods. This innovative approach positions a small rural university as a leader in biomedical engineering and research.

224. Briana Kiyomi Shimada, University of Hawaii at Manoa. **Loss of selenocysteine lyase increases redox imbalance in the hearts of female mice during diet-induced obesity.** Co-Authors: Marissa Watanabe, Nadia Apo Takayama, Kayla A. Colaruotolo, Princess J. Santiago, Sydonie Swanson, Naghum Alfulaij, Marla J. Berry, Lucia A. Seale. Co-Authors Institutional Affiliations: University of Hawaii at Manoa. COBRE Dietary deficiencies in selenium (Se) elevate the risk of cardiometabolic disorders. Consumption of fatty foods contributes to cardiac oxidative stress. Se maintains redox homeostasis by regulating the levels of antioxidant selenoproteins, such as glutathione peroxidases 1 and 4 (GPX1,4) and thioredoxin reductases 1 and 2 (TXNRD1,2). Se-dependent tissues such as the liver have a Se recycling mechanism to allow selenoprotein synthesis, especially when Se is limiting, carried out by the enzyme selenocysteine lyase (Scly). However, it is unclear if Scly modulates Se and selenoprotein synthesis in the heart, particularly in the presence of diet-induced obesity. We fed wild-type (WT) and Scly knockout (KO) male/female mice a high-fat diet (HFD; 45% kcal fat) with low (0.08 ppm) or adequate (0.25 ppm) selenomethionine (SeMet) for 8 weeks. Intriguingly, only female Scly KO mice on a low SeMet HFD gained weight. Echocardiography showed a slight decrease in percent fractional shortening (%FS) in female Scly KO mice on either diet and cardiomyocyte (CM) function was significantly reduced in female Scly KO mice on an adequate SeMet HFD. Proteomics analysis of hearts revealed GPX1 to be significantly decreased in both male and female Scly KO mice on low SeMet HFD. Furthermore, GPX4 levels and total GPX activity were reduced in both male and female Scly KO hearts while glutathione levels were lower only in Scly KO female hearts. In summary, loss of Scly and dietinduced obesity leads to increased oxidative stress and reduced CM function in female hearts through the loss of GPX activity.

225. Larisa Ryzhova, MaineHealth Institute for Research. **Mouse Genome Modification Core Facility at MaineHealth Institute for Research.** Co-Authors: Abigail Kaija, Anne Harrington, Lucy Liaw. Co-Authors Institutional Affiliations: Not Listed. CTR
In 2000, Maine Medical Center/MaineHealth received its first Center of Biomedical Research Excellence (COBRE) award, which supported the establishment of a core facility to develop mouse models of human disease. This shared resource has over two decades of experience generating mouse models, and performing mouse cryopreservation, recovery, and re-derivation. We offer complete CRISPR/Cas-mediated mouse strain development which includes the targeting strategy, genotyping protocols, in vitro reagents testing, embryo injection, characterization, and breeding of founders. In addition, we support procedures related to assisted reproduction, early embryo manipulation, and experimentation with small moleculemediated targeting, and maintain shared mouse strains. Our facility continues to provide these high-quality services for our internal and external investigators in over 15 institutions. Some examples of our most recent work include CRISPR/Cas mediated global and conditional null models (Rab27aGKO), tissue-specific inducible Cre driver strains (GhrelinCreERT2), targeted mutations to mimic human alleles (Cryab R123W), and the introduction of epitope tags (HA-Nr3C2). In addition, microinjection expertise is used for conventional transgenesis and the introduction of microRNAs into single-cell embryos. We are dedicated to providing the most advanced genome modification technologies, which soon will include prime editing and improved genome editing via oviductal nucleic acid delivery (iGONAD). We are proud of our contributions to the genome modification community and

have coauthored numerous papers. We are committed to the welfare of laboratory animals and have been an AAALAC-accredited facility since 2004. Investigators are welcome to contact us to discuss mouse strain needs. Please visit our website (https://mhir.org/?page_id=233) for more information.

226. Neha Bhatnagar, Furman University. **Examining the extracellular presence of necrotizing fasciitis causing strains of Acinetobacter baumannii in THP-1 macrophages and THP-1 viability after 24 hours.** Co-Authors: Adarsh Shidhaye, Elizabeth Hogue, Alia T. Sadek, Elias M. Wheibe, Kyleigh Connolly, Ryan F. Relich, Luis A. Actis, Steven Fiester, Maria Soledad Ramirez, Jennifer T. Grier. Co-Authors Institutional Affiliations: USC School of Medicine Greenville, Furman University, Indiana University School of Medicine, Miami University of Ohio, California State University Fullerton. INBRE
Acinetobacter baumannii is a global pathogen associated with severe nosocomial infections such as pneumonia and sepsis, particularly among immunocompromised patients. Infections with necrotizing fasciitis-causing strains of A. baumannii (NFAb) are currently rare but growing in frequency. During NFAb infections, it remains unclear how NFAb strains interact with macrophages, the first human immune cells to encounter pathogens. To understand the relationship between NFAb pathogenesis and the human immune system, we assessed the ability of NFAb bacteria to survive within and escape human macrophages over a 24 hour period. THP-1 macrophages were infected with A. baumannii strains and colistin (50 ?g/ml) was added two hours post infection to eliminate extracellular bacteria. We assessed intracellular and extracellular bacterial growth, as well as THP-1 cell viability with comparisons between Type (19606, 17978) or NF (NFAb1, NFAb2) strains. We observed that following colistin treatment and 24-hour incubation, both Type and NFAb strains demonstrated intracellular escape and extracellular growth, as demonstrated by quantification of colony forming units on LB agar plates. Concerningly, these results demonstrate that surviving intracellular bacteria are able to evade antibiotic treatment and may escape host cells during human infections, leading to new sites of infection or ongoing infections despite antibiotic treatment. Future work will aim to identify bacterial escape mechanism to identify how A. baummannii strains successfully egress from macrophage cells. Understanding the mechanisms driving NFAb survival and virulence can identify crucial avenues for the development of novel antibacterial therapeutics in the future.

227. Emily Curd, University of Vermont. **A multi-research core and multi-omic approach to understand neurodegeneration in the tiger bromeliad spider (Cupiennius salei).** Co-Authors: Emily Curd, James Lubkowitz, Kirsten Tracy, Kristiaan Finstad, Scott Tighe, Sydney Cohn Guthrie, Charlotte Pearson, Osmand Evans, Roxana del Rio-Guerra, Wai Lam, Heather Driscoll, Julie Dragon, Christopher Francklyn, Adam Weaver, Shane Lamos, Ruth Fabian-Fine. Co-Authors Institutional Affiliations: University of Vermont, Norwich University, Saint Michael's College. INBRE
Globally, neurodegenerative diseases affect millions of people and are a major cause of death. The tiger bromeliad spider (Cupiennius salei) is novel model organism for the study of neurodegeneration and shows the histological hallmarks of neurodegeneration. The cellular mechanisms triggering the neurodegeneration in these spiders are the dissociation of microtubules in the glia and neuron and microtubule-associated desmosomal junction weakening. This results in the unraveling of macroglia that insulate neurons, ultimately compromising neuron structural integrity. To identify the genetic mechanisms underlying the histological evidence for neurodegeneration in these spiders, genomic, flow sorted cell population transcriptomic, and proteomic data was generated and analyzed by the research cores of the Vermont Biomedical Research Network (VBRN) and the University of Vermont Center for Biomedical Shared Resources. Here we present the results of a collaborative multi-omic project that investigates age related expressional changes in C. salei. A reference genome was assembled from short and long read sequence data generated and processed using custom NextFlow workflow developed by a

VBRN summer intern and Data Science Core analyst. After annotation, this genome was used to map cell specific transcripts and proteins to spider genes and determine differential expression. Enrichment analysis was used to identify pathways associated with neurodegeneration in this species and determine if the omics data support the spider histological data.

228. Walden Ai, Benedict College. **Targeting KLF4-mediated cell fusion in trained immunity and cancer recurrence.** Co-Authors: Ava McCargo, Walden Ai, Daping Fan, Mitzi Nagarkatti. Co-Authors Institutional Affiliations: Benedict College, University of South Carolina School of Medicine. INBRE
Trained immunity refers to the ability of the first line defense of the organisms, named innate immunity, to form immunological memory and a mode of long-lasting protection. It has potent antitumor activities by generating memory immune cells including myeloid cells through epigenetic reprogramming. The challenging question is that peripheral myeloid cells are short-lived and they may not be responsible for the long-lasting effect of the antitumor activities. On the other hands, targeting breast cancer stem cells (BCSCs) as seeds of breast cancer recurrence has great potentials to prevent breast cancer recurrence. However, BCSCs are resistant to chemotherapy and can keep dormant for years before they initiate cancer growth again. In addition, they are heterogeneous. Whether some populations of BCSCs acquire memory as similarly in trained immunity in the early stage of cancer development leading to later protective effect on cancer recurrence is not known. We previously reported that KLF4 is important to maintain BCSCs. Our current hypothesis is that KLF4-mediated cell fusion of myeloid cells with tumor cells promotes the generation of dormant memory BCSCs by epigenetic reprogramming leading to reduced breast cancer recurrence. This is proposed based on the following observations: 1). KLF4 up-regulation was concomitant with generation of fusion cells between myeloid lineage monocytes with breast cancer cells in our preliminary studies. 2). Fusion cells generated in our studies have features of memory monocytes and dormant BCSCs bearing CD44+CD24- signatures. 3). Dormant BCSCs may inhibit proliferative BCSCs within the total BCSCs leading to reduced breast cancer recurrence.

229. LaKeisha Williams, Xavier University of Louisiana. **Bridging Research and Community: The Impact of LA CaTS Community Engagement Core on Health Disparities in Louisiana.** Co-Authors: Stephanie Broyles, Margarita Echeverri, Jennifer Caldwell, Dandra Odom. Co-Authors Institutional Affiliations: Pennington Biomedical Research Center, Xavier University of Louisiana. CTR
The Community Engagement and Outreach Core (CEO) is a vital component of the Louisiana Clinical and Translational Science (LA CaTS) consortium, dedicated to advancing the mission, research and community efforts aimed at reducing health disparities and improving outcomes for vulnerable populations in Louisiana. Led by Xavier University of Louisiana, with expertise from Pennington Biomedical Research Center, the CEO Core empowers community members by integrating them into the research process. Through initiatives such as Community Advisory Boards, the Community Scholars Program, the Translating Research into Practice (TRIP) Working Group, and the Community Research for Optimal Wellness Network (CROWN), the core collaborates with community stakeholders to identify research priorities and develop projects addressing chronic disease burden, disparities, and health inequities. By employing community-driven approaches, the CEO Core enhances recruitment and retention in clinical trials, thereby amplifying the impact of translational research efforts. Specific aims include: 1) to facilitate greater community involvement in biomedical research by identifying health priorities and increasing partnership opportunities, 2) to provide LA CaTS investigators and community partners with services and resources that improve bi-directional engagement in outreach activities, research, and communication of findings, and 3) to create and maintain strategic partnerships between researchers, healthcare practitioners, and the lay communities to promote community-engaged translational/clinical research and health promotion in mitigating health disparities. By fostering these

partnerships and initiatives, the CEO Core contributes significantly to bridging the gap between researchers, healthcare practitioners, and lay communities, ultimately advancing health equity and improving health outcomes for the diverse populations served in Louisiana.

230. John Talledo, Clemson University. **Investigating the role of chitin synthases 1 and 2 in encystation in the human pathogen Entamoeba histolytica.** Co-Authors: Cheryl-Ingram Smith. Co-Authors Institutional Affiliations: Not Listed. COBRE
Entamoeba histolytica is a human protozoan pathogen that relies on a two-stage life cycle for successful proliferation. Outside of its host, E. histolytica exists in its cyst form, which is a dormant, small, rounded cell protected by a strong chitin cell wall that protects it from environmental stressors and allows it to survive until it can be introduced to a host via contaminated food and water. Once introduced to the host, E. histolytica cysts undergo excystation within the small intestine, entering their motile disease causing trophozoite form. Trophozoites migrate to the large intestine where they multiply, causing amoebiasis in ~10% of infections. Trophozoites colonizing the large intestine can undergo encystation back to the cyst form to be shed into the environment to complete their life cycle. Currently, there is a lack of understanding of the exact molecular mechanism E. histolytica trophozoites use to initiate the encystation process. There are however several genetic factors that are established to have a role in encystation. We are studying the role of chitin synthases 1 and 2, which are involved in formation of the chitin cell wall. In particular, we are examining the regulation of expression of these two genes during encystation as well as their enzymatic activities in formation of the chitin shell. These enzymes could prove to be valuable targets for new therapeutics as blocking encystation would prevent spread of this disease.

231. Tanner Smida, West Virginia University. **Prehospital post-resuscitation vital sign phenotypes are associated with outcomes following out-of-hospital cardiac arrest.** Co-Authors: Tanner Smida, Bradley S. Price, Alan Mizener, Remle P. Crowe, James M. Bardes. Co-Authors Institutional Affiliations: West Virginia University School of Medicine, John Chambers School of Business and Economics, ESO Solutions. CTR
Introduction: Prehospital vital signs are strongly associated with outcome following out-of-hospital cardiac arrest. Machine learning techniques may identify phenotypes of post-resuscitation vital sign abnormalities that are associated with outcome. Our objective was to use k-means clustering to identify postresuscitation vital sign phenotypes and to determine if these phenotypes are associated with outcome. Methods: The ESO Data Collaborative 2018-2022 datasets were used to explore this question. K-means clustering was performed using minimum, maximum, and delta (last minus first) case-level systolic blood pressure, heart rate, SpO2, shock index, and pulse pressure to identify vital sign clusters/phenotypes. The assessed outcomes included mortality and rearrest. To explore the association between phenotype and outcome, multivariable logistic regression models adjusted for standard Utstein factors in addition to â€˜down timeâ€™ (dispatch to ROSC interval) and airway management strategy were used. StataSE 18 and R were used for data curation and analysis. Results: Within our total cohort of 12,320 patients, five clusters were identified. In order of increasing mortality, patients in cluster 1 (n=2,861; 23.2%) were hypertensive, patients in cluster 2 (n=3,206; 26.0%) were normotensive, patients in cluster 3 were hypotensive and tachycardic (n=2,164; 17.6%), patients in cluster 4 (n=1,856; 15.1%) were hypoxemic and exhibited increasing systolic blood pressure, and patients in cluster 5 (n=2,233; 18.1%) were severely hypoxemic and exhibited a declining systolic blood pressure. In comparison to the cluster with the lowest mortality (1), each phenotype was associated with greater adjusted odds of mortality (c2 aOR: 1.42 [1.04, 1.93]; c3 aOR: 2.32 [1.62, 3.31]; c4 aOR: 3.52 [2.38, 5.19]; c5 aOR: 2.60 [1.77, 3.82]) and rearrest (c2 aOR: 1.20 [1.03, 1.40]; c3 aOR: 1.42 [1.21, 1.68]; c4 aOR: 2.60

[2.21, 3.04]; c5 aOR: 2.89 [2.48, 3.36]). Conclusion: Unsupervised clustering yielded 5 post-resuscitation vital sign phenotypes that were associated with rearrest and mortality.

232. Lauren Kohntopp, University of Alaska Anchorage. **Copper chelation and zinc supplementation induce differential metabolomics responses in a treatment model of the Atp7b-/- Wilson Disease mouse.** Co-Authors: Zoey Grenier, Jason Burkhead, Patrick Tomco. Co-Authors Institutional Affiliations: Not Listed. INBRE
Wilson Disease (WD) is an autosomal recessive disease resulting in abnormal levels of copper accumulated in the brain, liver, and other vital organs. Metabolomic pathways affected in Wilson Disease are not entirely defined, nor is copper's effect on zinc homeostasis. Additionally, we want to look at how this model responds to WD treatments. In order to interrogate these pathways in Wilson Disease, we analyzed the impact of Wilson Disease treatments, copper chelation therapy (TTM), and zinc supplementation (Zn-) on liver and blood metabolites. Liver metabolites were extracted and analyzed via 400 MHZ NMR Spectroscopy and blood serum from experimental groups with Orbitrap-MS and ICP-MS analysis.

233. Thomas Gonnella, Mayville State University. **Utilizing Simple Coumarins as Fluorescent Lifetime Reporters for HSA Binding Sites.** Co-Authors: None. INBRE
Human serum albumin (HSA) contains nine binding sites and is an essential transport protein for drugs and endogenous compounds to target organs, Examining the binding of drugs to albumin is of high importance because it determines the pharmokinetics, biodistribution, and toxicity of a drug. Coumarins, which are typically fluorescent, comprise a very large class of compounds found throughout the plant kingdom. Many coumarins and their derivatives exert antitumor, antiviral, anticoagulant, anti-inflammatory, antioxidant, and antimicrobial properties. Recently coumarins have become important lead compounds in drug research development. Our group screened fifty-four simple coumarins and determined that ten candidates showed significant binding to HSA and three candidates displayed secondary binding to HSA. These HSA bound coumarins were then simply displaced from HSA using non-fluorescent drugs with recently publish x-ray crystal structures. The binding affinities of these drugs to HSA were determined and the published drug locations with HSA were used to try to identify the binding locations our coumarin probes within HSA.

234. Diane Smith, Boise State University. **Program Outcomes for Mentored Early Stage Investigator Career Development.** Co-Authors: Usha Acharya, Jim Browning, Ken Cornell, Julia Thom Oxford. Co-Authors Institutional Affiliations: Boise State University. COBRE
The National Institutes of Health Institutional Development Award Programs support the establishment and growth of biomedical research infrastructure in states that receive a low level of federal funding for biomedical research. The purpose of this investigation was to analyze the impact of the multifaceted mentoring program established at Boise State University by the COBRE in Matrix Biology program for participating early stage investigators between 2014 to 2024. To conduct this analysis, first we evaluated participating COBRE investigator achievements, including; career advancement, publications, proposals submitted, awards obtained, grant writing training, mentorship, and independence status. Secondly, bibliometric data was collected and social networking analysis was applied. Third, U.S. Department of Human Health & Services funding awarded to Boise State was collected to see NIH funding achievement at Boise State University. Results show that early stage investigators are participating in program interventions and meeting milestones. Social networking analysis indicates that communities of expertise are forming. Finally, we see increased NIH funding at Boise State University since the COBRE in Matrix Biology program has been established. The environment created as a result of IDeA Programs

facilitated the establishment of multifaceted mentorship programs. Early stage investigators experienced career success as assessed by program outcomes.

235. Kari Lynne Sisk, WVCTSI. **Empowering Tomorrow's Researchers: The Impact of INTRO Summer Research Program on West Virginia's Health Challenges.** Co-Authors: Sarah Haymond, Sally Hodder, Jodie Saunders, Joan Lakoski, Courtney DeVries, Ming Lei. Co-Authors Institutional Affiliations: ISCORE-RC WVCTSI, WVCTSI. CTR

Initiation to Research Opportunities Summer Research Program (INTRO), jointly sponsored by the West Virginia Clinical and Translational Science Institute (WVCTSI) and the West Virginia University Health Science Center and Office of Research and Graduate Education, provides first-year medical and pharmacy students an eight-week summer research experience. Faculty members with active research programs are matched with students-based interests and serve as a primary mentor during the summer experience. This mentored research experience prioritizes fundamental skills essential for clinical and translational research, such as identifying significant research questions, crafting innovative hypotheses, and devising appropriate experimental designs with robust data analysis and interpretation. The anticipated outcome is for the experience to culminate in presentations and publications of project results. Critically important is the guidance and support of the faculty mentor as evidenced by the following quotation from a 2021 INTRO student, “This program served as the catalyst for our collaboration, leading to a series of engaging projects that extended well beyond the program's completion”. Seventy-five students have participated in INTRO over the past 3 summers resulting in ten publications and sixteen abstract submissions and presentations. The INTRO program serves as a catalyst for advancing the development of research focused on addressing the health issues confronting the people and communities of West Virginia. By providing students with immersive research experiences and mentorship opportunities, the program cultivates a new generation of researchers equipped to tackle the unique health challenges prevalent in the state.

236. Ranjita Misra, West Virginia University. **Perceived Threat for COVID-19 and Long COVID-19 in Rural Patients with Underlying Medical Conditions.** Co-Authors: Brenna Kirk, Samantha Shawley-Brzoska, Daniel Totzkay, Catherine Morton, Summer Kuhn, Misty Harris, Mary McMillion, Elaine Darling. Co-Authors Institutional Affiliations: Not Listed. CTR

Background: West Virginia, a rural state with a disproportionate burden of chronic diseases. Older adults and patients with underlying medical conditions have higher risk for severe illness from COVID-19 and Long COVID-19. This study explored perceived threat (disease susceptibility and severity) among rural adults with pre-existing diabetes, heart disease, respiratory illness, hypertension, cancer and kidney disease. Methods: A convenience sample of 2117 rural adults participated in a statewide, community-based, brief COVID-19 educational intervention delivered by trained Health Navigators (11/2022 - 12/2023). Intervention included watching brief videos of trusted HCPs addressing COVID-19 questions and vaccine concerns, followed by survey data collection. Adjusted multivariable logistic regression model was used to explore association between multimorbidity (â‰¥ 2 medical conditions) and perceived threat, controlling for demographic and psychosocial factors (e.g., vaccine concerns, self-efficacy). Results: Mean age was 41.8 Â±17.8 years; 58% of participants were female and 53.5% had no college degree. One-fourth reported multimorbidity, yet, 16.1% and 16.5% were unvaccinated or had only the basic vaccine dose without a booster. Patients with multimorbidity had higher odds ratios of perceived threat of Long COVID (OR=1.07; p

237. Ngoc Hieu Hoang, University of Mississippi Medical Center. **Cardiac mitochondrial dysfunction in hyperandrogenemia rat model of PCOS.** Co-Authors: Kristin Edwards, Karen Brooks. Co-Authors Institutional Affiliations: Not Listed. COBRE
Polycystic ovarian syndrome (PCOS) is the most common endocrine disorder in women with approximately 80% suffering from hyperandrogenemia. Hyperandrogenemia causes PCOS women to suffer from cardiovascular comorbidities. Hyperandrogenemia leads to an increase in androgen receptor expression which can alter mitochondrial function. This study aims to investigate the mechanism linking the cardiac comorbidities of PCOS with cardiac mitochondrial dysfunction. The hyperandrogenemia female (HAF) rat model exhibits characteristics like PCOS women such as increased body weight, fat mass, and food intake. At 4 weeks of age, female rats received dihydrotestosterone (DHT, 7.5mg/90 days, s.c.) pellets. At 15 weeks of age, heart tissues were collected for mitochondrial isolation. Complex I-driven respiration and complex IIdriven respiration were measured simultaneously with mitochondrial reactive oxygen species (mtROS) using the Oroboros O2k-FluoRespirometer. Data was normalized to protein concentration. In the heart from HAF rats, we observed a decrease in mitochondrial complex I-driven respiration compared to the control (3449.13 vs 4208.47 nmol e-/min/mg protein, 18% decrease), complex II-driven respiration (3449.13 vs 4208.47 nmol e-/min/mg protein, 22% decrease). In addition, mtROS production increased 20% during complex I-driven respiration while no change was observed during complex II-driven respiration. The observed cardiac mitochondrial dysfunction in the HAF model suggests a potential involvement in the development of cardiovascular comorbidities. This study provides a better understanding of the role of mitochondria in the development of cardiovascular comorbidities with PCOS while also providing an avenue for the development of strategies to re-establish normal mitochondrial function in the treatment of these comorbidities.

238. Alicen James, University of Arkansas for Medical Sciences. **Stimulation of autophagy in osteoblast lineage cells via CRISPR activation of Tfeb increases bone mass and strength.** Co-Authors: Melda Onal. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE
Autophagy is a recycling pathway in which cellular components are delivered to lysosomes for degradation. Reduction or insufficiency of autophagy is thought to contribute to several diseases of aging including osteoporosis. Accordingly, elimination of autophagy from osteoblast-lineage cells reduces osteoblast number, bone formation, and bone mass. However, whether increasing autophagy in osteoblast-lineage cells would be beneficial for bone health is unknown. To address this, we stimulated autophagy in osteoblast-lineage cells using in vivo CRISPR activation of Transcription Factor EB (Tfeb). Tfeb is a master transcriptional regulator of autophagy and lysosomal biogenesis. This genetic maneuver increased Tfeb expression 2.5-fold in RNA isolated from bones. As expected, Tfeb overexpression (OE) stimulated autophagy and lysosomal biogenesis of osteoblasts. At 18 weeks of age, Tfeb overexpressing mice displayed increased femoral and vertebral cortical thickness and cancellous bone volume. Histomorphometric analysis revealed that the increase in femoral cortical thickness was due to increased periosteal bone formation. Tfeb OE elevated bone strength as determined by femoral three-point bending analysis. Serial DXA BMD measurements in Tfeb overexpressing mice revealed high bone mass that progressed up to 9 months of age and was maintained until 12 months. MicroCT analysis at 12 months revealed that Tfeb overexpressing mice maintain high cortical thickness and exhibit an increase in cancellous bone volume in femur and spine. These increases were due to elevated bone formation. In conclusion, Tfeb overexpression in osteoblastlineage cells is anabolic, results in mechanically stronger bones, and may represent an effective approach to combat age-associated bone loss.

239. Alexandra Robinson, Pittsburg State University**. Activated Maple Carbon as a Bio-Based Electrode Material for Lithium-Sulfur Batteries for Enhanced Performance.** Co-Authors: Alexandra N.

Robinson, Anjali Gupta, Wang Lin, Ram K. Gupta. Co-Authors Institutional Affiliations: Pittsburg State University. INBRE

As the demand for energy increases, researchers are searching for new, eco-friendly energy sources to replace fossil fuels. Lithium-sulfur (Li-S) batteries are attractive energy storage devices as they use low-cost materials such as sulfur and their performance is several times higher than current lithium-ion batteries. Despite their high electrochemical performance, Li-S batteries are not as popular as Li-ion batteries commercially due to some inherent obstacles such as the shuttling effect, volume expansion due to (de)lithiation process, and formation of dendritic lithium, among others. To find solutions for that, carbon with a high surface area was used. High surface area carbon was synthesized using maple leaves to allow simultaneous increment of conductibility as well as the presence of pores in the structure to give room for the expansion of sulfur through (de)lithiation. Carbon from the maple leaves was activated using various ratios of activating agents to understand the effect of activating agents on the surface properties of the carbons. These carbons were used to fabricate Li-S batteries. The effect of surface area on the electrochemical properties of Li-S batteries was investigated. These batteries were tested using cyclic voltammetry, electrochemical impedance spectroscopy, galvanostatic charge-discharge measurements, and cyclic stability at different C-ratings. The maple carbon: activating agent (KOH) with a ratio of 1:3 showed a high specific capacitance at 0.1 C of 1050 mAh/g, good stability, and good C-rating.

240. Megan Connell, Minot State University. **The Effects of Methamphetamine on Primary Cell Cultures of Bovine Chromaffin Cells.** Co-Authors: Michael Rayel, Tara Czemeres, James Foster, L. Keith Henry, Bryan Schmidt. Co-Authors Institutional Affiliations: Minot State University, University of North Dakota School of Medicine and Health Sciences. INBRE

Amphetamines trigger the release of norepinephrine (NE), epinephrine (EPI), and dopamine (DA) in the brain. The adverse effects of methamphetamine (MA) are similar to those of an EPI response, therefore suggesting the possibility of MA-stimulated EPI secretion in the peripheral nervous system via adrenal chromaffin cells. Chromaffin cells originate from the neural crest and thus it is conceivable that they may react to MA in a manner similar to efflux mechanisms in the brain. Our lab is primarily focused on the measurement and characterization of catecholamine (CA) release from MA-stimulated adrenal chromaffin cells as initial studies have consistently indicated CA release from chromaffin cells upon MA treatment. Our current efforts are to determine the mechanism of CA release in response to MA and as a first step we are characterizing the transcriptome of the heterogeneous adrenal cell population observed in our primary bovine chromaffin isolates using single-nuclei RNA sequencing. Our goal is to identify distinct cell populations with extracellular surface markers unique to EPI-producing cells so that these cells can be isolated using flow assisted cell sorting (FACS). This will provide an enriched cell population to accurately measure EPI production and release in the absence and presence of MA treatment and provide a more direct and relevant characterization of the mechanism of MA-mediated EPI release.

241. Minu Kesheri, Marshall University. **Artificial Intelligence as the futuristic eyes for deciphering environmental and community health.** Co-Authors: None.

Abstract: Artificial intelligence has the potential to leverage huge and significant information from an avalanche of crucial data engendered by the advances in omics technologies that seems to be a holy grail. In this new era of artificial intelligence, wastewater-based epidemiology serves as a low-cost fuel to drive the proactive policy making by health departments and ringing the bell for early warnings pertaining to perils of public health matters as well as the pandemic by its futuristic machine learning based predictions. Use of artificial intelligence at the interface of biomedical sciences, environmental sciences and informatics alludes to the application of machine learning/deep learning and various other

tools to better understand the underlying mechanisms and combat the challenges thereof. The availability of huge amounts of data on various public platforms is not junk or useless but is used less. Therefore, my talk would revolve around telling the tale of a detective which is none other but “Artificial Intelligence” that has skills to measure and transform the hidden treasure in the world of complex and challenging data science to the productive information that could be useful for the benefit of mankind and environment.

242. Andrew James Wegner, Creighton University. **Fabrication of Carbon-based Stencil Printed Gold Electrodes for Biosensor Applications.** Co-Authors: Erin M. Gross, Ethan Gomez, Rebecca Y. Lai. Co-Authors Institutional Affiliations: Creighton University, University of Nebraska Lincoln. INBRE
Folding-based nucleic acid electrochemical biosensors offer an inexpensive and fast method for clinical measurements and disease diagnosis. Previous work in our lab demonstrated the fabrication of electrochemiluminescent (ECL) based nucleic acid biosensors using commercial gold electrodes. Although the method is fast, the gold surfaces of these electrodes require extensive cleaning and preparation. This work looks to fabricate ECL sensors using chip-based electrodes, where, in just a few minutes, a fresh gold layer is fabricated onto a carbon base for each electrode, eliminating the need for lengthy cleaning. This allows for faster and less expensive sensors capable of ECL detection. This work focuses on optimizing gold deposition onto the carbon electrode, and the fabrication of an alkanethiol monolayer on the gold surface, which is necessary for stability. Specifically, the concentration of Au3+ solution, deposition time, and the deposition potential waveform were investigated. Gold concentrations studied include 5, 7.5, 10, 12.5, and 15 mM. Reduction of gold onto the carbon was facilitated by an electrical potential difference of âˆ’0.2 volts vs. Ag, AgCl. Potential was applied for 120, 135, 150, 165, 180, 195, and 210 seconds. Currently, square wave deposition is being examined to determine if gold deposition across of the surface of the carbon can be made more uniform. Thus far, a 7.5 mM gold solution and 165 second reduction time utilizing standard cyclic voltammetry have offered the most reproducible electrode surface.

243. Bashir M. Rezk Atteia, Southern University at New Orleans. **Combined toxic effects of Alcohol and Homocysteine.** Co-Authors: Asim B. Abdel-Mageed. Co-Authors Institutional Affiliations: Tulane University Health Sciences Center. INBRE
Excessive alcohol consumption is a global healthcare and socioeconomic problem that is associated with the development of more than 200 diseases and injury conditions. However, the precise mechanisms of alcohol-induced toxicity are not yet clear. One of the mechanisms underlying alcohol toxicity has to do with its interaction with homocysteine (HCY). The increased level of HCY in plasma, or hyperhomocysteinemia, is considered a major risk factor for vascular diseases. The development of vascular diseases is a multifactorial process that includes endothelial dysfunction, and vascular smooth muscle cell (VSMC) apoptosis, proliferation, and migration from the media to the intima. Under physiological conditions, cell proliferation and apoptosis are balanced since cell death triggers cell migration and proliferation. However, in pathogenic conditions, a selective increase in cell proliferation induces hyperplasia, and a selective elevation of apoptosis leads to atrophy. Galectins are a family of animal Î²-galactoside-binding lectins that are present intra- and extracellularly. This cellular distribution enables galectins to exert a broad spectrum of patho-physiological effects in several diseases, including cancer, atherosclerosis, diabetes, and wound repair. Galectin-1 (GAL-1) modulates tumor progression and metastasis via various biological events, including cell migration, adhesion, and angiogenesis. Galectin-3 (GAL-3) is highly expressed in humans and rodents and has important roles in cancer and immunity. This study is focusing on the cellular and molecular mechanisms of the combined toxicity of alcohol (EtOH) and homocysteine (HCY) in vitro. Our preliminary results showed that treatment with 100

ÂµM of EtOH and/or HCY enhanced the expression of GAL-1 at 48 h and 72 h. However, GAL-3 has been elevated at 24 h and 48 h. Furthermore, both HCY (100 ÂµM) and EtOH (100 ÂµM) decreased the percentage of exosomes that might affect the vesicular transport system at the cellular level.

244. John Agbo, University of Mississippi Medical Center. **Sex-specific Activation of Intra-renal Histone Deacetylase in Offspring Exposed to Maternal Hyperandrogenemia and Maternal Obesity In-Utero.** Co-Authors: Ruth Michelle Vinson, Jane F. Reckelhoff, Prerna Kumar, Noha M. Shawky. Co-Authors Institutional Affiliations: University of Mississippi Medical Center, Tulane University. COBRE Polycystic ovary syndrome (PCOS) is the most common endocrinopathy in young women. In-utero, PCOS children in the US are exposed to maternal hyperandrogenemia (HA) and obesity. Using a rat model of maternal PCOS, the HA dams, we previously showed that adult male, not female, offspring of HA dams (HAoff.) have exaggerated angiotensin (Ang) II hypertension (HTN). Histone deacetylase (HDAC)3 is a marker of epigenetic modifications and has been shown to play a role in Ang II HTN. The present study was designed to test the hypothesis that male HAoff. develop sex-specific intra-renal activation of HDAC3. Methods: At 4 wks of age, female Sprague Dawley rats were implanted with either dihydrotestosterone (7.5 mg/90 d, s.c.; HA) or placebo (CON) pellets. HA and CON were allowed to get pregnant and offspring (n=3-6, 1/sex/litter) were euthanized as adults. Renal cortical nuclear extract was used to measure HDAC activity (colorimetry) and HDAC3 expression (western blot). Results: Male HAoff. had higher HDAC activity compared to male and female CONoff. and female HAoff. (5+/-0.9 vs 1+/-0.1, 1+/-0.4 and 1+/-0.2 OD/min/mg protein, respectively, p

245. Katarzyna Rosikon, Delaware State University. **Effects of a Differential Overexpression of the Vesicular Acetylcholine Transporter on Synaptic Activity and Behavior in Drosophila melanogaster.** Co-Authors: Hakeem Lawal. Co-Authors Institutional Affiliations: Not Listed. COBRE Impairment in cholinergic neurotransmission is associated with normal and pathological aging, making cholinergic release a subject of sustained interest. However, the precise role of changes in central acetylcholine (ACh) release in mediating behaviors that range from locomotion to cognition has not been fully elucidated. The vesicular acetylcholine transporter (VAChT) is present in many species, including worms, flies, and humans, and is responsible for the packaging of ACh for exocytotic release. Although there is a plethora of knowledge about the molecular machinery that regulates ACh, the exact manner in which VAChT, an essential component of ACh regulation, alters ACh-linked neuronal function remains a subject of active investigation. Here, we use the overexpression of VAChT as a tool to increase the amount of ACh released into the synaptic cleft. And we are measuring the effect of that altered state on synaptic activity using two key behavioral circuits, locomotion and cognition. Previously, we showed that vast increases in VAChT expression cause severe behavioral deficits, including a sharp decline in lifespan. Our current study is focused on testing the hypothesis that more moderate increases in VAChT expression will not only lead to less severe effects but also beneficial ones. To test this idea, we used four VAChT overexpressing lines with varying levels of increased expression. We report the intriguing results that while strong increases in VAChT produced a corresponding decrease in lifespan, a less drastic overexpression of the protein led to a less steep decline in lifespan. Moreover, we show that in agreement with our previous published findings, our preliminary data show that VAChT overexpression caused an age-dependent decrease in locomotion ability in all lines tested. Further, immunohistochemical analysis showed that at least one VAChT overexpressor showed a strong increase in localization of the protein to punctate in the optic lobe, indicative of increased presence in synaptic vesicles. Taken together, these data indicate that morphological and behavioral effects of VAChT overexpression are driven by the levels of the protein's expression and inform further studies to be

aimed at identifying precisely which dial in VAChT expression could lead to a beneficial effect on synaptic neurotransmission.

246. Massimo Aloisi, Coastal Carolina University. **Evaluating the genotoxicity, carcinogenic potential, and disease-promoting effects of polystyrene nanoparticles using Drosophila melanogaster models of human disease.** Co-Authors: A.M.G. Poma, P. Morciano, C. Gamberi, D. Grifoni. Co-Authors Institutional Affiliations: University of L'Aquila, Coastal Carolina University. INBRE
The world's oceans are thought to contain more than 170 trillion plastic particles. Unknown amounts are present in both atmosphere and mainland. Thus, plastic pollution is a global emergency. Plastic degradation forms micro- and nanofragments that are ingested by living beings and bioaccumulated in fatty tissues that reduces survival, is genotoxic and causes metabolic alterations. We use Drosophila melanogaster as model organism to assess if 100 nm polystyrene nanoparticles (PSNPs) induce DNA damage, increase cancer risk and potentially worsen disease progression. Ingested fluorescent PSNPs are absorbed into intestinal cells and accumulated in fat bodies of wild-type flies. Compared with controls PSNPs-fed flies weighed considerably less and showed increased developmental time, and compromised starvation resistance and heat shock recovery. Feeding PSNPs to DNAlig4 mutants, known to be susceptible to dietary stressors, decreased climbing performance. Together, these findings imply that PSNPs influence fly development and metabolism. A qPCR analysis of the intestines of PSNP-fed wild type larvae revealed higher expression of cell damage response genes. Increased DNA damage was detected with the comet assay. Reinforcing the hypothesis of the PSNPs carcinogenic potential, PSNPs-fed warts mutants, known to spontaneously develop melanotic tumors even in heterozygous individuals, developed more aberrant masses than untreated ones. We are currently testing the potential effects of PSNPs on disease progression using a fly/Drosophila model of Polycystic Kidney Disease.

247. Sujoita Sen, University of Delaware. **Modulating HSP90 interactions with its client proteins as a therapeutic target in cardiac diseases.** Co-Authors: Logan Hallee, Adam Hetzelson, Julia Serjantova, Halley Wisner, Richard Roberts, Chi Keung Lam. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Modulating HSP90 interactions with its client proteins as a therapeutic target in cardiac diseases. Sujoita Sen1, Logan Hallee2, Adam Hetzelson1, Julia Serjantova1, Halley Wisner1, Richard Roberts1, Chi Keung Lam1; 1: Department of Biological Sciences, University of Delaware; 2: Department of Biomedical Engineering, University of Delaware; Cardiac disease has a complex etiology involving multiple molecular and cellular dysfunctions that the existing therapies fail to target simultaneously. Heat Shock Protein 90 (HSP90) regulates the proteostasis of several proteins relevant in cardiac signaling pathways and therefore, presents as a potential target for treatment. Past studies have shown that HSP90 interacts with HCLS1associated protein X-1 (HAX-1) to inhibit the activity of sarco-endoplasmic reticulum Ca2+ ATPase (SERCA) pump and cardiac contractility. Previous studies have also indicated that increased interactions of HSP90 with HAX-1 preserved mitochondrial integrity by preventing the activation of the mitochondrial permeability transition pore (mPTP). As impaired contractility and reduced cell survival are common attributes of most cardiac diseases, the goal of this study is to design cell-permeable interfering peptides to modulate the HSP90/HAX-1 binding to improve contractility and cardiomyocyte survival under stress. We have determined the specific interacting regions of HSP90 and HAX-1 on each other by protein binding assays to design the interfering peptides. The Antennapedia peptide sequence has been added to these domains to make the interfering peptides cell permeable. Our preliminary data from interfering peptide treatment of iPSC-derived cardiomyocytes suggest enhanced contractility and improved mitochondrial integrity after hydrogen peroxide challenge. We then designed AAV vectors coding for the interfering peptides with targeting sequence for SR/ER membrane, mitochondrial

intermembrane space or matrix. Mitochondria targeting, but not SR/ER targeting interfering peptides enhances protection against mPTP opening. Thus, our findings suggest that HSP90/HAX-1 interaction may serve as an interesting target to enhance cardioprotection and contractility.

248. Vincent Melemai, West Virginia University. **Utility of GPT-4 in assisting orthopedic residents preparing for the AAOS board exam.** Co-Authors: Ryan A. Lacinski, Garrett Yoder, Brody M. Fitzpatrick, Michael Hu, Brock Lindsey. Co-Authors Institutional Affiliations: West Virginia University School of Medicine, Akron General Medical Center - University of Akron, Johns Hopkins University School of Medicine. CTR

Background: ChatGPT has demonstrated its exceptional knowledge base and human-like reasoning by passing professional board examinations including the United States Medical Licensing Examination (USMLE). In this study, we sought to determine whether GPT-4 could act as a resource to assist orthopedic residents during board preparation by testing its ability to answer American Academy of Orthopedic Surgeons (AAOS) Orthopedic In-Training Examination (OITE) questions. Prompt engineering techniques were also assessed to determine best practices for obtaining the highest fidelity responses. Methods: Using the 2023 AAOS OITE question set, plain prompting was completed for all 207 questions. Prompt engineering techniques, including direct prompting, were then assessed to improve the accuracy of responses for those questions with incorrect or no response. Questions containing images or laboratory data were also incorporated into a “missing piece” prompt to determine if GPT-4 could identify the appropriate diagnostic test required to answer the question. Results: Overall, plain prompting in GPT-4 yielded a correct percentage of 63.7%, with the chatbot performing significantly better in both “Basic Science” and “Shoulder and Elbow” question categories ($p < 0.05$). An unpaired t-test demonstrated a statistically significant improvement in performance of directed prompting when compared to plain prompting ($p < 0.01$). Conclusion: While plain prompting of GPT-4 failed to meet the minimal passing score of 68.6%, secondary use of directed prompting increased the overall percent correct to 72.9%. Further analysis of our data set is required to determine the quality of references provided by GPT-4 in terms of relevance to current clinical standards.

249. Holly LaVoie, University of South Carolina. **MMP14 overexpression and its impact on cardiac function and extracellular matrix markers in pregnant and postpartum mice.** Co-Authors: Ridha Fatima, Emily Walliser, Aiden Maragh, Jessica Simpson. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine. INBRE

Physiological remodeling of the heart occurs during pregnancy and reverses postpartum. Elevated Matrix metallopeptidase 14 (MMP14) is associated with pathological remodeling of the heart. We aimed to determine if overexpression of MMP14 in mice would alter maternal cardiac function and extracellular matrix (ECM) parameters during pregnancy and postpartum remodeling. We utilized mice expressing a human MMP14 (hMMP14) transgene under control of the murine Col1a2 promoter which expresses predominantly in fibroblasts. Wildtype and hMMP14 adult female mice were mated and underwent a series of echocardiogram measurements and were euthanized for tissue collection at day 17 of pregnancy or postpartum day 49. Age-matched virgins were also analyzed. Heart weight normalized for tibia length (HW/TL) was highest in pregnant mice of both genotypes. The only genotype difference in HW/TL was between the younger age-matched virgin groups. In both genotypes, stroke volumes (SVs) at ppd 2, 7, 14, and 21 were higher than their respective virgin levels. In addition, in hMMP14 mice at ppd28 SV was higher than starting virgin levels. Investigation of mRNAs for ECM molecules found differences in reproductive status and/or genotype in specific TIMP and collagen genes. COL1A1 isoform levels were altered by pregnancy, but no difference was observed in picrosirius red stain quantification of collagen types 1 and 3. Overall, there were few differences in cardiac function, ECM proteins and their

mRNAs between genotypes. The largest impact on cardiac function, ECM mRNA and protein expression was pregnancy. Acknowledgments: Dr. Frank Spinale for mice and funding from SC INBRE P20GM103499.

250. Geanina R. Swanay, Vermont State University - Castleton. **Accuracy of body mass index vs bod pod when assessing body composition: a pilot study.** Co-Authors: Andrea Corcoran. Co-Authors Institutional Affiliations: Not Listed. INBRE
PURPOSE: This study challenges the Body Mass Index (BMI) chart and its validity as a body composition assessment tool. Using air displacement plethysmography (Bod Pod) as a reference method, we evaluated the correlation between BMI and %body fat (%BF) obtained by the Bod Pod. METHODS: Twenty-five participants (11 male, 14 female; 19-85 years) underwent %BF assessment using the Bod Pod. Height and weight were measured and used to calculate BMI. RESULTS: Measurement s obtained were used to categorize both BMI and %BF values, resulting designated categories were compared individually. We observed the most agreement of %BF with BMI when someone falls into the “Obesity” category (>30.kg/mÂ²). When the BMI places a person in “Underweight” category the Bod Pod places them in the â€œVery Leanâ€• category. Within the Bod Pod the average female body fat percentages was 34.64% obese. The average male body fat percentage was 24.12%, overfat. The average BMI measured was 27.94kg/mÂ², the overweight category, while the rang was 18.51-39.81 kg/mÂ². A significant positive correlation was found between BMI and %BF in males (r=0.805, p

251. Anya Goropashnaya, UAF. **Skeletal muscle preservation in arctic ground squirrels during hibernation season.** Co-Authors: Amy L. Confides, Inigo Yoldi Bergua, Kelly L. Drew, Esther E. Dupont-Versteegden, Vadim B. Fedorov. Co-Authors Institutional Affiliations: University of Kentucky, UAF. INBRE
Reduced skeletal loading leads to muscle atrophy in humans and most mammals. By contrast, hibernating mammals demonstrate limited loss of skeletal muscle mass and strength by the end of winter after being physically inactive for several months. The present study objective was to establish potential underlying processes for the lack of muscle loss during the hibernation season of arctic ground squirrels (AGS). Our hypothesis was that early in the the hibernation season, protective mechanisms of AGS are not yet mobilized and muscles show signs of atrophy, while compensatory processes for preventing muscle loss appear at a later time point. Quadriceps muscles of juvenile male AGS were collected shortly before hibernation, and on 2, 6, 10-12 and 16-22 weeks during hibernation. Pre-hibernating animals were used as controls. We found that fiber cross-sectional area (CSA) was not different between the groups ($P > 0.05$). No difference was detected in myofiber composition between the hibernation groups compared to the control. Muscle atrophy marker FBXO32 and autophagy related genes MAP1LC3A and BECN1 did not show different level of expression between the groups. Only another muscle atrophy marker TRIM63 was significantly overexpressed at the time point of 2 weeks of hibernation. These results indicate that throughout the hibernation season, AGS preserve muscle fiber CSA showing limited signs of muscle atrophy only during the first weeks of hibernation, and yet-to-be determined processes exist to suppress protein degradation in AGS muscles during hibernation. The work was supported by Center of Biomedical Research Excellence under grant number [P20GM130443].

252. Sara Akhtar, Pittsburg State University. **Gene expression of oncolytic virus receptors in human head and neck squamous cell carcinomas.** Co-Authors: Silas Rosiere, Christopher Simmons, Phillip Harries. Co-Authors Institutional Affiliations: Pittsburg State University. INBRE
Head and neck squamous cell carcinoma (HNSCC) is the 6th most common cancer worldwide. HNSCC affects 600,000 new patients every year with over 250,000 annual deaths attributed to the disease. Oncolytic viruses are those that kill cancer cells and they have been increasingly utilized as an adjuvant

therapy paired with more traditional forms of treatment to attack a wide array of cancers. Although a handful of studies have tested oncolytic viruses on HNSCC, there is relatively little known about which viruses may be most effective for this specific type of cancer. In order for any oncolytic virus to kill cells, it must first initiate an infection by binding to and entering the host cell. This initial interaction is generally mediated by binding of a protein on the surface of the virus particle with a receptor on the surface of the host cell. In this study, we compare gene expression patterns of known oncolytic virus receptors in HNSCC compared to a healthy control. We further examine the potential role of cytosine methylation in such patterns. The overall goal of this work is to identify oncolytic viruses that might have the best chance of infecting HNSCC compared to normal health tissue.

253. Claudine Jurkovitz, ChristianaCare Health Services, Inc. **Impact of the COVID-19 Pandemic on Lung Cancer Diagnosis and Screening in Delaware.** Co-Authors: Yeonjoo Yi, Kevin Ndura, Krishna Vasireddy, Kiran Kattepogu, Brian Nam. Co-Authors Institutional Affiliations: ChristianaCare Health Services, Inc., Delaware Health Information Network. CTR

COVID-19 has greatly impacted the U.S. health system. While lung cancer incidence and screening have been affected, whether pre-existing racial and socioeconomic disparities worsened is unknown. The purpose of this study is to analyze the impact of COVID-19 on lung cancer care in Delaware. We analyzed claims data from the Delaware Health Care Claims Database for the years 2019-2020. Patients with a new lung cancer diagnosis and those who had undergone lung cancer screening were identified. The intervention of interest was the onset of care restrictions at the end of March 2020. We used an interrupted time series analysis to evaluate baseline levels and overall trend changes. The number of new lung cancer diagnoses and lung cancer screenings decreased after initiation of COVID-19 lockdown. No significant differences were seen between the two time-periods in mean age, gender, race, insurance or income level among those with new cancer diagnosis. The weekly count of new lung cancers declined at the beginning of the pandemic and did not recover by the end of 2020. This effect was most pronounced among 80-90 years old. The weekly count of lung cancer screenings decreased sharply following the services restriction but subsequently returned to pre-pandemic levels. Patients on Medicaid resumed screening more rapidly than those on commercial insurance or Medicare. COVID-19 had a significant impact on new lung cancer diagnosis specifically in elderly patients while screening-related services recovered promptly. These findings offer valuable insights for shaping health policy in preparation for future pandemics.

254. Braden Allphin, Fort Hays State University. **RNA Interference of TorsinA and Heat Shock 70 kDa proteins in Acyrthosiphon pisum.** Co-Authors: Griffin Davies. Co-Authors Institutional Affiliations: Fort Hays State University. INBRE

Acyrthosiphon pisum, more commonly known as pea aphids, are a pest to many species of Febaceae (legumes) mainly due to the species being prone to carrying Febaceae diseases. Protection against A. pisum currently includes insecticides and natural predators, both of which bring potential negative effects to other organisms in the surrounding area. In this study, the use of RNA interference (RNAi) provides an alternative and species-specific elimination of A. pisum. The targeted proteins in this study, Heat Shock 70 kDa Protein 1L (HSPA1L) and TorsinA (TOR1A), are involved with the stabilization of existing proteins, mediating the folding of newly translated proteins in the cytosol and organelles, and catabolizing misfolded proteins. Targeting the HSPA1L and TOR1A genes could potentially result in an increase in improperly folded proteins in the cytosol and other organelles, which would eventually result in increased apoptosis (cell death) and death of the organism. In this study, RNA was isolated from A. pisum and reverse transcribed into cDNA. This cDNA was combined with HSPA1L and TOR1A primers to

synthesize HSPA1L and TOR1A dsRNA that would be fed to multiple groups of A. pisum. In preliminary studies, this method has shown reasonable evidence of increased death rate of A. pisum.

255. Jaden Nienhueser, University of Nebraska Omaha. **Spanning paradigms: using immunotherapy to enhance human natural killer cell antibody dependent cell-mediated cytotoxicity against cancer and infectious disease.** Co-Authors: Paul W. Denton. Co-Authors Institutional Affiliations: University of Nebraska Omaha. INBRE

A primary goal of the Denton Immunobiology laboratory is to evaluate immunotherapy strategies with the goal of improving the killing capacity of human natural killer (NK) cells. To date, this work has been in the context of killing cancer cells. Malignancy is a paradigm of disease with a near-immeasurable scope. However, infectious diseases operate in a similarly large sphere. This project's goal is to determine whether immunotherapy findings in cancer can span paradigms and similarly impact treatment approaches in infectious disease. Our goal is to perform infectious disease-related experiments without incorporating fully infectious agents into our approach. To do this, we obtained cells that express human immunodeficiency virus (HIV) envelope proteins constitutively. HIV was chosen as the pathogen to represent the infectious disease paradigm because its treatments exist but are not curative. Our goal is to contribute to many research efforts focused on helping to “train” the immune system to fight HIV in the absence of other treatments (e.g., antiretroviral therapy). These target cells expressing HIV envelope protein appear as “infected” to human NK cells. To allow NK cells to recognize the presence of HIV protein, we utilized an antibody specific for the envelope, an antibody capable of directing the NK cell to perform the killing function known as antibody-dependent cell-mediated cytotoxicity (ADCC). Data to date will be presented. The project described was supported in part by an Institutional Development Award (IDeA) from the NIGMS of the National Institutes of Health under Grant # 5P20GM103427.

256. Mackenzie Hall, West Liberty University. **Screening Resorufin Pentyl Ether Analogs for Enhanced Antimicrobial Activity Against Francisella tularensis and Neisseria gonorrhoeae.** Co-Authors: Emily Young, Jordan Gibson, Ryleigh Morgan, Caroline Woody, Emma Beatty, Blaze Oxier, Deanna Schmitt, Tanvir Ahmed, Jada Berg, Gregory Dudley. Co-Authors Institutional Affiliations: West Liberty University, West Virginia University. INBRE

Antibiotic resistance is an urgent public health threat. The CDC estimates there are approximately 2.8 million new cases of antibiotic-resistant infections annually resulting in 35,000 deaths and billions of dollars in health care costs. The development of new drugs is imperative to combat this crisis and prevent the loss of additional lives from once â€œcurableâ€• diseases. Resazomycins, a novel family of antibiotics, have bactericidal activity against Francisella tularensis and Neisseria gonorrhoeae. One resazomycin, resorufin pentyl ether (RPE), significantly reduces vaginal colonization by N. gonorrhoeae in a mouse model of infection. Repeated administration of RPE, however, fails to clear the infection, in contrast to a single dose of ceftriaxone, an antibiotic commonly used to treat gonorrhea, which clears the infection within 24 hours. Further characterization of resazomycins revealed the efficacy of these compounds is limited by interaction with serum albumin and reduced oxygen concentrations found within mammalian tissues. Therefore, we hypothesize that novel resazurin analogs that maintain antimicrobial activity in the presence of serum albumin and low oxygen will have improved therapeutic efficacy in vivo. Resazurin has been chemically modified to generate ether and deoxygenated compound derivatives. Six ether derivatives and two deoxygenated analogs exhibited robust antimicrobial activity against F. tularensis and N. gonorrhoeae. In the presence of serum albumin, however, reduced efficacy was observed in the six ether analogs yet activity was maintained in the deoxygenated analogs. We plan to screen the efficacy of additional ether and deoxygenated analogs against F. tularensis and N. gonorrhoeae.

257. Sharon Elaine Sanders, Arkansas Children's Research Institute: Center for Childhood Obesity Prevention. **The Bi-Directional Experience for Community and Academic Partners.** Co-Authors: Anna Huff Davis, Taren Swindle. Co-Authors Institutional Affiliations: Not Listed. COBRE

The Center for Childhood Obesity Prevention Community Engagement (CE) Core launched a Bi-directional Experience to promote CE in research. Part I, the Academic Experience (AEX), was attended by 73% (11/15) of the Center's Community Advisory Board. The CAB toured research facilities and attended lay-friendly science presentations. The CAB also networked and engaged in a perspective sharing panel discussion with researchers. Researchers (n=16) attended the Community Experience (CEX) to explore the realities of life and health in the Arkansas Delta. Researchers joined community-led tours in southeast Arkansas and listened to a community panel about health in the Delta. Each group completed a feedback survey and focus group. The CAB survey participants (n=8) strongly or somewhat agreed that the AEX was helpful in providing opportunities to discuss mutual interests (88%), network (100%), and collaborate (75%). The CAB also appreciated "pulling back the curtain" to see the behind scenes of research, listening to lay science presentations, and discussing sustainability. Researchers (n=16) somewhat or strongly agreed that the CEX increased their understanding of factors that contribute to child health in the southeast Arkansas Delta. Researchers said the CEX influenced their intentions to develop new collaborations with communities (75%), serve the community (69%), design new research projects (63%), and encourage their colleagues to attend future CEXs (88%). Researchers underscored the value of leveraging community assets, CE, and potential collaborations. Both groups expressed a deeper appreciation of the other's perspective. Bidirectional Experiences may enhance community and academic collaborations and foster new interests for CE in research.

258. Laurel Stone, West Virginia University. **Targeting Stress Circuitry: A Novel Approach for Improving PostIschemic Stroke Outcomes.** Co-Authors: Morgan Bridi. Co-Authors Institutional Affiliations: West Virginia University School of Medicine. COBRE

Ischemic Stroke (IS) has profound consequences on long-term functional impairment and is a leading worldwide cause of disability and death. The dysregulation of the hypothalamic-pituitary-adrenal (HPA) axis exacerbates post-stroke complications, including hypercortisolism and neuronal damage, and contributes to post-IS morbidity. Gaining insight into the neuroendocrine responses to stroke is essential for devising effective therapeutic interventions. Here, we propose a novel strategy targeting stress-processing neuronal populations in the hypothalamic paraventricular nucleus (PVN) and bed nucleus of the stria terminalis (BNST) to mitigate HPA axis hyperactivation and improve post-IS outcomes. Building on evidence implicating hippocampal modulation of stress responses, we are utilizing chemogenetic tools to selectively modulate PVN and BNST neurons in mouse models of transient middle cerebral artery occlusion (tMCAO) via AAV injections. Preliminary data demonstrate the efficacy of chemogenetic manipulation in the modulation of stress circuitry. We hypothesize that attenuating HPA axis activation in the acute post-IS phase will reduce corticotropin-releasing factor (CRF) signaling, lower plasma corticosterone levels, and mitigate hippocampal neuronal loss. Experimental protocols include chemogenetic manipulation after tMCAO, followed by assessments of infarct size, hippocampal integrity, and behavioral outcomes. We anticipate that the targeting of specific stress nuclei and neuronal subtypes will offer treatment outcomes for post-IS recovery, potentially improving long-term functional and behavioral outcomes. This research accentuates the importance of stress modulation in stroke pathophysiology and underscores the potential of targeted neuronal interventions in the improvement of patient outcomes.

259. Chris WD Jurgens, University of North Dakota. **Advanced Light Imaging: INBRE Microscopy Core Facility at the University of North Dakota.** Co-Authors: Van A Doze, Don A Sens. Co-Authors Institutional Affiliations: University of North Dakota School of Medicine & Health Sciences. INBRE
The North Dakota INBRE Microscopy Core Facility (IMCF) at the University of North Dakota provides advanced light imaging technologies to support cutting-edge research in the sciences. The IMCF serves researchers of all experience levels from diverse institutions and fields. The core is located on the 4th floor of the School of Medicine & Health Sciences Building. The facility is open to all members of the research community, with priority given to IDeA-funded investigators and projects. The IMCF provides tools for routine fluorescence and confocal microscopy (including live cell imaging), laser microdissection, stereology and has dedicated high performance workstations to support available image analysis software. Near-IR confocal microscopy will soon be offered. Adjacent laboratory space allows outside investigators to prepare cells for viewing using both available bench space and the cell culture and related facilities of the Department of Pathology. The IMCF also provides training and consultation services to help researchers of all levels to collect, analyze, and interpret their images. The IMCF aims to promote research productivity and improve STEM training in imaging science by providing: well-managed and maintained equipment; methodological and technical expertise; training in image acquisition and analysis; and an interface for interaction of researchers to facilitate collaborations. The facility is supported in part by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health (P20GM103442), the Department of Pathology, the UND School of Medicine and Health Sciences and the North Dakota Cancer Collaborative on Translational Activity (DaCCoTA).

260. Ranjeeth Reddy Kondati, Southern University and A&M College. **TCHQ-induced Damage in HepG2 Cells: A Molecular Perspective.** Co-Authors: Nandini Bidarimath, Druthi Mutyala, Manisha Thakur, Sanjay Batra. Co-Authors Institutional Affiliations: Not Listed. COBRE
Pentachlorophenol (PCP) has been a potent pesticide, fungicide, herbicide, and insecticide since 1936. The chlorinated aromatic organic compound has biocidal properties. In 1984, the US government prohibited its utilization because of its cancer-causing and poisonous characteristics. Despite the prohibition, a staggering 36 million utility poles exist in the United States that have been subjected to the application of pentachlorophenol (PCP), hence amplifying the potential for exposure and associated risks. Exposure to wood surface volatilization either through skin contact or inhalation is the mechanism for coming into contact with the substance. The environmental persistence of PCP leads to extensive contamination. The duration of its impact is enduring, with a lifespan of up to 200 days in water and 33 to 16 days in individuals. The process of oxidative dichlorination of PCP results in the formation of TCHQ, which is a carcinogen that poses significant health risks. Nevertheless, the precise mechanisms behind the genotoxicity and mutagenic effects of TCHQ remain unidentified. Our results demonstrate that contrary to PCP, TCHQ exhibits detrimental effects on HepG2 epithelial cells. We observed that TCHQ triggers apoptosis, pyroptosis, and necroptosis (PANoptosis) pathways in liver epithelial cells, concurrently. In future, we aim to study the molecular processes regulated by TCHQ in HepG2 cells, specifically focusing on the PANoptosome formation. The objective of our research is to shed light on the molecular events regulated by TCHQ, in order to facilitate the development of treatment strategies and mitigate the associated health hazards.

261. Cady Burnside, University of Delaware. **Antibiotic fragments targeting the tuberculosis ClpP1P2 peptidase possess a secondary binding site.** Co-Authors: Monika Prorok, Fan Fei, Jason K. Sello, Karl R. Schmitz. Co-Authors Institutional Affiliations: Not Listed. COBRE

Tuberculosis is the world's leading infectious killer, causing over 4,000 deaths each day. The emergence of multidrug-resistance in the causative pathogen, Mycobacterium tuberculosis, drives an urgent need for drug development against novel molecular targets. Mycobacterial Clp proteases, which play essential roles in protein homeostasis and pathway regulation, are one promising group of antibacterial targets. These proteolytic enzymes consist of a protein unfoldase (ClpX or ClpC1) that threads protein substrates into a tetradecameric peptidase barrel (ClpP1P2) for destruction. Acyldepsipeptides (ADEPs), a class of nonribosomally encoded peptide antibiotics, are known to inhibit Clp proteases by binding to the surface of ClpP1P2 and blocking unfoldase binding. ADEPs can kill mycobacteria in culture and in models of infection, but their potency is relatively low. Efforts to improve ADEP potency are constrained by its peptide macrocycle, which offers few opportunities for structural optimization. Here, we examine the binding and activity of ADEP fragments that possess only a partial linearized macrocycle. Co-crystal structures of ADEP fragments in complex with M. tuberculosis ClpP1P2 confirm that these simpler compounds bind similarly to full ADEPs, but provide new opportunities for structural elaboration. Interestingly, our structures also reveal ADEP fragments bound to peptidase active sites within the barrel. Biochemical assays suggest that this secondary binding mode provides an additional mechanism through which ADEP fragments can dysregulate Clp protease function. Taken together, these studies provide a path for future development of ADEP derivatives to achieve improved potency and target selectivity.

262. Jia Fan, Tulane University. **Exploring Adipocyte-Derived Extracellular Vesicles as Early Indicators of Diabetes in Obese Individuals.** Co-Authors: Sudipa Maity. Co-Authors Institutional Affiliations: Not Listed. COBRE

Adipocyte-derived extracellular vesicles (AdEVs) serve as intercellular messengers, facilitating communication between adipose tissue and various organs. Accumulating evidence underscores the pivotal roles of AdEVs in metabolic regulation and the development of Type 2 Diabetes (T2D). To elucidate the involvement of AdEVs in T2D and assess their potential as markers for diabetes predisposition in obese populations, we employed massâ€"spectrometry-based proteomics to scrutinize AdEVs isolated from both lean and obese cohorts. Our analysis revealed 140 proteins exhibiting differential expression between lean and obese AdEVs, with 30 proteins implicated in pathways associated with T2D through pathway enrichment analysis. Among these proteins, we further investigated to ascertain their selective enrichment in EVs, thereby designating them as EV markers. Expression proteomics in EVs and their respective cells unveiled caveolin-1, CD316, and cell cycle and apoptosis regulator protein 2 (CCAR2) preferentially enriched in AdEVs. Interestingly, while the expression of these proteins in adipocytes of lean and obese populations appeared insignificant, they were elevated in the corresponding EVs. Subsequent examination of their expression in tissue unveiled caveolin and CCAR2 enrichment in tissue EVs, alongside elevated expression in obese EVs compared to lean EVs, a phenomenon not observed directly in tissues. However, CD316 was rendered undetectable in the tissues. In conclusion, our findings underscore the role of AdEVs in T2D pathogenesis and suggest caveolin-1 and CCAR2 as potential EV markers indicative of diabetes predisposition in obese populations. These results offer insights for further research into diagnostic applications targeting EV proteins in diabetes.

263. Savannah Noblitt, University of South Carolina. **Web Application for Searching and Displaying Cancer Patient Database.** Co-Authors: Ali Firooz, Julie Martin, W. Jeffery Edenfield, Anna Blenda, Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina, Prisma Health Cancer Institute. INBRE

Introduction: Personalized care for cancer patients is vital due to the intricate nature of cancer's development and progression, influenced by factors such as the patient's health status, genetic mutations, and environment elements. Hypothesis: To tailor an individualized treatment to a patient, it is essential to present multifaceted data in a format that can easily be accessed and analyzed by healthcare providers. Methods and Results: The initial data, from the Prisma Health Cancer Institute Biorepository, includes 2,800 cancer-critical gene mutations, profiles of five serum galectins, and serum/biopsy glycan structures, and healthy control values. This data, along with patient clinical and demographic information, was integrated into a MySQL Relational Database Management System (RDBMS), with the primary database relation focusing on basic patient information tied to anonymous IDs. A Flask web application connected to the RDBMS via SQLAlchemy was developed. Authorized users can conduct customized searches through the web app. Such searches will generate the appropriate SQLAlchemy statements for querying the RDBMSand will display the results logically. The alpha-stage database and web app enable researchers and physicians to merge cohorts and analyze data for molecular signatures or correlations. Conclusions: Our project introduces an expanding, interactive database framework and web app for analyzing molecular and clinical patterns in cancer, enhancing diagnostic and prognostic capabilities. Grant Support: This research received support from SC INBRE Award Number P20GM103499 and Prisma Health.

264. Alejandro Q. Nato, Jr., Marshall University. **Computational 3D analysis of the Cidec mutation (R46S) potentially involved in obesity.** Co-Authors: Vinicius Magalhaes Borges, Natalia Fagundes Borges Teruel; James Denvir, Jung Han Kim. Co-Authors Institutional Affiliations: Marshall University, Universite de Montreal, INBRE

Cell death-inducing DFFA-like effector c (Cidec) gene is a potential candidate for tabw2a, an obesity quantitative trait locus on chromosome 6 in obese diabetic TALLYHO/JngJ (TH) mice. Cidec is a crucial regulator of cellular lipid storage and lipolysis, associated with lipid droplet formation, and predicted to be involved in apoptosis. Mutations in its human ortholog (CIDEC) may be involved in insulin-resistant diabetes. A single nucleotide substitution (136C>A) in Cidec coding sequence of TH mice results in an amino acid substitution (R46S; p.Arg46Ser). When on high-fat diet, Cidec R46S knock-in mice (homozygous for S46) exhibited significantly larger body fat mass than wild-type mice (homozygous for R46). Here, we assessed the impact of the R46S missense mutation by computationally evaluating protein-protein interactions on the binding interfaces of Cidec. Leveraging the experimentally-solved dimeric structure of Mus musculus Fsp27 CIDE-N domain (4MAC) from RCSB, we employed Modeller to model the missense mutation (p.Arg46Ser) caused by SNP rs252980716 (chr6:113410092-113410092 [mm39]). Surfaces analysis was employed to assess the binding interfaces across all residues between the two monomers constituting the Cidec structure, both in wild-type and modeled (R46S) forms. Our analysis revealed a significant reduction in the favorability of the interface between monomers in the R46S mutant compared to the wild-type structure, with estimated binding Î”Î”G values of -9.490 kcal/mol and -7.767 kcal/mol, respectively. These findings suggest that the active site potentially disrupted by the R46S mutation may affect interactions of Cidec with other relevant proteins, which may contribute to the etiology of obesity.

265. Sherri Davis, West Virginia Clinical and Translational Science Institute. **Strategies to enhance clinical resources to increase SARS-CoV-2 testing among rural primary care clinics.** Co-Authors: Jada HeathGranger, Stacey Whanger, Sally L Hodder. Co-Authors Institutional Affiliations: West Virginia Clinical and Translational Science Institute. CTR

West Virginia's (WV) predominantly rural population has been at increased risk for severe disease and death due to SARS CoV-2 as shown in assessments of comorbidities impacting the virus and health

outcomes. Rural communities also heavily depend on their community health centers for their health and medical needs. To assess a series of community-identified strategies to enhance SARS CoV-2 testing support in WV primary care clinics a county-based, non-randomized study was designed. Participating clinical sites received testing supplies, personal protective equipment for testing staff, and dedicated personnel for testing. Nasal or nasopharyngeal swabs were also procured and sent to the clinics' partner commercial laboratory for polymerase chain reaction (PCR) results. Fifty-one primarily rural clinics participated. The clinics represented eleven health systems and were distributed across twenty-eight counties in WV. A total of 223,437 tests were provided to patients by the WVPBRN participating sites. Rural sites supported with testing enhancements conducted significantly higher rates of testing per site during surge months (July 2021 "November 2021 and December 2021" April 2022) than rural sites not supported in the same time period. When stratified by urban and rural counties, there was a significant improvement in rural counties, in comparison to urban counties. This SARS CoV-2 RADX project provided support to community health centers by providing clinical staff support and resources. Future research and support needs directed to the community health centers to sustain local, quality health care in areas with limited access to inform how to effectively test patients in future pandemics.

266. Angela Ngoc Truong, Univeristy of Nebraska - Omaha. **Surface CD16 Modulation by Toll-Like Receptor 9 (TLR9) Agonism on Human Natural Killer Cells.** Co-Authors: Paul W. Denton, Anna Mahr, Maia BennettBoehm. Co-Authors Institutional Affiliations: Univeristy of Nebraska - Omaha, Kansas University Medical School. INBRE

Human CD16, a Fc-gamma-III receptor, binds to the constant fragment (Fc) of IgG (gamma) antibodies and leaves the Fab, or antigen-binding fragment, ends of the antibody free to bind to its specific antigen. An antibody's structure is associated with a Y-shape. The two binding sites at the top of this "Y" are the Fab ends and the singular binding region at the bottom is the Fc end. When one or both the Fab binds to its specific target, the Fc is free to bind to an Fc receptor. This series of bindings is critical for a killing mechanism mediated by human natural killer (NK) cells called antibody-dependent cell-mediated cytotoxicity (ADCC). In NK cell mediated ADCC, an IgG antibody's Fab binds to a pathogenic cell's marker while the Fc binds to a Fc receptor on a NK cell. In the Denton Immunobiology Laboratory, we observed an unexpected circumstance where an immunotherapy drug, a toll-like receptor 9 (TLR9) agonist, reduced CD16 surface levels on NK cells. Due to this reduction, the immunotherapy did not boost the NK cells' ability to perform ADCC as suggested by other research groups in prior publications. In this poster, data will be presented regarding the impact of TLR9 agonism on CD16 expression and how this could be relevant for the use of TLR9 agonism in anti-cancer clinical contexts. The project described was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under Grant # 5P20GM103427.

267. Stacie Deslich, Charleston Area Medical Center Institute for Academic Medicine Health Services and Outcomes Research. **Pulmonary Limitations from Covid-19 and Effects on Robotic Prostatectomy.** Co-Authors: Mary Novak, Samuel Deem. Co-Authors Institutional Affiliations: Charleston Area Medical Center. CTR

Robotic-Assisted Laparoscopic Radical Prostatectomy (RALP) is a commonly performed treatment for prostate cancer however, the steep Trendelenburg position required for the surgery limits the procedure in instances with pulmonary comorbidities. Effects of Covid-19 include inflammation within and around the airways that result in airway constrictive bronchiolitis, leading to persistent dyspnea. The use of steep Trendelenburg position could lead to reduced intraoperative pulmonary compliance and airway edema in those suffering post Covid19 bronchiolitis. Our study aimed to determine risk associated with pulmonary limitations during RALP due to Covid-19. We hypothesized that COVID-19 infection is a risk

factor for pulmonary complications post RALP. This was a retrospective study of patients who underwent RALP with or without a prior Covid-19 infection identified on the TriNetX database from January 16, 2020 to August 29th 2022. TriNetX is a global federated health research network providing access to statistics on electronic medical records. Only aggregated counts and statistical summaries of de-identified information was received. We queried the network to form cohorts of patients who had and had not received a COVID vaccination, and who had and had not had pulmonary complications post RALP. Statistical analysis was performed within the TriNetX enclave. Preliminary analysis indicated that individuals who had a COVID-19 infection prior to RALP had a higher risk of pulmonary complications within 90 days post procedure (RR=2.03, CI 1.64, 2.52). We have demonstrated that COVID-19 infection can lead to pulmonary complications post RALP when the steep Trendelenburg position is used.

268. Analilia Cardenas-Garza, LSU Health Sciences Shreveport. **Glucocorticoids Diminish Estrogen's Cardioprotective Effects in Hypoxia by Reducing Nrf2 Levels and Elevating Oxidative Stress in Female Cardiomyocytes.** Co-Authors: Lesly Rodriguez-Vicens, Xinggui Shen, Christopher G. Kevil, Diana CruzTopete. Co-Authors Institutional Affiliations: Not Listed. COBRE

Heart disease is a leading cause of death among women, with a significant increase in myocardial infarction (MI) incidence observed among young females in recent years. Mental stress is a significant risk factor for both the development and exacerbation of MI in this demographic. However, the precise molecular mechanisms underlying the impact of stress hormones on MI outcomes in premenopausal women remain elusive. This study aims to elucidate potential molecular pathways contributing to the effects of stress on female cardiomyocytes. Building upon recent findings indicating that heightened systemic levels of glucocorticoids, the primary stress hormones, exacerbate MI injury in female hearts by promoting reactive oxygen species synthesis and reducing Nrf2 levels “a key regulator of antioxidant response” in a glucocorticoid receptor (GR)-dependent manner, we hypothesize that glucocorticoids diminish estrogen's regulation of Nrf2 expression levels and antioxidant effects in female cardiomyocytes. To test this hypothesis, we treated mouse cardiomyocytes with estradiol, dexamethasone, a synthetic glucocorticoid specific for GR, or a combination of both hormones while being challenged with periods of hypoxia (1% O2, 16 hours) followed by a period of reoxygenation (6 hours). We assessed cell survival, Nrf2 expression, protein levels, and superoxide production. Our results indicate that combined hormone treatment led to decreased cardiomyocyte survival, reduced Nrf2 levels, and an increase in superoxide production. Our findings shed light on the intricate interplay between stress hormones, estrogen, and oxidative stress in female cardiomyocytes under hypoxia/reoxygenation. This study underscores the importance of understanding these molecular mechanisms to develop targeted therapies for women.

269. Jack Howard Hoen, University of Alaska Anchorage. **Assessing Toxicity of Weathered Microplastics in the Altered Metabolomic State of Bay Mussels (Mytilus trossulus).** Co-Authors: Jack Hoen, Monica Brandhuber, Annette Jarosz, Logan Wieland, Brian DiMento, Maile Branson, Zachary Redman. Co-Authors Institutional Affiliations: Not Listed. INBRE

Microplastics (MPs) are plastic particulates less than five millimeters in size, created through the breakdown of plastic waste and use of plastic materials. In recent years, MPs have become a heavily researched topic as the potential effects to health are coming to light, as well as their prevalence as a pollutant. We created “weathered” MPs by mechanically grinding them down and exposing them to sunlight, and compared them to “pristine”, lab-created MPs. Utilizing Bay Mussels (Mytilus trossulus), an ecologically important species with great potential to bioaccumulate MPs, our aims were to investigate the differential impact of weathered and pristine MPs on the metabolic pathways of Bay Mussels. After exposure to MPs, we dissected the mussels to determine the effect of weathering and particle size on

the uptake and distribution of MPs within the mussels, and identify metabolite biomarkers of MP exposure. Upon analysis, a notable array of metabolite biomarkers were observed, indicating significant alterations in metabolic pathways. Weathered microplastics elicited a more pronounced shift in these pathways compared to pristine microplastics, suggesting a heightened stress response in Bay Mussels when exposed to weathered plastics. As Bay Mussels are a keystone ecological species, the presence of weathered MPs in the environment could contribute to a cascade of negative effects for the ecosystem, and this work reveals a need to better understand how environmental weathering of plastics may influence MP toxicity. Further projects are underway to determine uptake of MPs over time, and distribution within the mussels using a novel Iridiumlabeling analysis.

270. Neishaliz Cotto-Heredia, Pontifical Catholic University of Puerto Rico. **Analysis of SOD1's protein family and mutant SOD1-G93A associated to Amyotrophic lateral sclerosis.** Co-Authors: Ceidy Torres-Ortiz, Luis E. Vázquez-Quiñones. Co-Authors Institutional Affiliations: Pontifical Catholic University of Puerto Rico, Interamerican University of Puerto Rico in Arecibo. INBRE
Over 100 missense mutations in the SOD1 gene have been identified in a subset of familial amyotrophic lateral sclerosis (fALS), a disease characterized by the degeneration of motor neurons. The SOD1 gene codes for the superoxide dismutase 1 (SOD1) enzyme. Mutations in this gene can cause SOD1 to misfold and accumulate into neurotoxic aggregates within cells. Studies suggest that mutant SOD1 proteins can impair the mitophagy process, which is essential for cell viability. Mitophagy is a selective autophagy that targets damaged or dysfunctional mitochondria. Our goal is to identify structural changes upon human SOD1-G93A mutation and label functional mitochondria in yeast cells. We performed a bioinformatic report of human SOD1's protein family and identified the members of the Cu-Zn SOD protein family using classification libraries. We searched for homologous proteins for each member and performed a multiple sequence alignment. We found three fully conserved residues in all 88 sequences: Gly83, Asp84, and Asp125. We identified that residue Gly93, involved in ALS mutation G93A, is highly conserved throughout the protein family. Gly93 has a role in the enzyme's overall structure. Next, we will evaluate the structural motifs related to mutant SOD1 and docking analysis between protein-protein interactions. To evaluate the mitochondrial abundance in yeast strains, we optimized the concentration of Mitotracker Green probe to obtain a specific mitochondrial visualization in fluorescent microscopy. We concluded 15nM of Mitotracker Green allows optimal mitochondria visualization in 1x10 7 Â cells/mL. Investigating how the SOD1-G93A mutation affects mitophagy is essential for understanding the pathological mechanisms underlying ALS.

271. Robyn Kent, OUHSC. **Uncovering bradyzoite heterogeneity in Toxoplasma brain cysts.** Co-Authors: Argenis Arriojas, Bruno Martorelli Di Genova, Kourosh Zarringhalam, Gary Ward. Co-Authors Institutional Affiliations: UMass Boston, UVM. COBRE
The apicomplexan parasite Toxoplasma gondii chronically infects around one third of the global population. Cysts can be found, life long, in the brain, eyes, heart and skeletal muscles of intermediate hosts, including humans. How the parasites survive within these very different tissues and microenvironments is poorly understood. Uncovering the essential and tissue specific components required for survival and host cell manipulation forms the basis of my CoBRE project. Here we show that within a single tissue, the brain, encysted bradyzoites exhibit unexpected heterogeneity. This includes the presence of a bradyzoite specific G1 cell cycle state, multiple routes for cell-cycle progression and variable expression of previously identified canonical bradyzoite proteins and essential cyst wall proteins. This work represents the first step in mapping the essential bradyzoite survival transcriptome allowing survival across these disparate environments.

272. Seetharama D Jois, Louisiana State University. **EGFR dimers in non-small cell lung cancer: Inhibition of dimers by orally available peptides as therapeutic agents.** Co-Authors: Prajesh Shrestha, Vivitri Prasasty, Daniel Billadeau. Co-Authors Institutional Affiliations: Not Listed. INBRE
Human epidermal growth factor receptors (EGFRs) protein overexpression or mutation play a key role in the development as well as resistance to drug therapy in NSCLC therapy. The protein HER2 is known to interact with other EGFRs and form dimers/heteromers. Peptides can be targeted to unique sites on EGFR extraccellular domain and inhibit the protein-protein interactions of EGFR dimers. The goal of the study is to design stable grafted peptides to target protein-protein interactions of EGFRs and modify these grafted peptides for oral bioavailability. A grafted peptidomimetic molecule has been designed that specifically binds to the HER2 protein and inhibits the dimerization of EGFR proteins. Using xenograft model of lung cancer, we have shown that the grafted peptide can suppress the tumor growth in mice when administered orally. To understand the structural aspects of EGFR dimers, we have conducted molecular dynamic (MD) simulations on EGFR heterodimers and proposed a model for binding of the grafted peptide to HER2 protein. The model suggested that the grafted peptide designed binds to C-terminal part of domain IV of EGFR and inhibits EGFR dimers. This research was supported by funding from the National Cancer Institute of the National Institutes of Health, Grant/Award Number: 5R01CA255176-03 (SJ and DB) and Institutional Development Award from the National Institutes of General Medical Sciences of the national Institutes of health under the grant number P20 GM103424.

273. Eryn Matich, University of Arkansas for Medical Sciences. **UAMS Bioanalytical Core.** Co-Authors: Milesh Joseph, Shelbie Stahr, Ashley Lavender, Marjan Boerma, Ping-Ching Hsu. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE
The UAMS Bioanalytical Core serves as an analytical resource for the UAMS research community. The goal of the core is to provide services for the detection and quantification of chemical compounds, elements, and heavy metals in samples. The core houses three liquid chromatography mass spectrometry instruments, including a triple quadrupole mass spectrometer for targeted assays, a single quadrupole mass spectrometer also for targeted analyses, and a quadrupole time of flight mass spectrometer for high resolution analyses. The core also includes an inductively coupled plasma-mass spectrometer for elemental analyses, which can be coupled to a dedicated liquid-chromatography system for speciation. This core is supported by the COBRE Center for Studies of Host Response to Cancer Therapy (Marjan Boerma) and the UAMS Department of Pharmaceutical Sciences (John Imig). The equipment and instruments used for the analysis of small molecules are in Biomedical Research Building II and are managed by Milesh Joseph and Eryn Matich. The equipment and instrumentation for elemental analyses are in the Winthrop P. Rockefeller Cancer Institute and are managed by Shelbie Stahr. Ashley Lavender is the Administration and Billing Manager. Ping-Ching Hsu is the Managing Director (PHsu@uams.edu). Please reach out to us about the core and its capabilities.

274. Michael Shtutman, University of South Carolina. **Functional Genomics Core, University of South Carolina COBRE Center for Targeted Therapeutics and SC INBRE.** Co-Authors: Diego Altomare, Hao (Emily) Ji. Co-Authors Institutional Affiliations: University of South Carolina. COBRE
The Functional Genomics Core (FGC) serves as the research cornerstone for the COBRE Center for Targeted Therapeutics (CTT) at the USC College of Pharmacy. Offering cutting-edge genetic, genomic, transcriptomic, and bioinformatics services, FGC caters to investigators at USC's main and regional campuses and institutions statewide and nationally, including Historically Black Colleges and Universities (HBCUs). FGC's support extends from the initiation of projects and grant applications to the finalization of research papers. The core's personnel collaborates and closely engages with interested investigators, providing comprehensive assistance across the spectrum of modern genetics, genomics,

transcriptomics, and epigenomics methodologies. The FGC is embraced in the promotion of diversity by developing and implementing a minority-inclusive bioinformatics pipeline based on the alignments to the graph-based panhuman genome. The core services included standard RNA-seq service, small and mRNAs library preparation from ultra-low input samples, and detection of circular and lariat RNAs. The FGC performed single-cell RNAseq analysis using a variety of methodologies (10x Genomics, Parse Bioscience, and Fluent Bioscience). The specific focus of the core is the identification of RNAs associated with RNA-binding proteins with crosslinking immunoprecipitation (CLIP) and RNA modification technologies, such as TRIBE (targets of RNA binding proteins identified by editing) and STAMP (surveying targets by APOBEC-mediated profiling). Additional FGC was performed, and analyzed high-throughput screening of CRISPR-cas9 sgRNA and shRNA libraries was analyzed. The core supports high and medium throughput experiments utilizing liquid handling robotics systems.

275. Joseph Yarbrough, University of Delaware. **Modeling Expanding Viral Capsids.** Co-Authors: Caitlyn Zeller, John R. Jungck, Donald Plante. Co-Authors Institutional Affiliations: University of Delaware, University of New Hampshire. INBRE
Viruses often have protein shells known as viral capsids which protect the RNA or DNA found inside. Capsids with icosahedral (20-sided polyhedron) symmetry have been observed expanding and collapsing in a breathing-like motion under certain environmental conditions in order to release their genetic material, and these have been coined as “expandohedra”. Developing macroscopic models for these microscopic organisms is a great way to better understand their function and later reapply these models to concepts beyond virology. What is the best way to model a biotic structure using only abiotic materials while still remaining true to the structure’s nature? Our study is focusing on a particular expandohedron “the icosidodecahedron” which is common among icosahedral capsids. Several different techniques were applied including origami, kirigami, magnets, and simple mechanics, with a preference for models that best demonstrated both structure and function. A jitterbug model, an expanding polyhedron connected by hinges, proved to be the most helpful in illustrating dynamics, while origami and magnets were able to appropriately demonstrate the static forms. The concepts that went into the construction of this jitterbug model could be applied to shapes other than the icosidodecahedron in order to demonstrate the nature of more complex viral capsids. Future models can be made from different materials for better durability and automation. Better understanding the expansion and collapse of these capsids has immediate implications for the field of virology and medicine as a whole. The tensegrity mechanics of these structures could further be applied to architecture, prosthetics, and disaster relief.

276. Allie Conner, University of Maine. **Uncovering Factors Involved in Bacterial-Drug Synergy Against Candida.** Co-Authors: Siham Hattab, Lindsey Stover, Robert Wheeler. Co-Authors Institutional Affiliations: University of Maine. COBRE
The yeast, Candida albicans, and the bacterium, Pseudomonas aeruginosa, are opportunistic pathogens that co-colonize multiple sites within the human host, particularly in the immunocompromised lungs of Cystic Fibrosis (CF) and mechanically ventilated patients. CF patients co-colonized with both C. albicans and P. aeruginosa experience reduced lung function and poorer prognosis. We recently described how P. aeruginosa increases the effectiveness of the antifungal treatment Fluconazole (FLC) both in vitro and during co-infection in a vertebrate zebrafish infection model. We concluded that iron starvation by P. aeruginosa is one important component of this antagonistic interaction; however, it does not account for most of the effect. Here, we report that Pseudomonas-FLC synergy influences the fungal calcineurin pathway, a key fungal virulence factor. Specifically, it leads to a reduction in the translocation of transcription factor crz1 to the nucleus. Reduced translocation of crz1 diminishes the expression of

calcineurin target genes related to fungal virulence. We will also report preliminary results from screening a genome-wide nonredundant library of P. aeruginosa strain PA14 transposon insertion mutants to identify loss-of-synergy mutations. Identification of relevant bacterial pathways involved in Pseudomonas-FLC synergy will expand our knowledge of how bacteria communicate with Candida during co-colonization and infection, as well as provide insight into increasing the effectiveness of clinical treatments.

277. Jared M. Saletin, EP Bradley Hospital. **Bradley Hospital COBRE Center for Sleep and Circadian Rhythms in Child and Adolescent Mental Health: A Sleep and Circadian Methods Research Core in a Child Psychiatry Hospital.** Co-Authors: Alexandros Markowitz, Caroline Gredvig-Ardito, David H. Barker, Mary A. Carskadon. Co-Authors Institutional Affiliations: EP Bradley Hospital, Bradley Hasbro Children's Research Center. COBRE
Introduction: The objective of the Sleep and Circadian Methods Research Core (SCMRC) is to support researchers in the use of multimodal sleep and circadian methods in mental health contexts. We provide multidisciplinary resources focused on all aspects of the research process, from study design, data acquisition, and quality control, to data processing, analysis, and interpretation. We place particular focus on adapting these methods to the demands of mental health research in a pediatric psychiatry hospital. Methods: The aims of the SCMRC are 1) support Center investigators in the selection, acquisition, scoring, analysis, and interpretation of sleep and circadian measures, 2) facilitate access to facilities, instrumentation, software, and database resources, and 3) cultivate current best practices and while identifying methodological, measurement, and analytic advances in sleep and circadian assessments suitable for pediatric mental health populations. Results: To date, the SCMRC has provided 217 research consultations (181 within Bradley Hospital). Additional activities include training workshops, including in child/parent-report sleep dairies, watch/wearable sleep-wake actigraphy, dim-light melatonin assessment, and wearable sleep EEG. Conclusions: The SCMRC's long-term goal is to integrate pediatric sleep and circadian methods into the Bradley Hospital clinical and research infrastructures to create an enduring resource to support research. Our near-term goals involve preparing easy-to-use web-based tutorials and data pipeline examples, publishing refined protocols, collating a library of best practice educational content, and training pediatric mental health clinical faculty in sleep and circadian rhythms science. Clinical Implications: Integrating sleep and mental health research will improve mental health care for youth.

278. Melissa Jauregui, California State University of Fresno. **Fluorescent chalones to study the nematocidal effects of chalcones in Caenorhabditis elegans.** Co-Authors: Eema Quadri, Zoie Gavel, Nayeli Saldaña, Ramakrisha Kandi, Carolynn Chin Arpin, Alejandro Caleron-Urrea. Co-Authors Institutional Affiliations: Not Listed.
Nematodes present a significant challenge to agriculture, resulting in estimated annual losses of $157 billion due to plant parasitic nematodes. While methyl bromide was once widely used as a nematicide, its environmental and health impacts have led to its discontinuation due to its harmful effects on the environment and humans. Alternative nematicides are needed to guarantee food security in an ever increasing world population. Our research focuses on developing eco-friendly alternative nematicides, with a specific interest in chalcones. Chalcone 17 and 30 have shown significant nematicidal characteristics, causing mortality at concentrations as low as 10-5 M. However, the underlying mechanism of their effectiveness remains unclear. We have introduced pyrene into the chalcone structure, creating fluorescent chalcones. These compounds emit light in the UV-Blue spectrum (375-405 nm), allowing for the determination of their accumulation locations before nematode death. Lifespan experiments comparing fluorescent and regular chalcones revealed that Chalcone 17 Fluorescent

outperforms Chalcone 30 Fluorescent in inducing nematode mortality. Worms treated with Chalcone 17 Fluorescent began to die by day 7, with complete mortality by day 25, while those treated with Chalcone 30 Fluorescent began to die by day 10, with complete mortality by day 28. However, using a Lionheart microscope equipped with a DAPI filter (Part number 1225100, EX 377/50 nm, EM 447/60 nm), preliminary findings indicated potential challenges related to nematode autofluorescence and that emitted by fluorescent Chalcones. We are working in a collaboration with ThermoFisher to synthesize a different set of fluorescent chalcones.

279. Micah Penn, University of North Dakota. **Hypoxia upregulates epidermal growth factor receptor (EGFR) expression and phosphorylation in CD133+/CD24+ kidney progenitor cells.** Co-Authors: Seema Somji, Scott Garrett, Sarmad Al-Marsoummi. Co-Authors Institutional Affiliations: University of North Dakota. INBRE

The proximal tubules of the kidney are susceptible to hypoxia which is one of the leading causes of kidney injury. This is due to the high oxygen/energy requirement of the kidney to perform the tubular reabsorption function. The stem/progenitor cells of the kidney can perform the repair function but if the process is inadequate, it can lead to chronic kidney injury and end-stage renal disease. The role of the Epidermal Growth Factor Receptor (EGFR) pathway in kidney injury is not clear with some studies showing that its activation can enhance recovery from acute kidney injury whereas other studies showing that its activation can lead to the development and progression of renal diseases. In this study, we investigated the role of EGFR signaling in renal progenitor cells after hypoxia induced injury. Renal progenitor cells co-expressing CD133+ and CD24+ and non-progenitor cells expressing CD24+ were isolated from the human proximal tubular cell line RPTEC/TERT1. The cells were cultured under hypoxic (2.5% oxygen) or normoxic conditions for two, three, and seven days. RT-qPCR and Western blot were used to analyze mRNA and protein levels. Hypoxia significantly upregulated both the expression and phosphorylation of EGFR. The expression of TGFï•¡, a ligand of EGFR was also increased in the progenitor cells. Knockdown of CD133 upregulated the expression of EGFR and TGF-ï•¡ in the progenitor cells. Our results suggest that activation of the EGFR pathway is a critical response to hypoxic injury and CD133 could function as a negative regulator of EGFR pathway.

280. Alfredo Ghezzi, University of Puerto Rico - Rio Piedras. **Alcohol-induced sleep dysregulation in Drosophila is dependent on the neuropeptide PDF.** Co-Authors: Maria Ramirez, Nicolas Fuenzalida-Uribe, Christian Del Valle, Airined Montes, Miguel Alvarez, Sebastian Morales, Jose L. Agosto. Co-Authors Institutional Affiliations: University of Puerto Rico - Rio Piedras. COBRE

Alcohol exposure is known to trigger homeostatic adaptations in the brain that lead to the development of tolerance and dependence. These adaptations are also believed to be the root of a series of disturbances in sleep patterns that often manifest during the development of alcoholism and can have significant clinical and economic consequences. Unfortunately, the neuronal and genetic pathways that control the effects of alcohol on sleep are currently unknown, thus, limiting our efforts to find effective treatment. In this study, we conduct a mechanistic exploration of the relationships between alcohol and sleep alterations using a Drosophila model system. We show that the genetic manipulation of the ventral lateral neurons (LNv) “a set of neurons known to control sleep in Drosophila” disrupts alcohol sensitivity and tolerance. Moreover, we show that alcohol exposure induces a series of alterations in sleep patterns that last for several days. Our results demonstrate that a single alcohol exposure promotes daytime sleep, alters sleep structure during the night, and reduces morning anticipatory behavior. In addition, we show that some of these alterations are partially dependent on the activity of the neuropeptide PDF, a key element in the regulation of sleep architecture. We propose that alcohol-induced sleep disruption

stems from alterations in the activity of the PDF-releasing LNv neurons and that these alterations are similar to those that produce alcohol tolerance.

281. Ning Liu, Tulane School of Medicine. **Cerebrovascular metabolic dysregulation in obesity-related dementia of females.** Co-Authors: Yinghua Jiang, Yuwen Xiu, Yinjie Wang, Mengxuan Shi, Di Zhou, Aim Niamnud, Winna Wang, Samuel J Vodovoz, Xiaoying Wang. Co-Authors Institutional Affiliations: Not Listed. COBRE

Obesity is linked to a heightened risk of cognitive impairment, particularly in obese women. Due to the obesity epidemic, the associated economic costs, and the increasing aging population, it is imperative to understand the mechanisms underlying obesity-related cognitive decline and develop therapies. There is mounting evidence indicating that the cellular metabolic dysregulation of brain microvascular endothelial cells plays a role in cerebral microvascular dysfunction. This suggests that metabolic disturbances in the cerebral microvasculature induced by obesity may contribute to microvascular dysfunction and cognitive deficits in obese women. To test this hypothesis, we conducted a pilot study to investigate the cellular metabolic alterations within the cerebral microvasculature using LC-MS/MS-based metabolomics and isotope tracing methods in a mouse model of high-fat diet (HFD)-induced obesity. Our initial findings indicate that HFD leads to cognitive decline in 18-month-old (postmenopausal) but not in 8-month-old female mice, and it worsens age-related cerebrovascular metabolic dysregulation in 18-month-old females, but not in males. Furthermore, bulk RNA sequencing analysis of cerebral microvasculature reveals that gene expression related to vascular inflammation and fatty acid synthesis is significantly upregulated in the microvasculature of obese female mice. These results suggest that addressing microvascular metabolic dysregulation might be a viable strategy for preventing and treating dementia in obese women.

282. Stephanie T. Broyles, Pennington Biomedical Research Center. **The Community Research for Optimal Wellness Network (CROWN): Infrastructure to enhance the reach and quality of community engagement in Louisiana.** Co-Authors: Dandra Odom, Jennifer Caldwell, Margarita Echeverri, LaKeisha Williams. Co-Authors Institutional Affiliations: Pennington Biomedical Research Center, Xavier University of Louisiana. CTR

The Community Research for Optimal Wellness Network, or CROWN, is an initiative from the Community Engagement and Outreach (CEO) Core of the Louisiana Clinical and Translational Science (LA CaTS) Center to engage with community members and community organizations across the state of Louisiana. The CROWN network is an infrastructure to enhance the reach and quality of LA CaTS's community engagement. Engagement opportunities distributed through CROWN will be targeted to network members according to the interests they express during enrollment, which range from traditional activities (e.g., â€˜learning about researchâ€™ and â€˜participating in a research studyâ€™) to the more engaged (e.g., â€˜partnering with health researchers to design better or more relevant studies,â€™ â€˜suggesting topics for future research,â€™ or â€˜serving on a community advisory board for a health research studyâ€™). Tailored content distributed through CROWN will range from knowledge-sharing, such as sharing resources for health improvement/wellness and disseminating lay summaries of research results, to capacity-building activities that not only builds community capacity for engaging in research but also allows LA CaTS to meaningfully invest in communities and to build trust. The idea for CROWN was proposed in 2020 by LA CaTS's community advisory boards (CABs) when providing input on new CEO Core activities that would have the greatest impact on community health. From 2020-2024, the CEO Core designed CROWN based on ongoing input from CABs and from an internal CROWN Advisory Group that includes representatives from multiple LA CaTS cores. CROWN will launch Summer 2024.

283. Victoria Barbone, University of Delaware. **A variable single amino acid position in bacteriophage DNA polymerase I affects in vitro enzyme biochemistry and in vivo infection dynamics.** Co-Authors: Barbra D. Ferrell, Rachel A. Keown, Andrew P. Sikkema, Gregory J. S. Lohman, Jeffry J. Fuhrmann, K. Eric Wommack, Shawn W. Polson. Co-Authors Institutional Affiliations: Not Listed. INBRE
Viruses are the most genetically diverse and environmentally abundant biological entities. Two infection strategies impact host communities and ecosystems differently. Lytic infection rapidly lyses the host cell, affecting nutrient cycling and community composition. Temperate infection incorporates viral genomes into the hosts, contributing to gene transfer and affecting host biology. The DNA polymerase I gene (PolA) is carried by ~25% of dsDNA phage and can serve as a marker gene for investigating phage infection types. Variations in the PolA 762 residue (E. coli numbering) correlate with the speed and accuracy of DNA replication in vitro and are distributed disproportionately among different infection types of phage. Three residue variations have been identified at the 762 position: tyrosine, a fast, inaccurate T7 wild type PolA associated with lytic phage; phenylalanine, a slower, more accurate E. coli wild type PolA associated with lytic phage; and leucine, the slowest, most accurate PolA associated with temperate phage. Bioinformatic analysis of metagenomic samples has identified a histidine 762 variant. The life cycle and biochemistry of the histidine variant enzyme is unknown, but we predict that phage carrying this polA will exhibit a temperate lifestyle. In vivo mutagenesis experiments on all four mutant enzymes are being performed to determine infectivity characteristics. Biochemical characterization of the histidine mutant enzyme will identify in vitro replication dynamics. The in vitro and in vivo data will strengthen our genome to phenome hypotheses about PolA-carrying phage and their host and environmental impacts, and predict the infection strategies of viral populations observed.

284. Minu Kesheri, Marshall University. **Deciphering anti-cancer potential of novel cyanobacterial pharmacophores using molecular docking.** Co-Authors: Swarna Kanchan, Travis B. Salisbury. Co-Authors Institutional Affiliations: Not Listed. INBRE
Introduction: Cancer is the second leading cause of death worldwide, after cardiovascular diseases according to the World Health Organization. Survivin is a member of an Inhibitor of Apoptosis Protein (IAP) and is expressed in cells associated with various cancer types. Survivin expression was observed to be minimal in normal tissues and overexpressed in cancerous cells therefore, it can be used as a target for tumor diagnostic/prognostic as well as for anti-cancer therapies. Hypothesis: Survivin protein includes Nterminal BIR (Baculovirus IAP Repeats) domain which is crucial owing to their anti-apoptotic function. Blocking the BIR domain of survivin can prevent the anti-apoptotic activity of the protein especially in cancerous cells. Therefore, we posit molecular docking studies to investigate the cyanobacterial photoprotective compounds as novel pharmacophores that may be potential inhibitors of survivin protein. Results and discussion: Results of molecular docking elucidated that among 16 photoprotective compounds, six compounds exhibited binding energy less than -7.0 kcal/mol, 13 illustrated the binding energy less than -6.0 kcal/mol. Visualization of molecular interaction studies and hydrogen bonding interactions of top two selected photoprotective compounds Scytonemin and Dimethoxyscytonemin against survivin protein binding pocket residues was evident which supports the potential of these two compounds as anti-cancer pharmacophores.

285. Sermin Aras, The University of Southern Mississippi. **Community Outreach Research (COR) Undergraduate Scholars Program: Learning Research at the Heart of Community.** Co-Authors: Jennifer L. Lemacks, Tammy Greer. Co-Authors Institutional Affiliations: The University of Southern Mississippi. INBRE
Cohort-based, experiential research opportunities with a health disparities focus may introduce undergraduate students to research that may be underreached by traditional biomedical programs. The

Community Outreach Research (COR) Scholars program was initially developed with support of an R15 award in 2016 with expanded development supported by MS-INBRE from 2019-2023. The program has shown to improve the scholars' research knowledge (p = .007) and their science-identity (p = .006). Students who completed the program indicated that joining the program influenced their decisions to participate in other research programs, apply for graduate school, and pursue careers in research-related fields. The curriculum has been further developed to support a membership service to minimize the cost and maximize the translation of the program to other institutions in IDeA states. The purpose of this presentation is to describe the development and implementation of COR Scholars program and new membership services. The program includes three components: research, community outreach and professional development. The program curriculum is designed as a 10-week summer intensive program and includes workshops and activities to complete primary research abstract and poster, and outreach activities to engage community in research. The program curriculum also offers activities for soft skills development, including leadership, communication, and other professional skills. Implementation of the COR Scholars program supports building of community outreach research infrastructure by exposing future professionals in the life sciences to community health issues, the role of research

286. Wesley Sumida, University of Hawaii. **Patient and Pharmacist Perspectives on Asking About Social Determinants of Health.** Co-Authors: Agnes Malate Adrienne Dillard Tauasosi-Posiulai, Tina Kimberly Yamauchi Dee-Ann Carpenter Karen Pellegrin Deb Taira Emily Makahi. Co-Authors Institutional Affiliations: Not Listed. CTR
Understanding patients' social determinants of health(SDOH) is crucial as these factors influence health outcomes. The goal of our study was to understand patient and pharmacist perceptions toward having pharmacists ask patients about social determinants of health. Our focus was on Native Hawaiian, Filipino, and Pacific Islander patients in Hawaii, and pharmacists who care for these patients. Three focus groups of Native Hawaiian, Filipino, and Pacific Islander patients with heart disease or diabetes were conducted, along with three focus groups of hospital, retail, and ambulatory pharmacists. Focus group participants were asked about 9 questions from the Family Practice Social Needs Tool. Community feedback were that many of the questions were too personal to be asked by the pharmacist, that pharmacists should focus on medication-related questions, that pharmacists need solutions if they are going to ask the questions, and that the questions might be okay in the context of strong relationship between patient and pharmacist. They also offered suggestions for changing the questions. They also felt the questions would be best asked as a written survey (not verbally). Pharmacists said these questions might be appropriate in the context of an ongoing relationship, that pharmacists should explain the rationale, and that the questions could be softened. They also raised ethical questions about raising these issues if they were not prepared to help and that pharmacists may need to be incentivized to add this to their already busy schedules and that a team based approach might be best.

287. Isaiah Davis, University of South Carolina School of Medicine Columbia. **Combinatorial Therapeutics for Pancreatic ductal adenocarcinoma.** Co-Authors: Karthik Gourishetti, Hannah Taylor Mills, Deepak Bhere. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine. INBRE
Pancreatic adenocarcinoma (PDAC), constituting 3% of US cancers, exhibits a dismal 5-year survival rate below 11%. Despite surgical and conventional treatments, resistance to chemotherapeutics hampers efficacy. Dysregulated microRNA (miR), particularly miR-7, correlates with aggressive PDAC. Investigating a novel approach, our approach combines miR-7 modulation with Herpes Simplex Virus-1 luciferase (HSVLuc). Our approach offers potential breakthroughs in overcoming PDAC treatment resistance and improving patient outcomes. The goal of this study is to evaluate the potential therapeutic synergism with a combinational approach of restoring miR-7 levels through exosomes and HSV-Luc on various

PDAC cells in vitro. We have evaluated the mechanism underlying the effect of the proposed combinatorial approach on various PDAC cells in vitro. We have performed a time-course experiment using two PDAC cell lines: SW 1990, and Hs 766T. Cells were treated with exosomes (exo)-miR-7 followed by varying doses of HSV-Luc. PDAC cell viability was assessed at 24h, 48h, 72h, and 96h post-HSV addition. Mechanisms of the combinatorial approach were evaluated by immunoblotting. Our cell viability studies demonstrated a significant reduction in PDAC cell viability as compared to controls in a dose dependent manner. Further, immunoblotting studies revealed activation of cell death markers together with halting of cell proliferation which contributes to the overall effect on PDAC cell viability. Outcomes from our preliminary studies shed light into the mechanism underlying our proposed therapeutic intervention to target PDAC. Further in vivo studies are warranted to further evaluate the effects on host immunity and its mediated effects on therapeutic efficacy.

288. Naya Habr, The Miriam Hospital / Brown University, Boston University. **Perceptions of newly diagnosed reproductive aged women of color with sleep apnea regarding the healthcare system.** Co-Authors: Melissa Guillen, Rachel Moody, Meghan Sharp, Marian Gonzalez, Kate Guthrie, Ghada Bourjeily. Co-Authors Institutional Affiliations: The Miriam Hospital / Brown University.
Background: Obstructive sleep apnea (OSA) is common in adults but racial differences exist in OSA severity and adherence to therapy. OSA is significantly underdiagnosed and data examining OSA and adherence is limited to older individuals. We examined the perceptions of the healthcare system and management of OSA among reproductive age women of color with a new diagnosis of sleep apnea. Methods: Reproductive age women newly diagnosed with (OSA) and prescribed positive airway pressure (PAP) therapy were interviewed (qualitative, remote, 60-90 minutes) 4-8 weeks following PAP initiation. Questions focused on participants' perception of diagnosis of OSA and their interactions with clinicians, medical equipment providers and healthcare logistics. Thematic analysis was performed. Results: Eight women identifying as Black or Hispanic were interviewed. Patient-Provider Communication: Some participants reported suboptimal communications with providers: lack of understanding of the impact of OSA or PAP, or having their symptoms dismissed, leading to misconceptions that OSA must not be a concerning diagnosis. Trust in health care varied significantly: Many trusted their specialist: "she knows what she's doing", "very kind and informative and felt comfortable asking questions". One participant stated that although she thought her doctor was honest and trustworthy, she did not feel that she could fully trust the science behind medication safety. DME: PAP machines, overall, were a source of stress, confusion and frustration for many; cost was also a significant concern. Conclusion: OSA diagnosis and therapy initiation needs improvement to align impact of OSA on overall health with methods to deliver care in this population.

289. Anatoliy Chornyy, University of Puerto Rico Medical Science Campus. **Assistant of Metabolite Selection in GC-MS Experiments. Basic Application.** Co-Authors: None. INBRE
In metabolic investigations using gas chromatography and mass spectrometry (GC-MS) the process of data preparation requires a significant time and effort due to a large number of metabolites. The software supplied with GC-MS equipment provides a chromatogram and parameters for derivatives, including retention characteristics, height, and name. However, for the statistical analysis it is necessary to create the table of a special format metabolites vs observations, where each entry is an abundance or concentration normalized by some biological entity (number of cells, RNA, etc.). Usually, data preparation for statistical analysis is performed manually. The presented program designed to facilitate this work. The software provides following functionalities: The construction of supporting file system, and templates for parameters and data. Editing of factors, their levels, as well as the generation of maximum number of identities, and the ability for their manipulations. Retrieving metabolite names

from their derivatives, producing the metabolite and derivative lists, and providing tools of their modifications. Selection of metabolite main peaks, calculation of their concentrations, and biological scaling (normalization). The results are presented in two tables for abundance and concentration, convenient for subsequent statistical analysis. The result tables can be saved to the designed file system. There are two format styles, the one is presenting the observation as a row, and the other as a column. The above-mentioned functionalities significantly simplify and accelerate the preparation of initial data for the consequent analysis. Acknowledgment: This research was supported by the NIH/NIGMS-PRINBRE Grant 5P20GM103475.

290. Lily Sabol, Saint Michael's College. **Determining the effects of a patient mutation in moesin on T cell development.** Co-Authors: Lyndsay Avery. Co-Authors Institutional Affiliations: Not Listed. INBRE
Moesin is an actin-binding protein linking the cytoskeleton to the plasma membrane. Cycling between an open and closed conformation, it plays a role in cell shape change and cell migration. The importance of moesin in T cells, specifically, is exemplified by the disease Xlinked Moesin-Associated Immunodeficiency (X-MAID) caused by a single-point mutation (moesinR171W). These patients exhibit profound lymphopenia causing persistent and recurrent, infections, with bone marrow transplant being the only known treatment. Based on characterization of patients and mouse models, T cells with moesinR171W have defects in migration. Because T cell differentiation relies on a functioning cytoskeleton and migration, we hypothesize that this mutation results in the inability of hematopoietic stem cells (HSCs) to properly differentiate to lymphoid progenitors, contributing to patient lymphopenia. In this study we aim to elucidate the effects of the X-MAID mutation on the differentiation of HSCs to T cell progenitors in an in vitro setting. To do this, HSCs from WT and X-MAID mouse bone marrow are isolated and differentiated using FLT3L and IL-7 on an OP9DL1 stromal cell line. We expect fewer T cell progenitors in the X-MAID samples suggesting that the mutation in moesin affects the differentiation process. However, in this reductionist system, it is possible that we don’t observe any significant difference in numbers. This would suggest that migration is the primary defect in XMAID T cell progenitors. The results of this study are critical to understanding the role of moesin in T cell differentiation with clear implications for future therapeutic development.

291. Gavin Brown, Arkansas State University. **Synthesis of novel pyrazole containing compounds as potent antibacterial agents.** Co-Authors: Shailesh Budhathoki, Mohammad A Alam. Co-Authors Institutional Affiliations: Arkansas State University. INBRE
Antimicrobial resistance is a global concern, worsened by the overuse and misuse of antibiotics and the rise of multidrug-resistant bacteria. The COVID-19 pandemic has further strained healthcare systems, leading to an increase in hospital-acquired infections, including carbapenem-resistant Acinetobacter baumannii, multidrug-resistant Pseudomonas aeruginosa, vancomycin-resistant Enterococci (VRE), methicillinresistant Staphylococcus aureus (MRSA), which caused well over 1,000,000 global infections in 2019. This study explores the development of new potential antibiotics, specifically pyrazole containing compounds. The synthetic process involves hydrazone formation, pyrazole formation followed by reductive amination to synthesize the target compounds. The structure of these novel compounds have been established by using nuclear magnetic resonance (NMR) spectroscopy and mass spectrometry. In preliminary antibacterial studies, most of the synthesized compounds inhibited the growth of bacteria with minimum inhibitory concentration values as low as 0.5 μg/mL.

292. Kirsten Dunn, University of Nevada - Las Vegas. **History of Cholesterol Medications Predicts MoCA Scores in a Longitudinal Study of Mild Cognitive Impairment and Alzheimer's Disease.** Co-Authors:

Kaley Brouwers. Co-Authors Institutional Affiliations: Cleveland Clinic Lou Ruvo Center for Brain Health. COBRE
This study investigated whether a history of cholesterol medication predicted Montreal Cognitive Assessment (MoCA) scores among participants. Using a linear mixed model, MoCA scores were analyzed with age, body mass index (BMI), and medication history (cholesterol, metabolic, and thyroid medications) as predictors. Subject ID and visit number were considered, with a specific covariance structure employed. While initial models included interactions, only main effects were significant. Results indicated age as significant, and importantly, a history of cholesterol medications significantly predicted MoCA scores. These findings suggest a potential link between prior use of cholesterol medications and cognitive performance, highlighting the need for further exploration into the cognitive effects of high cholesterol and its potential role in these conditions.

293. Alan E Woessner, University of Arkansas - Fayetteville. **High Resolution Assessments of Cellular Metabolism.** Co-Authors: Timothy Muldoon, Narasimhan Rajaram. Co-Authors Institutional Affiliations: University of Arkansas – Fayetteville. COBRE
The Arkansas Integrative Metabolic Research Center (AIMRC) is a NIH-funded COBRE that was established in March 2021 to study metabolism in cells and tissue. The metabolic imaging and spectroscopy core is one of three research cores that were established as fee-for-service resources in the AIMRC. We will present the technologies and capabilities available within the imaging and spectroscopy core for utilization by university researchers and industry. The core currently houses state-of-the-art multi-photon microscopes that allow high-resolution visualization of cell and tissue structure, function, and biomolecular composition. Twophoton microscopy enables quantification of cellular metabolism through endogenous fluorescence intensity and lifetime of the metabolic coenzymes, NADH and FAD. Additionally, Raman microscopy leverages Stokes and anti-Stokes scattering to provide high-resolution visualization of lipid distributions in cells and tissue. The core also contains a confocal Raman microscope capable of generating high-resolution 3D maps of Raman spectra for characterizing biomolecular distributions within cells and tissue. We also provide access to portable diffuse optical spectrometers that can quantify total hemoglobin concentration and vascular oxygenation in bulk tumors in pre-clinical animal models and accessible tumors in patients.

294. Zumana Noor, Nemours Children's Health. **Combatting Racism in Support of Student Mental Health: Educator Perspectives on Implementation Challenges.** Co-Authors: Tia Barnes, Melissa Stoffers, J.J. Cutuli, Michelle Goodreau, Danika Perry, Kim Graham, Kira Branch, Danielle Hatchimonji. Co-Authors Institutional Affiliations: University of Delaware, Nemours Children’s Health, Delaware State University. COBRE
Racism threatens the mental health of students of color in public education settings. Despite increased attention toward explicitly combatting racism in schools, limited evidence details how to support educators in implementing these practices. A race(ism) conscious adaptation of the Consolidated Framework for Implementation Research (CFIR) offers an approach to identifying barriers and facilitators to combatting racism in schools. We used a semi-structured interview protocol with questions guided by the CFIR to examine educators' perceptions of challenges related to mental health and racial equity practices. We interviewed district leaders (n=2), teachers (n=6), and student support providers (n=4) from a mid-Atlantic state (50% Black; 16% White; 16% Multiracial; 58% Female). Qualitative content and thematic analysis are ongoing, with anticipated completion by April 2024. We identified three preliminary themes. Theme 1: School staff demonstrate ambivalence toward addressing racism, sometimes characterized by helplessness or by a feeling of apathy toward change. Theme 2: Educators feel unsupported in pursuit of racial equity, describing limited time and materials to adjust instruction and

support students' unmet needs (e.g., food, mental health). Theme 3: Educators describe that level of engagement is superficial and combatting racism is treated as a "checklist," with a lack of follow-through from administrators and other staff. This theme also captured perceptions of insufficient attention to recruiting, retaining, and supporting educators of color. If strategies to combat racism are going to be effective in supporting student mental health, schools must cultivate educator buy-in, provide adequate resources, and support meaningful engagement throughout educational systems.

295. Mystera Samuelson, UNMC. **The UNMC Animal Behavior Core: Providing Ethological Support in the Lab.** Co-Authors: None. COBRE

Conducting rigorous and reproducible behavioral and cognitive studies requires thorough training in the field of ethology, which is leveraged in the design of nearly all established laboratory assays involving non-human animal behavior and cognition. Further, the continued development and use of novel rodent strains in biomedical research requires that investigators conduct their own foundational assessments of strain differences to determine behavioral changes, differences in sensory capabilities, and other changes â€" both targeted and unexpected. The UNMC Animal Behavior Core supports investigators in this endeavor by providing access to the specialized procedural space, equipment, software, training, and expertise needed for effective assessments conducted with mice and rats. Offerings include standard and customized cognitive and behavioral assays, as well as telemetric arrays, implantable miniscope, auditory and vestibular testing, bioacoustic assessments, and other physiological assessments used to confirm and support behavioral findings. The UNMC Animal Behavior Core also provides support for behavioral and cognitive assessments involving other species, including nonhuman primates, swine, and others as needed. This work has included, but is not limited to, study design, consulting on the development of customized equipment, as well as support for large animal training to facilitate voluntary participation in assessments.

296. Tyler D. Twedt, Millsaps College. **Pyridine-based HIV Integrase Inhibitors: Side-Chain Development.** Co-Authors: A. Margaret Miller, Christopher T. Bruni, Jacques J. Kessl, Matthew G. Donahue, Wolfgang H. Kramer. Co-Authors Institutional Affiliations: Millsaps College, The University of Southern Mississippi. INBRE

Retroviruses employ three unique enzymes "reverse transcriptase, integrase, and protease" that are essential for their life cycle. Antiviral therapy targets those enzymes, preferably, as fewer side effects are expected. Human immunodeficiency virus (HIV), which can develop into acquired immunodeficiency syndrome (AIDS) if left untreated, is generally combated with triple therapy, consisting of two reverse transcriptase inhibitors and one integrase or protease inhibitor. As the high mutation rate of the virus causes resistance, HIV drugs are constantly optimized. HIV integrase inhibitors are mostly based on aromatic heterocycles such as pyridine and quinoline. This project aims to synthesize new HIV integrase inhibitors based on the pyridine core to interrupt the enzyme's incorporation of the viral DNA into the host cell genome. The heterocycle is generated by reaction of substituted malonic esters with an aminocrotonate ester; this is followed by the extension of the side chain in the 3-position, which consists of a methine carbon carrying a tert-butoxy group and a carboxylic acid. Several methods of the side chain synthesis have been attempted and are discussed, while further incorporation of substituents on the pyridine core will determine the efficiency of the inhibitors. Acknowledgement: This work was supported by the Mississippi INBRE, funded by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM103476.

297. Krystal Ann Hughes, West Virginia University. **Polymeric lipid hybrid nanoparticle allows for precise intracellular drug delivery into B-cell acute lymphocytic leukemia cells.** Co-Authors: Bishal Misra, William Pentz, Werner Geldenhuys, Sharan Bobbala. Co-Authors Institutional Affiliations: West Virginia University. COBRE
Acute lymphocytic leukemia (ALL) is a hematological malignancy caused by abnormal lymphocyte production and overabundance within the bone marrow. Initial remission following chemotherapy is often achievable; however, recurrence is common, and the subsequent chemotherapeutic resistance leads to poor prognoses. This calls for an urgent need to develop novel therapeutic strategies that can precisely deliver small-molecule therapeutics to the leukemic cells and the bone marrow microenvironment, which may help overcome drug-resistant mechanisms. Here, carbohydrate-based pH-responsive acetalated dextran (Ac-Dex) nanoparticles are employed to precisely deliver therapeutics to leukemic cells. In addition, oleic acid (OA), an amphiphilic unsaturated fatty acid, which is notably one of bone marrow's main fatty acid components, was incorporated into nanoparticles for drug accumulation in the bone marrow. We hypothesize that Ac-Dex OA nanoparticles can efficiently transport therapeutics to the bone marrow and release payloads inside the leukemic cells. Ac-Dex OA nanoparticles were monodisperse and inherently non-toxic to cells. These nanoparticles were taken up by B-cell ALL cells in a time-dependent fashion and exhibited a cytosolic release of payloads. These nanoparticles were further validated using a small-molecule ligand of a mitochondrial outer membrane protein (MitoNEET) called NL-1, which has previously demonstrated its anti-leukemic activity in acquired and de novo drug-resistant cells. Lastly, in vivo studies demonstrated an accumulation of nanoparticles in the bone marrow. Taken together, the Ac-Dex OA nanoparticle platform is a promising platform to deliver therapeutics to the bone marrow for the treatment of B-cell ALL.

298. James Van Leuven, University of Idaho. **Bacteriophage resistance evolution in a honey bee pathogen.** Co-Authors: Tuan Phan. Co-Authors Institutional Affiliations: University of Idaho. COBRE
For the past century bacteriophages were sporadically used to treat bacterial infections in humans. Despite this long history, the widespread adoption of phage therapy has not occurred. Among the barriers hindering the use of bacteriophages (phages) as therapeutics is a gap in understanding of how and in what conditions bacteria will evolve resistance, especially in the context of an animal microbiome. Utilizing honey bees as an animal model system, we investigated the evolution of phage resistance in the bee pathogen, Paenibacillus larvae. This pathogen can quickly evolve resistance to several different phages on agar plates. Among the mutations conferring resistance is a possible receptor protein. Resistance to one type of phage often provides cross-resistance to closely related phages, but not more distantly related ones. However, there are notable exceptions to this generalization. Phage resistance does not so readily evolve in liquid culture and is only observed at certain host and phage densities. We model phage-host dynamics with a series of ordinary differential equations to try and understand the conditions in which resistance arises and test for phenotypic effects of resistance in honey bees.

299. Jay DeLoriea, Coastal Carolina University. **Using a Drosophila melanogaster model to create high throughput populations for drug screens.** Co-Authors: Cassandra Millet-Boureima, Chiara Gamberi. Co-Authors Institutional Affiliations: McGill University Health Centre, Coastal Carolina University. INBRE
The fruit fly Drosophila melanogaster is an established model to study how genes function in human disease and screen for genetic and chemical modifiers to influence new therapeutics. Our lab has modeled Polycystic Kidney Disease (PKD) in the Bicaudal C (BicC) mutants and TANGO2 deficiency disease (TDD) in TANGO2 mutants. Both models were successfully used to test prototype drugs with a tailored, controlled, fly testing pipeline. We identified several cyst-reducing molecules including rapamycin, mimics of the second mitochondria-derived activator of caspases (Smac) and melatonin. TDD

flies showed reduced pathological phenotypes when supplemented with vitamin B5. A newer drug administration method, capillary feeding, may help to minimize drug use and be suited for testing molecules synthesized in analytical scale in drug development efforts. Aiming to compare drug administration protocols in fly disease models for reliable drug activity testing, we use a robust pipeline to generate large populations of testing flies of reliable quality. Sterile BicC flies were generated through genetic crossing of BicC heterozygotes and selected on the base of their phenotype. Stable TANGO2[G517] and control wild type Ore[R] flies were cultured in controlled conditions. Drug administration through food supplementation in different culture scales was used to test molecules for cyst-reduction, negative geotaxis assays, survival and perform timelines and dose-response assays. The capillary feeding method was also used in survival studies. Consistent culturing and administration protocols are critical to obtaining reproducible results and sustain medium to high throughput assays in pharmacological studies using Drosophila pathological models.

300. Paula Andrea Medina Diaz, Geisel School of Medicine at Dartmouth. **Sunburn Susceptibility and Its Role in Early Melanoma Development.** Co-Authors: Margaret Karagas. Co-Authors Institutional Affiliations: Geisel School of Medicine at Dartmouth. COBRE
This study examines the association between children's skin reactions to their first exposure to strong sunlight during summer and the prevalence of nevi, which are considered precursors to melanoma. Utilizing data from the New Hampshire Birth Cohort Study, researchers investigated the impact of sunburn, categorized by reactions to one hour of unprotected sunlight exposure, on the occurrence and size of nevi. The primary outcomes were the counts of children with nevi larger than 2mm but not exceeding 5mm and those with nevi 5mm or larger. We analyze the relationship between sunburn reactions and nevi presence and size using logistic and multinomial regression models adjusting for confounders. The analysis of 151 children aged 3.5 years revealed a significant correlation between severe sunburns with blistering or peeling and increased nevi size of 2mm or greater, as opposed to reactions that led to tanning without sunburn. Notably, children exhibiting larger nevi were more likely to have blond hair and blue eyes. The findings suggest a tendency to sunburn may increase children's risk of nevi, which may represent melanoma precursor lesions. The study's limitations include its small sample size. Further work using a larger sample size will be conducted. Future observational studies will aim to deepen the understanding of the relationship between sunburn exposure and melanoma development.

301. Van A. Doze, University of North Dakota. **INBRE Behavioral Research Core Facility at the University of North Dakota: Infrastructure and Advanced Equipment for Behavioral Phenotyping in Rodents.** Co-Authors: Chris W.D. Jurgens, Don A. Sens, Ellen M. Olson. Co-Authors Institutional Affiliations: University of North Dakota School of Medicine & Health Sciences. INBRE
The Behavioral Research Core Facility (BRCF) at the University of North Dakota School of Medicine & Health Sciences is a state-of-the art facility where investigators can conduct behavioral phenotyping for both mice and rats. The BRCF is located in the basement of Columbia Hall .The facility consists of multiple rooms, which are directly accessible from the institution’s animal facility. These rooms include four testing rooms which allow simultaneous usage of the facility by multiple research groups. Three rooms are designated for mice and one room for rats. The rat behavior suite is located within the Center for Biomedical Research. The BRCF has 25 different pieces of specialized equipment and offers over 30 different behavioral tests. Available tests include models of attention, learning and memory, anxiety, depression, locomotor activity and coordination, food intake, and metabolic measures. There is also a tissue preparation room and a surgical suite with stereotaxic instruments and an adjacent vivarium room for housing. The BRCF is a fullservice core managed by Senior Research Specialist, Ellen Olson.

The facility is supported in part by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM103442. The BRCF aims to promote research productivity and improve STEM training in behavioral science by providing for the following needs: Wellmanaged and maintained equipment; Methodological and technical expertise; Training in behavioral testing and analysis; an Interface for interaction of researchers to facilitate collaborations.

302. Matthew Rizzo, University of Nebraska Medical Center. **Large language model tools to enhance public understanding and access to national clinical trials.** Co-Authors: Bill Lynch, Kati Cordts, Joan Severson. Co-Authors Institutional Affiliations: CTO HumanTrue, University of Nebraska Medical Center. CTR

Health literacy underpins access to healthcare, ground-breaking treatments available via clinical trials, and better health outcomes for all. ClinicalTrials.gov is a premier national public resource for recruitment into clinical trials, where content complexity may deter persons with lower health literacy. This obstacle is reinforced by disparities in technology access and use associated with age, economic status, rurality, and distrust of complex content. The consequence is underrepresentation of diverse populations, which critically hinders the reach, generalizability, and effectiveness of needed national research, and the overall NIH mission. Our overarching goal is to enhance patient-centered communication for greater public access to national clinical trials. For this purpose, we implemented a novel AI platform and patient-facing application that uses a fine-tuned large language model (LLM). This transforms dense medical narrative and terminology of ClinicalTrials.gov into plain language that can be understood by persons with a sixth-grade reading level. A user-friendly conversational interface provides real-time personalized support to clarify study protocols, and address user question, expectations, and needs. Ongoing usability testing with diverse user groups is refining the LLM's assimilation of complex trial narratives, translation of content to comprehensible language for potential subject consideration, tool acceptability, and ready interface use. This includes interactive real-time voice cues, embedded graphics, mobile applications, integration with tools for eConsent, chatbots, and "co-pilots" for institutional review board (IRB) documentation. This integrated approach offers to enhance accessibility of national clinical trials information, engage underrepresented groups, advance public health through more inclusive research practices, and democratize understanding of clinical trials for a broader audience.

303. Sweta Mahato, West Virginia University. **COVID-19 Perceived Threat and Vaccine Uptake Association Differs by Gender and Age Among Rural Adults with Chronic Diseases: Results from A Community-Based COVID-19 Educational Intervention.** Co-Authors: Ranjita Misra. Co-Authors Institutional Affiliations: West Virginia University. Higher perceived threat is associated with higher COVID-19 vaccine uptake. Hence, health communication messaging interventions use threat appeal as an effective strategy for increasing vaccine uptake. Yet, none have explored this association disaggregated by age or gender among adults. This study examines if age or gender moderates the association between perceived threat and COVID-19 vaccine uptake in rural adults with chronic diseases. Participants comprised of a convenience sample of rural adults living with chronic conditions (n=2117) who received a brief educational intervention delivered by trained Health Navigators (HNs). The COVID-19 educational intervention included watching brief videos addressing their vaccine concerns, followed by survey data collection. Binary logistic regression analysis was conducted to examine the differences by age and gender on the relationship between perceived threat and vaccine uptake controlling for education, race, employment, multimorbidity. Participants were grouped as 1) unvaccinated or primary series only, and 2) vaccinated with primary series along with 1-2 boosters. Mean age of the participants was 41.8 Â±17.8

years and 58% were female. Association of perceived threat and vaccine uptake was significantly moderated by gender (p=0.002) and age group (p=0.014). Controlling for multimorbidity, age, race, education, employment in the model, the strength of association was stronger in men (OR=1.11, p

304. Horrick Sharma, Southwestern Oklahoma State University. **Synthesis and biological characterization of novel ldha inhibitors against pancreatic cancer.** Co-Authors: Somrita Mondal, Landon, Santa-Pinter, Colter Esparza, Madalyn White, Lerin Luckett-Chastain, Anne Cooper, Pragya Sharma, Scott Lovell, Michael A. Ihnat, Surendra K. Shukla. Co-Authors Institutional Affiliations: Southwestern Oklahoma State University, University of Oklahoma Health Sciences Center, The University of Kansas, OU Health Stephenson Cancer Centre. INBRE
Cancer cells differ from normal cells by up-regulating glycolysis and glucose uptake and converting pyruvate to lactate even in the presence of oxygen (Warburg effect). Despite having functional mitochondria, cancer cells reprogram their metabolism from oxidative phosphorylation to aerobic glycolysis for survival and growth. Lactate dehydrogenases (LDH) mediate the Warburg effect and convert pyruvate to lactate, producing NAD+, which drives glycolysis for ATP production. Lactate dehydrogenase-A (LDHA) is the major isoform of LDH that is overexpressed and linked to poor survival in many cancers, including pancreatic ductal adenocarcinoma (PDAC). We performed virtual screening of a large database of 15 million compounds and carried out hit to lead efforts to discover a new class of LDHA inhibitors comprising a novel succinic acid monoamide chemotype. The lead compounds exhibit good binding affinity, and the cocrystal structures showed that the compounds bind to an allosteric site on LDHA. The two most potent compounds, 4 and 5, demonstrated potent inhibition of LDHA with IC50 of 46 nM and 72 nM, respectively. Lead compounds inhibit lactate production and glycolysis in pancreatic cancer MIA PaCa-2 cells. Compounds 4 and 5 inhibited the proliferation of human pancreatic cancer cell lines and patient-derived 3D pancreatic cancer organoids. Compounds 4 and 5 demonstrated favorable pharmacokinetics with up to 73% oral bioavailability and a cumulative half-life of 4.5 h. The efficacy and toxicity of compounds are being evaluated in preclinical models of pancreatic cancer. These compounds could be further developed into a drug-like lead that targets metabolic reprogramming and lactate production in PDAC.

305. Tyler McGaughey, West Virginia Clinical and Translational Sciences Institute. **WVCTSI Biomedical Imaging Core.** Co-Authors: None. CTR
The WVCTSI Biomedical Imaging Core is a new service offered by our CTR. These services aid clinicians and researchers alike in developing translation research projects. Our group provides a wide variety of services such as; medical imaging data pulls directly from the medical record, HIPAA safe-harbor complaint deidentification with crosswalk maintenance, image processing services, study design consultation, manuscript preparations, data analysis services, high-performance computing assistance, medical model creation, data curation services, grant writing assistance, and a variety of trainings.

306. Abby Bolt, University of Delaware. **Novel PI3P-binding Legionella pneumophila effector proteins target degradative host compartments.** Co-Authors: Ramona Neunuebel. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Phosphoinositide (PIP) lipids are integral regulators of eukaryotic membrane trafficking acting as molecular beacons that recruit and activate protein complexes. The seven PIP species are each specifically enriched on distinct cellular membrane compartments and play a key role in defining membrane identity. Recently, PIPs have emerged as a target of bacterial pathogens that exploit host membranes. The intracellular pathogen, Legionella pneumophila, infects and proliferates within lung macrophages. During infection, Legionella secretes over 300 effector proteins into the host cell allowing

the pathogen to establish a replication permissive compartment. Previous studies revealed a growing number of these effectors bind host PIPs. We believe Legionella effectors utilize PIP-binding to target host membrane compartments, which can be used as a molecular handle to identify effectors that manipulate host membranes. Here we employed a three-pronged approach to identify and validate novel PIP-binding effectors. First, we screened an E. coli expression library of His-tagged effectors using lipid-coated beads followed by mass spectrometry. Subsequently, we used protein-lipid overlay assays with purified PIP-binding candidates and examined their intracellular colocalization with PIP-biosensors. We identified and validated 27 novel PIP-binding effectors. Remarkably, the majority of these bound PI3P and displayed a preference for PI3P-positive membranes. We are currently uncovering which PI3P compartments are targeted by each PI3P-binder. PI3P is enriched on endocytic and autophagic membranes, the exact degradative compartments Legionella is trying to avoid. These results indicate that the newly identified PI3P-binding effectors directly target detrimental compartments to facilitate Legionella's ability to avoid degradation and survive intracellularly.

307. Emma Foley, Creighton University. **Characterizing the role of a mutant PCNA protein in nucleosome assembly.** Co-Authors: Lynne Dieckman. Co-Authors Institutional Affiliations: Creighton University. INBRE

When a cell divides, its genome must be replicated and passed on to the next generation of cells. During replication, newly synthesized DNA is organized into nucleosomes, the fundamental units of chromatin. Proliferating cellular nuclear antigen (PCNA) and chromatin assembly factor 1 (CAF-1) are two proteins required for this process. The interaction between PCNA and CAF-1 is essential for nucleosome assembly to occur. However, the mechanism of this interaction is not well understood. Our lab has discovered an amino acid in PCNA, R44, that resides in a potential novel interaction site for CAF-1. I performed protein-protein binding studies between R44A PCNA and CAF-1 or other PCNA-interacting proteins and determined that the R44A mutation results in increased binding in some but not all PCNA-binding proteins. These studies provide insight into a potentially inhibitory role of R44 in PCNA, which highlights the importance of this residue in the maintenance of DNA organization and genome stability.

308. Ryan Mortenson, Southcentral Foundation. **Developing and Implementing a Culturally-Centered Advance Care Planning Initiative for the Alaska Tribal Health System.** Co-Authors: Rona Johnson, Chris Piromalli, Rajinder Sigh, Christina Fieldhouse, Jennifer Shaw. Co-Authors Institutional Affiliations: Southcentral Foundation, University of Arkansas for Medical Sciences, University of Alaska Fairbanks. INBRE

Introduction: Advance care planning (ACP) and advance directives (ADs) can improve health outcomes among seriously ill patients and their families. Alaska Native and American Indian (ANAI) people have lower rates of ACP than the general population. A quality improvement initiative in the Alaska Tribal Health System (ATHS) developed culturally-centered resources for ACP among ANAI adults with serious illnesses and their caregivers. Methods: Healthcare experts and patients collaborated to plan ACP initiative activities. Providers completed needs assessment surveys while patients provided feedback on ACP materials through focus groups to ensure cultural acceptability and relevance. These data were used to inform ACP resource development and refinement. Results: This initiative developed ACP resources for 160,000 ANAI patients and caregivers in 12 Alaska regions, including a culturally-centered AD guide, education modules, trainings, and workflows for healthcare personnel. A public relations campaign raised ACP awareness. Electronic health record (E.H.R.) was modified to store and retrieve ACP documents, and integrated quality metrics for measuring effectiveness. A pilot of the new materials in one primary care clinic resulted in an increase from 30% of documented ADs in the E.H.R. among patients age 40. The materials were implemented in all primary care clinics in Anchorage after the pilot.

Conclusion: Culturally-centered ACP resources are highly needed and acceptable among ANAI adults with serious illness and their caregivers. This initiative increased ACP utilization among ANAI patients in Alaska and provides a model for health systems aiming to increase ACP engagement and health equity among ANAI and other populations.

309. Cindy Nguyen, University of Hawaii at Hilo. **Mitotic Protein Expression in Eukaryotic Cells.** Co-Authors: Harrison Maurus, Brianna Bratt, Adam Thatcher, Sinni Vo, Li Tao. Co-Authors Institutional Affiliations: University of Hawaii at Hilo. INBRE
Mitosis is a cell division process where a single cell divides into two identical daughter cells. Mitotic errors can result in multiple diseases, including cancer, which makes cytokinesis a crucial step. Cytokinesis serves as the final stage for error correction during cell division. Centralspindlin, an essential protein complex composed of RacGAP and Kinesin-6, regulates this pivotal stage of mitosis. To elucidate the functions of centralspindlin, efficient expression of this protein complex is imperative. However, the active full-length centralspindlin complex has never been expressed due to the large molecular mass and difficulty in isolating the active form of centralspindlin from the E.coli expression system. Our lab uses the baculovirus expression system and insect cell culture to express this full-length protein for further studies into its function. Our hypothesis posits that the combination of insect cell culture and baculovirus expression can express the active full-length protein complex. In this study, we clone Kinesin-6 and RacGAP genes into baculovirus and use the recombinant baculovirus to infect SF9 cells. The protein was purified through Ni-NTA affinity chromatography. In vitro, motility assay demonstrated that this protein is active by translocating microtubules using energy from ATP hydrolysis. Our results validate the hypothesis, demonstrating the successful expression of centralspindlin through the baculovirus expression system. The successful expression of centralspindlin paves the way for further investigations into its functional roles in mitosis and its regulation in cancer biology.

310. Ranjita Misra, West Virginia University. **Diabetes Retinopathy and Diabetic Macular Edema in Rural Patients with Diabetes.** Co-Authors: Joel Palko, Annahita Amireskandari, Prashnna Gyawali, Vishvanathan Ramamurthy, Carol Laxson, Co-Authors Institutional Affiliations: Not Listed. COBRE
Background: West Virginia (WV), an entirely Appalachian state, ranks 1st nationally in the prevalence of diabetes (16.3%). Diabetic retinopathy (DR) and diabetic macular edema (DME) disproportionately impacts rural adults with diabetes, a leading cause of preventable blindness. This study explored screening, follow up and predictors of DR/DME in rural WV patients. Methods: Using data from the statewide teleophthalmology program that included fundus images, we examined the number of patients with suspected DR/DME at the primary care clinics that followed-up with retina specialists for confirmation of DR/DME at the West Virginia University (WVU) Eye Institute. Results: Participants included 2756 rural adults with fundus image. Mean age was 61.5 Â± 13 years. Preliminary screening for patients with at least one gradable eye suggested 289 patients (12.4%) were suspected with DR/DME at the primary care clinics. However, 152 patients (53%) had a follow-up visit with retina specialists. Two-third of these patients (n=100) were confirmed to have DR/DME. Predictors of DR/DME in the binomial logistic regression analysis showed patients with type 2 diabetes (OR=3.14; p=0.02) and high HbA1c (OR=1.15; p=0.016) had higher odds of confirmed DR/DME. Age, diabetes duration and having gradable fundus image approached significance (p

311. Samuel Lawton Evans, Presbyterian College. **Impacts of Dietary Iron on Taxonomic Composition and Function of Zebrafish Gut Microbiome.** Co-Authors: Stuart Gordon. Co-Authors Institutional Affiliations: Not Listed. INBRE

A.healthy gut microbiota is essential to promote host health and well-being, and it plays a crucial role in the gastrointestinal tract. As this system often serves as a major route of infection, it is important to investigate the effects of dietary components on the gut microbiome. Iron, an essential component of heme and ironsulfur proteins, plays a central role in many biological activities, including oxygen transport and cellular respiration. In particular, the iron homeostasis system is one of the best characterized due to iron's causative relationship with iron-deficiency anemia. Dietary iron supplementation is a commonly used treatment for iron deficiency anemia; however, the known direct impacts of iron on the gut microbiome functional potential remain limited. In the present study, using Zebrafish (Danio rerio) as a model organism, we sought to determine if increases in dietary iron would cause changes in taxonomic composition and gut microbiome function. Based on our analysis, an increase in dietary iron significantly altered the zebrafish microbiome taxonomic composition with specific increases in Firmicutes and Proteobacteria. Analysis of taxa for functional potential suggested that iron enriches physiological functions such as aerobic respiration. In addition, gas chromatography mass spectrometry and liquid chromatography mass spectrometry were utilized to measure primary metabolites and lipids, respectively. Among analyzed primary metabolites, a significant increase in amino acids was observed when iron levels were increased. However, there was no significant change within the lipid data when dietary iron was altered.

312. Sam Freeman, University of Delaware. **Brain-mimetic PEG-based hydrogels induces dormancy in brain metastatic triple negative breast cancer.** Co-Authors: John Slater. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Tumor dormancy is regulated by many mechanisms including extracellular matrix (ECM) composition and degradability. Disseminated tumor cells (DTCs) can enter dormancy and remain there for months to decades before reactivation and new tumor formation. Colonization of the brain by breast cancer DTCs is difficult to treat effectively and severely reduces the patient’s duration and quality of life. Recapitulating the brain microenvironment in vitro is a critical step in advancing our understanding of how organ-specific ECM contributes to dormancy. We implemented brain-mimetic hydrogel formulations by tuning the adhesive peptides and degradability of poly(ethylene glycol) (PEG) based hydrogels. To quantify the impact of these formulations, we utilized two cell lines, the aggressive breast cancer cell line, MDA-MB-231 (P231), and a brain-homing sub line, MDA-MB-231-BrM2a-831 (BrM2a). These cells were encapsulated for 15 days in five, PEG-based hydrogel formulations composed of proteolytically degradable PEG, either a generic or brain mimetic adhesive peptide formulation, and the non-degradable comonomer N-vinyl pyrrolidone. These formulations compose three classes of gels, a permissive formulation which is highly degradable and adhesive, a degradation restricted formulation which is less degradable but still adhesive, and adhesion restricted formulation which is highly degradable but non-adhesive. Within the brain mimetic degradation restricted gels, BrM2as show higher viability and lower proliferation compared to the generic degradation restricted gels and P231s show increased viability in the generic degradation restricted gels. These data indicate the brain-homing BrM2a cells survive better and proliferate less when subjected to the brain mimetic formulation and induce a dormant phenotype as may be seen in vivo.

313. Elisabet Borsheim, Arkansas Children's Research Institute. **Metabolism and Bioenergetics Core: Services in Stable Isotope Methodologies.** Co-Authors: Craig Porter, Matthew Cotter. Co-Authors Institutional Affiliations: Arkansas Children’s Research Institute. COBRE
The Metabolism and Bioenergetics Core (MBC) is part of the COBRE-funded Center for Childhood Obesity Prevention (CCOP) at Arkansas Children’s Research Institute. The MBC aims to support research focused on the role of substrate metabolism and bioenergetics, especially as it pertains to the development,

treatment, and prevention of obesity, and to train investigators in key methodological approaches used to quantify metabolism and bioenergetics. The services provided by the MBC can be broadly grouped into three areas of focus: stable isotope technologies, bioenergetics, and clinical chemistry. A unique aspect of the MBC is the ability to support users in the application of stable isotope techniques to compute metabolic fluxes and substrate turnover rates in vivo. This allows the direct determination of various metabolic processes, e.g., energy expenditure, protein, fat, and/or carbohydrate metabolism. We provide services in the planning and execution of protocols using stable isotope methodology in preclinical and human studies, including participants in free-living conditions. Further, the MBC performs analyses of stable isotope enrichment in blood, tissue, urine, saliva, and breath samples using both mass and IR laser spectrometry. The Core offers an annual Metabolism and Bioenergetics Core Seminar Series in "Quantifying Metabolism and Bioenergetics: Basic Principles to Application" which includes an introduction to stable isotopes in metabolic research; considerations and applications, including quantifying glucose, protein, and lipid metabolism and metabolic rate. For accessing services, interested parties can submit service requests through provided forms. Preliminary service request:https://base.uams.edu/redcap/surveys/index.php?s=LNK39HJTNX. Service request form: https://base.uams.edu/redcap/surveys/index.php?s=HPREKRXRMR. Supported by NIH/NIGMS P20 GM109096.

314. Damien Parrello, University of North Dakota. **UND Genomics Core: Sequencing Excellence and Analysis Empowerment.** Co-Authors: Santosh Bhatt, Michael Hill, Sara Faraji Jalal Apostal, Sarah Johnson. Co-Authors Institutional Affiliations: Oracle, University of North Dakota. COBRE
The University of North Dakota (UND) Genomics Core provides a large panel of sequencing services, along with an innovative cloud-based bioinformatics platform. The UND Genomics Core offers a diverse set of sequencing technologies from Nanopore, Illumina, 10X, NanoString and AtlasXomics. Leveraging these technologies, the Core provides various sequencing services including bulk, single-cell or spatial RNA-seq & ATAC-seq, methylation analysis, targeted and whole genome sequencing. Understanding the growing need of the great majority of biologists to independently analyze genomics data, the UND Genomics Core has developed an innovative bioinformatics platform, genomEX, in collaboration with our partner Oracle Corporation. This platform provides fully personalized (adjustable CPU/GPU numbers & memory/storage capacity), dedicated (resources available 24/7 without any queue) and customizable (users have administrator rights) cloud-based high-performance computing environments. With Oracle-powered built-in security features and compliance certifications, users can securely work with their data. GenomEX offers a full range of one-click pipelines, from RNA-seq to genome assembly, all accessible and editable as needed. Providing admin privileges, genomEX is not limited in its offerings and can be expanded to accommodate any project specifically. Last but not least, Oracle enables genomEX to offer unbeatable pricing. Through the combined expertise of Oracle and the UND Genomics Core, genomEX emerges as a powerful and unique bioinformatics platform, providing every biologist with the freedom to explore genomics data independently, regardless of their coding proficiency. Overall, the UND Genomics Core is a center of excellence where stateof-the-art technologies cutting-edge ideas converge to advance the field of genomics.

315. Zhaojie Zhang, University of Wyoming. **Challenges and Strategies of Running a Successful Imaging Core in the Wild West.** Co-Authors: None. COBRE
The Integrated Microscopy Core (IMC) at University of Wyoming (UW) is part of the Wyoming Sensory Biology COBRE (WSBC). The IMC provides services in microscopy imaging to the research community, from fluorescence, confocal, two-photon to electron microscopy. Because of the unique geographic location, imaging cores in the wild west like Wyoming face unique challenges. Cores must be creative

and strategic to meet the challenges. Wyoming is the least populated state in the US with less people than the state of Alaska; and UW is the only four-year research university in the state. One of the challenges is to bring in the most advanced imaging technology to the “middle of nowhere”. Thanks to the COBRE and INBRE grants, we are able to secure funding to bring new imaging instruments to the Core. In recent years we have expanded the IMC to include instruments for molecular and genomics analysis, such as the 10X genomics, Illumina sequencer and Merscope. We organize workshops and seminars to bring in experts from around the world to educate ourselves with new technology. Another challenge we often face is to train students, especially undergraduate students, who have no previous experience and knowledge, in using our advanced instruments. We learned that we must be creative in explaining various techniques using “simple” terms and use multiple media to assist the training. Staff shortage is a challenge to many cores. With limited staff and multiple types of equipment, the core staff must be willing to learn and become “experts” on “everything”.

316. Kaitlyn Bailey, West Liberty University. **The Characterization of Antimicrobial Compounds Extracted from Rhus typhina.** Co-Authors: Reagan Gray, Joseph Horzempa. Co-Authors Institutional Affiliations: West Liberty University. INBRE
Rhus typhina, a plant native to eastern North America, has previously been discovered to exhibit antibacterial activity against various ESKAPE pathogens including Staphylococcus aureus and Acinetobacter baumannii. The purpose of this work is to examine the therapeutic potential of compounds extracted from a crude extract of Rhus typhina leaves on A.baumannii and S.aureus. Both bacteria are major causes of nosocomial infections due to their ability to resist multiple antibiotics. As multi-drug resistance becomes more prevalent, there is a growing demand for research on new therapeutic agents. Supporting previous unpublished research from our laboratory, the data here suggest that ethanolic extracts of R.typhina contain compounds that exhibit antibacterial capabilities against both S. aureus and A. baumannii. Ongoing studies are focusing on determining the structure of the antimicrobial chemicals and the mode of action of these compounds.

317. Grace Kim, Louisiana Health Sciences Center New Orleans. **Approximating Clinical Severity of Influenza Infection for the 27 Most Common HLA Class I Alleles During the 2024-2025 Flu Season.** Co-Authors: Lucio Miele, Judy Crabtree. Co-Authors Institutional Affiliations: LSUHSC. CTR
Based on the World Health Organization’s recommendations, the trivalent egg-based Influenza vaccine for the 2024-2025 season is composed of a 2022 (H1N1)pdm09-like virus, a 2022 (H3N2)-like virus, and a 2021 (B/Victoria lineage)-like virus. However, it remains unclear how CD8+ T cell epitope diversity is affected by newer influenza strains on both an individual and epidemiological level. We believe differences mediated by variations in Influenza Hemagglutinin (HA) and host HLA alleles may affect the clinical severity of Influenza infection in vaccinated individuals during the 2024-2025 season. We utilized a bioinformatic pipeline previously validated on SARS-CoV-2. MHC-I epitope binding predictions were determined through the Immune Epitope Database and Analysis Resource, TepiTool, utilizing the recommended default prediction for the 27 most frequent MHC Class I alleles. CD8+ T cell epitope repertoires of the trivalent influenza were compared against epitopes of 6 Influenza strains sequenced between Feb 2023-2024 in the District of Columbia and uploaded to the GISAID EpiFlu database. The 6 viruses, two (H1N1)pdm09-like viruses, two (H3N2)-like viruses, and two (B/Victoria linease)-like viruses, were selected to reflect the genetic drift seen in trivalent specific clades during 2023 and 2024. Our analysis found CD8+ epitope conservation to be estimated at 82.2-82.9% for (H1N1)pdm09-like viruses, 87.3-94.2% for (H3N2)-like, and 94-98.5% for (B/Victoria lineage)-like viruses. HLA-A*01:01, -A*11:01, and -B*44:03 are estimated to have the worst clinical outcomes for (H1N1) pdm09-like, (H3N2)-like, and (B/Victoria lineage)-like viruses respectively. Protective effects are estimated for HLA-B*53:01 for

(H1N1)pdm09-like, -A*23:01/-A*24:02 for (H3N2)-like, and -A*68:02 for (B/Victoria lineage)-like Influenza clades.

318. Deborah Ith, University of Montana. **Decreasing Mental Health Disparities Through Co-Creating Culturally Responsive SEL Programs.** Co-Authors: Jingjing Sun, Jaida Lilly, Anna Reszewicz, Anisa Goforth. Co-Authors Institutional Affiliations: University of Montana. INBRE
Indigenous American children experience significant mental health disparities and barriers to mental health care (Center for Native American Youth, 2019). Mental health prevention through social-emotional learning (SEL) that is universally embedded within schools (Colizzi et al., 2020; Taylor et al., 2017) and is culturally responsive for Indigenous communities (Jagers et al., 2019) is an especially effective way to reduce barriers while tapping into the strengths and resources within communities. This presentation highlights the process of co-adapting a SEL program for K-2nd grade students through community advisory board (CAB) meetings that included researchers, educators, and Indigenous community members (N = 7). Seventeen lessons were developed to teach five core values (resilience, responsibility, reverence, respect, and reciprocity) using Indigenous ways of teaching. Preliminary results showed the power of having multiple voices within the cocreation of the SEL program. This is highlighted by an expression of gratitude made by an Indigenous CAB member who noticed that both Indigenous and non-Indigenous members of the CAB were no longer using Western terminology and had "adopted the cultural value words as ways of talking about the lessons." Overall, given the lack of research on culturally responsive SEL in Indigenous communities, this presentation provides specific approaches to culturally responsive adaptations of mental health prevention programs for Indigenous communities. Our ultimate goal was to enhance mental health outcomes and reduce health disparities for children in a Tribal Nation through co-creating culturally responsive programs within their own communities as a means of reducing barriers to preventive mental health care.

319. Megan Brozik, Black Hills State University. **Evaluation of Alkene Selectivity with Olefin Metathesis-Based Fluorescent Detectors.** Co-Authors: Koni Hamilton, Katrina Jensen, Brian Michel. Co-Authors Institutional Affiliations: Dakota Wesleyan University, Black Hills State University, University of Denver. INBRE
Ethylene is the simplest alkene, which is an organic compound with a carbon-carbon double bond. Ethylene is a plant hormone that signals ripening. As a clear, odorless gas, ethylene is hard to detect, but monitoring ethylene levels is helpful in the shipment of foods and for further research of cellular processes involved in ripening. In previous studies, our collaborators developed a sensor that fluoresces in the presence of ethylene through an olefin metathesis reaction. Unfortunately, this sensor is not selective for ethylene, but also reacts with other alkenes. Our goal is to synthesis different alkenes to test the reactivity with two different sensors and modify the sensors to improve the selectivity for ethylene. The alkene compounds were synthesized under a nitrogen atmosphere and purified using column chromatography. Proton and carbon NMR spectra were collected and analyzed to confirm the structure and purity of each compound. The structure of each synthesized alkene was confirmed using nuclear magnetic resonance by analyzing the chemical shift, integrations, and peaks observed. By using the synthesized alkenes, we can test the selectivity and reactivity of the two sensors using a fluorimeter to measure how fast each alkene reacts with the sensor by quantifying the fluorescence. We hope to understand what structural changes can be made to develop a more selective sensor for ethylene.

320. Edna Acosta Perez, University of Puerto Rico - CTR Hispanic Alliance. **Importance of community participation & engagement in research.** Co-Authors: Jose Rodriguez Orengo, Marizaida Sanchez

Cesareo, Loyda Mendez Torres, Yari Valle, Yashira M. Sanchez Colon, Mayra L. Roubert Rivera. Co-Authors Institutional Affiliations: INBRE-PR, CTR- IDEA Alliance. INBRE
The long-term collaboration between the Puerto Rico INBRE and the Hispanic Alliance for Clinical and Translational Research have been able to expand the multi-sectorial coordination to address the impacts of social, economic injustice, and structural disparities on health by focusing on community health priorities and integrating sectors. We have focused on three main activities: 1) catalyze and support meaningful Community-Academic Partnerships ; 2) updated community need assessments for the development of health priorities and action plans, and 3) maximize capacity building and training opportunities for students, researchers, and community members. We expect to stimulate the interest of researchers to address the primary health needs identified and to support Community-Academic Partnerships with mentoring, education, and dissemination.

321. Kylie Hall, University of Pikeville. **Efficient Production of Serine Proteases Using Plant Transient Expression Systems: A Sustainable Alternative to CHO Cell Cultures.** Co-Authors: Savannah McKendree, Laikin Tackett, Russell Goins, Kevin Wang. Co-Authors Institutional Affiliations: University of Pikeville. INBRE
Abstract: Producing proteases in CHO cells can be problematic due to the degradation of essential cellular proteins and the product itself, leading to reduced yield and cell viability, and compromising product quality and stability. In contrast, our research has utilized plant transient systems for producing serine proteases, capitalizing on their safety, cost-effectiveness, scalability, and rapid production capabilities. The inherent resistance of plants to protease activity contributes to higher yields and supports an environmentally sustainable method. Within just four days after agroinfiltration treatment, we successfully expressed various serine proteases, including t-PA, lumbrokinase, and Nattokinase, in plant-based system. These plant-derived serine proteases were functional and demonstrated the ability to dissolve fibrin and blood clots effectively. Our results indicate that transient expression in plants offers a feasible and efficient alternative for the production of serine proteases.

322. Sherri Kelly Davis, West Virginia Clinical and Translational Science Institute. **Using Data Visualizations to Drive Clinical Study Performance.** Co-Authors: Connie Cerullo, Shelley Welch. Co-Authors Institutional Affiliations: West Virginia Clinical and Translational Science Institute. CTR
Beginning in September of 2021, the West Virginia Clinical and Translational Science Institute began its tenure as the hub managing site for 13 clinical study cohort sites across the United States, as they participated in the RECOVER study. The RECOVER observational study is designed to take an in-depth look at the long-term effects of COVID. This study aimed to recruit many participants in a short period of time from rural and medically underserved populations during a pandemic and follow those subjects with multiple and sometimes invasive tests for up to four years. A series of reporting tools were developed by the West Virginia University RECOVER study team using Tableau and REDCap. The tools were designed to monitor recruitment, retention, additional triggered test completion, and data completeness. These visualizations were shared with the hub cohort sites regularly. The data visualizations developed helped to maximize efficiency by directing staff effort where data missingness or trends in data entry errors were observed. Review of the enrollment and retention dashboards allowed sites to share recruitment experiences and retention strategies and challenges. Viewing participation trends in additional tests identified targeted trouble areas where resources and support should be directed. These data-based views allowed the hub to proactively address common issues in clinical study implementation and to maintain a high level of data awareness and integrity. Data visualization can be used to improve real-time awareness of study challenges, expedite enrollment,

reduce data errors, and ultimately improve the quality, quantity, and speed with which data are collected.

323. A. Jerrod Anzalone, University of Nebraska Medical Center. **Building a Collaborative Ecosystem Across the IDeA-CTR Networks in Response to a Public Health Emergency.** Co-Authors: Sharon Patrick, Amber Abel, Brad Price, Sally Hodder. Co-Authors Institutional Affiliations: West Virginia University. CTR
The COVID-19 pandemic highlighted the urgent need for collaborative responses to public health crises, leading to the creation of the National COVID Cohort Collaborative (N3C). The N3C Institutional Development Award (IDeA) Clinical and Translational Research Centers (CTRs) Consortium was pivotal in advancing COVID-19 research. Employing a sociotechnical model significantly improved research productivity by enhancing data sharing, investigator engagement, community outreach, and resource pooling, laying a foundation for future collaborative efforts. This model, grounded in shared governance, includes a governance committee and two main workstreams: operations and Navigation, Education, Analysis, and Training (NEAT). Operations focus on data management and regulatory compliance, while NEAT supports educational, analytical, and navigational initiatives. Emphasizing collaborative culture, inclusive decision-making, and equitable resource distribution, this approach has enhanced COVID-19 research efficiency and reach. The consortium's participatory method fostered a collaborative ecosystem that addresses pandemic challenges and sets a blueprint for future public health emergencies. Promoting interdisciplinary collaboration and utilizing shared data and resources has significantly advanced data driven research and improved health outcomes for underrepresented and medically underserved populations. The socio-technical model's success showcases its scalability and adaptability for collaborative research across health domains, cutting down the original text while retaining the essence of the consortium's impact and methodology.

324. Gian DePamphilis, Butler Hospital. **Serum malondialdehyde (MDA) levels following repetitive transcranial magnetic stimulation (rTMS) in patients with treatment resistant depression (TRD).** Co-Authors: Andrew M. Fukuda, Linda L. Carpenter. Co-Authors Institutional Affiliations: McLean Hospital, Butler Hospital | Warren Alpert Medical School. COBRE
Repetitive transcranial magnetic stimulation (rTMS) is an effective treatment option for treatment resistant depression (TRD); however, the full effects of rTMS are still being elucidated. Recent advancements have suggested that an imbalance in reactive oxygen species (ROS) play a role in the pathogenesis of depression, but limited evidence exists exploring the relationship between ROS and rTMS. As ROS are highly reactive and unstable, lipid peroxidation byproducts such as malondialdehyde (MDA) are often used to quantify oxidative stress. The current research sought to investigate changes in oxidative stress by examining MDA serum levels before and after a course of rTMS. Venous blood samples were drawn at baseline and follow-up for sixteen patients with TRD. Pre and post MDA serum levels were measured using lipid peroxidation assays and depression severity was assessed using the Inventory for Depressive Symptomatology, Self-Report (IDS-SR). Independent sample t-tests indicated that there were no significant differences in MDA percent change from pre to post rTMS between non-responders (M = 3.42%, SD = 33.43%) and responders (M = 1.48%, SD = 34.80%) or between remitters (M = -10.3%, SD = 24.63%) and non-remitters (M = 8.42%, SD = 35.48%) of the IDS-SR ($t(14) = .113$, $p = .911$; $t(14) = 1.06$, $p=.307$). Current results indicate that MDA serum levels/lipid peroxidation do not play a role in the efficacy of rTMS. However, MDA is but just one component of the pathological cascade involving ROS and analysis of other molecules are also underway.

325. Nicholas Todd Johnson, Kentucky Wesleyan College. **Development of Novel 3D-Bioprinted L. rh Containing Silicone Catheters to Treat Catheter Associated Urinary Tract Infections.** Co-Authors:

Anthony Kyser, Mohamed Mahmoud, Hermann Frieboes. Co-Authors Institutional Affiliations: University of Louisville. INBRE
Catheter Associated Urinary Tract Infections (CAUTIs) are a serious threat in healthcare. A study by Vicki Parker et al explains that roughly 1.7% of patients catheterized for a minimum of 48 hours contract a UTI. Antibiotics are a possible treatment for CAUTIs, but their use increases risk of antibiotic resistance. Alternatively, using probiotics, pathogenic bacteria can be outcompeted, safeguarding the urinary microbiome. Probiotics, such as Lactobacillus rhamnosus, provide a healthy microbiome through release of antimicrobials and a decrease in pH. L. rh-silicone bioink was bioprinted and cured for 24 hours at 50° C to replicate response of a 12 fr female foley catheter. Scaffold integrity and pH response was evaluated in artificial urine media (AUM) for 14 days. Cross sections of scaffolds were imaged under scanning electron microscope (SEM) to demonstrate probiotic viability and proliferation. Scaffold swelling with respect to initial mass had shown a 15% total increase. The pH had shown a decrease to 3.5 by 4 day corresponding to less pathogenic bacteria. Images provide evidence of sustained viability through day 7.

326. Denise Giuvelis, University of New England. **Unleashing the Potential of UNE's Rodent Behavior Core.** Co-Authors: Tamara King, Ian Meng. Co-Authors Institutional Affiliations: University of New England. COBRE
The rodent behavior core is located within the Center for Pain Research at the University of New England (UNE). We provide a comprehensive approach of rodent behavior services for UNE researchers and the external research community. The core offers the highest level of expertise, training, and instrumentation for behavioral analyses in rodents. We offer a variety of models and measures commonly used in the research setting including general behavioral phenotyping, neurobehavioral tests, and in vivo drug screening. The core also provides in-house validation of cutting-edge models of pain and relevant co-morbidities to advance the pain field and early-stage drug discovery. We also perform sample collection for ex vivo analyses by our inhouse histology and imaging or cell signaling cores or that can be shipped for analyses to external cores offering proteomic and genomic services. The core offers training to UNE students, professional staff, and faculty on any of our services and equipment. Lastly, we provide a non-credit bearing badge program that digitally validates and documents knowledge, skill sets, qualifications, and competencies that can be shared with prospective employers, or graduate schools. The core is currently funded by NIGMS grant number P30GM145497, PI-Meng.

327. Craig Porter, Arkansas Children's Research Institute**. Development of rodent metabolic and behavioral phenotyping service at Arkansas Children's Research Institute.** Co-Authors: Elisabet Borsheim. Co-Authors Institutional Affiliations: Arkansas Children's Research Institute. COBRE
Laboratory rodents are widely used as model organisms for human disease. In order to support reproducibility and to ensure the translational value of preclinical rodent models, it is essential that researchers have access to state-of-the-art rodent metabolic phenotyping platforms that provide critical physiological data on their rodents models. We leveraged a NIGMS administrative supplement to acquire a multiplexed rodent metabolic phenotyping platform that utilizes indirect calorimetry and real-time behavioral monitoring to determine total energy expenditure and its components in rodents. This system is housed within environmental cabinets that allow for parameters such as temperature and light intensity and cycle to be tightly control. We have employed this system to support COBRE investigators in demonstrating the significant metabolic impact of transitioning mice from standard (24Â°C) to thermoneutral (30Â°C) housing temperatures. We have also supported various COBRE, NIH and USDA funded investigators in developing and refining rodent models to study the impact of early life stress on offspring health, the efficacy of anti-obesity strategies, and the metabolic stress response to burn

trauma. In providing state-of-the-art rodent metabolic phenotyping services, we have enhanced the impact of several NIGMS funded research programs. By developing a charge back system for this core, our future goals are to make these services more broadly available to research colleagues in the IDeA State network.

328. Chalisa Longden, Northeastern State University**. Constructing a Novel Human Cell Line Harboring POLE1 Patient Mutations Using CRISPR-Cas9.** Co-Authors: Matthew Girard. Co-Authors Institutional Affiliations: Not Listed. INBRE

Polymerase Epsilon is an enzyme responsible for leading-strand synthesis during DNA replication. Mutations of the catalytic subunit, POLE1, have been implicated in connection with a disease causing facial dysmorphism, immunodeficiency, livedo, and short stature (FILS). Specifically, a single base pair substitution in intron 34 of POLE1 results in a truncated protein that causes impairment of T lymphocyte proliferation from G1 to S-phase. To better understand the mechanisms behind these pathogenic mutations, we are constructing a novel cell line that mimics the FILS patient mutations. However, because POLE is an essential gene, the novel HEK293T cell line will be created by knocking in a gene containing a POLE1-FILS mutation to the genome at the AAVS1 safe harbor site using CRISPR-Cas9. The transgene knock-in kit selected uses a pAAVS1-puro-DNR plasmid that contains AAVS1 homologous arms, puromycin resistance, and Myc-DDK tags. We have successfully cloned the POLE1 gene with FILS mutations into the pAAVS1-puroDNR plasmid. Ligation was confirmed via DNA sequencing and mutant protein expression by Western blot. HEK293T cells were co-transfected with the pAAVS1-POLE1-FILS-puro-DNR donor and pCas-Guide-AAVS1 plasmids. This was followed by several rounds of passaging and puromycin selection. In the future, limiting dilution and tissue direct PCR will be used to isolate individual colonies and select positive clones, respectively. Data from these experiments will be discussed at the meeting. Construction of this stable cell line promises insights into FILS pathology, as well as deciphering DNA replication and repair mechanisms crucial for the formulation of therapeutic strategies.

329. James C. Walton, West Virginia University. **West Virginia University Stroke CoBRE Rodent Behavior Core.** Co-Authors: Terri J. Poling, Randy J. Nelson, James W. Simpkins, A. Courtney DeVries. Co-Authors Institutional Affiliations: West Virginia University. COBRE

The Rodent Behavior Core (RBC) at West Virginia University assists in conducting functional assessments of rodents to enhance understanding of neurological diseases and other disorders, and to elucidate possible therapeutic interventions. We coordinate with the WVU Experimental Stroke Core to perform functional analyses during recovery from experimental stroke. Additionally, RBC equipment is available to all WVU researchers for the evaluation of rodents across functional domains including addiction, affective behaviors, cognition, sensorimotor function/skilled movement, nociception, and social behaviors. In addition to housing and maintaining general and specialized behavioral testing equipment, the RBC offers other services to facilitate behavioral research, including expert consultation on experimental design and task selection, individualized training in behavioral methods, assistance in grant and manuscript writing, assistance with animal use protocols, and statistical analysis of behavioral data. We maintain video tracking systems and high throughput automated testing equipment covering multiple behavioral domains to enhance rigor and reproducibility in the behavioral data generated in the core. Furthermore, we are actively integrating in vivo imaging technologies into our behavioral tasks to provide state of the art behavioral testing to our users. The Rodent Behavior Core at West Virginia University is supported by the National Institute of General Medical Sciences, P20 GM109098. The content of this poster is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.

330. Lacey L. Knudsen, MaineHealth Institute for Research. **Adenosine deaminase activity in plasma elevates in patients with poor outcomes after cardiac arrest.** Co-Authors: Joanne T. deKay, Jonathan Rud, Mary Sorcher, Christine Lord, Meghan Searight, Teresa L. May, Douglas B. Sawyer, Richard R. Riker, Sergey Ryzhov, David B. Seder. Co-Authors Institutional Affiliations: MaineHealth Institute for Research, MaineGeneral, Maine Medical Center. COBRE
Cardiac arrest (CA) is a leading cause of mortality and morbidity worldwide. Inflammation caused by the immune response after CA causes damage to cardiac tissues which may lead to poor survivorship outcomes. Adenosine deaminase (ADA) is an enzyme that decreases the levels adenosine, an antiinflammatory and immunosuppressive nucleotide. It is present in humans in two isoforms, ADA1 and ADA2. The role of ADA after cardiac injury has not been explored. We hypothesize that increased ADA activity after CA may be associated with poor outcomes in patients resuscitated after CA. In this study, we investigated ADA activity in 38 CA patients after return to spontaneous circulation (ROSC). Platelet-free plasma was obtained from whole blood samples via double centrifugation and ADA activity was measured using an ADA enzymatic activity kit. ADA isoforms were isolated using Pentostatin and EHNA inhibitors for total ADA and ADA1 activity. Our data demonstrated that ADA activity increases in the acute inflammatory phase after CA in patients with poor outcomes and stays elevated for 48 hours after CA. Isoform activity results reveal an increase in ADA1 activity 6 hours after ROSC and no change in ADA2 activity. Additionally, our research revealed a correlation between ADA1 activity and adenosine concentration. These data suggest that the isoform ADA1 may play a role in the progression of post-cardiac arrest syndrome and secondary tissue damage after cardiac arrest. Results from this study provide rationale for further investigation into the effect of ADA inhibition after CA.

331. Jessica J. Johnson, University of Alaska Fairbanks. **Developing a biomarker of animal protein intake using plasma carbon and nitrogen isotope ratio in a controlled feeding study of postmenopausal women.** Co-Authors: Shirley A. A. Beresford, Charles B. Eaton, Ying Huang, Johanna W. Lampe, Simin Liu, Sandi L. Navarro, Marian L. Neuhouser, Ross L. Prentice, Patricia M. Rivera, Thomas Rohan, Lesley F. Tinker, Sowmya Vasan, Cheng Zheng, Diane M. O'Brien. Co-Authors Institutional Affiliations: University of Washington, Brown University, Fred Hutchinson Cancer Center, University of Alaska Fairbanks, Albert Einstein College of Medicine, University of Nebraska Medical Center. INBRE
Dietary biomarkers help address measurement errors associated with self-reported intake when estimating specific diet-disease relationships. Our objective was to develop a biomarker model for animal protein intake using carbon and nitrogen stable isotope ratios (CIR and NIR) to investigate the relationship between protein source (animal vs. plant) and chronic disease risk among postmenopausal women. The Nutrition and Physical Activity Assessment Study Feeding Study (NPAAS-FS), an ancillary study of the Women's Health Initiative (WHI), was a 2-week controlled feeding study, approximating usual intake, in Seattle, WA. We measured CIR and NIR in post-feeding plasma samples from participants (n = 153) who completed the study. We calculated Pearson correlations between plasma CIR and NIR and intakes of animal protein (g/d), plant protein (g/d), and animal protein ratio (APR, animal/total protein). We modeled these intakes using a stepwise selection of CIR, NIR, and participant characteristics and assessed model performance using leave-one-out cross-validation (LOOCV). Biomarker models were considered valid with a LOOCV-R2 â‰¥ 0.36. Plasma CIR and NIR were most highly correlated with APR (r = 0.59, P

332. Thomas Palys, Dartmouth Geisel School Medicine. **The COBRE Center of Molecular Epidemiology Biorepository Core at Dartmouth: Comprehensive support for diverse and large-scale research.** Co-Authors: Brock Christensen, Michael Passarelli, Margaret Karagas. Co-Authors Institutional Affiliations: Geisel School of Medicine Dartmouth. COBRE

The COBRE Center for Molecular Epidemiology Biorepository Core at the Geisel School of Medicine at Dartmouth utilizes a combination of manual and robotic specimen processes and automated archival storage systems to provide support to members of the Dartmouth community and beyond. The Core performs an array of services including specimen fractionation (e.g., of blood and breastmilk), processing of a wide range of biologic samples (e.g., urine, stool, nail, teeth, hair, saliva), human and microbial nucleic acid extraction, tissue separation and fixation, as well as post-archival processing and referral management services. Since its inception in 2013, the Core has handled >400,000 aliquots, created about 300,000 aliquots and maintained a highly secure, annotated archive of >600,000 diverse specimens. The Biorepository Core capabilities are well positioned to fully support large and diverse studies that integrate genetic, epigenetic, metabolomic, metagenomic, metallomic, and a broad range of other analyses. The Core has provided comprehensive support for large scale collaborative cohort and population-based cancer studies such as the New Hampshire Birth Cohort Study, New England Bladder Cancer Study, the New Hampshire Health Study, the Vitamin D and Calcium Polyp Prevention Study and the national Environmental influences on Child Health Outcomes Program. Additionally, the Core supports COBRE projects and pilot studies, and is leveraged by trainees as well as early-staged investigators and more senior investigators to launch innovative research studies that lead to discoveries on the drivers of human health over the life course.

333. Julio Cesar Hernandez, University of Puerto Rico. **Fusing Scientific Expertise to Redefine Food Security Assessment.** Co-Authors: Meredith Niles, Jennifer Laurent, Maria Nazario, Winna Rivera, Myrna Comas, Alicia Barriga, Gary Stein, Evangelia Morou-Bermudez, Clifford Rosen, Carlos Luciano. Co-Authors Institutional Affiliations: University of Vermont, University of Puerto Rico, MaineHealth Institute for Research. CTR

A collaborative initiative of the NNE-CTR and the Hispanic Alliance for Clinical & Translational Research aims to develop a program to address shared regional challenges of nutrition/food insecurity in Vermont and Puerto Rico. Food security is a social determinant of health/health equity that disproportionately affects racial and ethnic minorities, older, low-income and rural households. In Vermont and Puerto Rico, the many unique and shared food security challenges include disparities related to transportation, rural regionality, older populations, and climate change. Food security, achieved through four pillars (availability, access, utilization, and stability), is currently only measured within the U.S. by considering economic access to food, despite the other barriers to food security. Data on food security does not currently exist in Puerto Rico, limiting understanding of food security and solutions. Building upon years of food security research and reciprocal experiences in their respective regions, this program utilizes a team science approach, bringing together interdisciplinary, cross-cultural researchers to: 1) develop and validate an integrated food security assessment tool that considers monetary and non-monetary ways of acquiring food and assess multiple dimensions of food security across cross-cultural contexts; and 2) establish and strengthen an interdisciplinary, multi-cultural scientific team well-trained and equipped to assess and address food insecurity across all dimensions in diverse cultural contexts in the future. This work is critical to developing a more comprehensive food security assessment tool that measures all four dimensions of food security and will create the baseline for future studies and data collection in both regions and beyond.

334. Sergey Tsibulnikov, MaineHealth Institute for Research. **The absence of ErbB3 receptors on endothelial cells increases myocardial fibrosis in remote myocardium after infarction.** Co-Authors: Lacey Knudsen, Elena Chepurko, Vadim Chepurko, Joanne T. deKay, Douglas B. Sawyer, Sergey Ryzhov. Co-Authors Institutional Affiliations: Not Listed. COBRE

Experimental studies demonstrated that ligand-specific stimulation of ErbB receptor signaling in endothelial cells (EC) increases survival and proliferation, activates angiogenesis, and controls paracrine signaling to promote cardiac repair. The ErbB family includes four receptors, ErbB1 - ErbB4. The expression of ErbB3 on EC in the heart varies significantly in humans. Little is known about the role of ErbB3 signaling in EC. We generated a tamoxifen-inducible mouse model with a knockout of ErbB3 in EC (ErbB3EC/KO). To determine the role of ErbB3 in EC, we induced myocardial infarction (MI) in these mice. We compared cardiac function and myocardial infarction size in ErbB3EC/KO mice versus control animals (ErbB3EC/WT) after MI. The mice were generated using ERT2/Cdh5 Cre and ErbB3fl/fl mice. The absence of ErbB3 on EC in ErbB3fl/fl/Cdh5 cre+ mice (ErbB3EC/KO) and the presence of ErbB3 at the cell surface of EC in control ErbB3wt/Cdh5 cre+ animals (ErbB3EC/WT) were confirmed using flow cytometry analysis. The cardiac injury was induced by ligation of the left coronary artery. Echocardiography was performed in unsedated mice using a VisualSonics Vevo 2100 imaging system. Immunohistochemistry analysis was done using the Masson trichrome staining. Quantification of infarction size was performed using ImageJ software. Normally distributed variables are expressed as mean Â± SEM. Comparisons between multiple groups were performed using ordinary one-way ANOVA with Tukey's multiple-comparisons post-test. No differences were found in heart function and scar size. However, significantly increased fibrosis was found in the remote area of the myocardium of the ErbB3EC/KO compared to the control ErbB3EC/WT animals.

335. Pradip Kumar Jaiswara, University of Oklahoma Health Sciences Center. **Targeting ROS homeostasis to overcome therapeutic resistance in pancreatic cancer.** Co-Authors: Surendra Kumar Shukla, Ravi Thakur. Co-Authors Institutional Affiliations: Not Listed. INBRE
According to the American Cancer Society, pancreatic cancer accounts for about 3% of cancer cases and 7% of cancer-related deaths. Pancreatic ductal adenocarcinoma (PDAC) represents about 95% of pancreatic cancer and is the leading cause of cancer-related death with a dismal mortality rate. The high lethality in pancreatic cancer is partly due to the acquired therapeutic resistance of pancreatic tumors toward most chemotherapeutic agents. Pancreatic tumors exhibit a wide range of metabolic and physiological adaptations, including altered reactive oxygen species (ROS) homeostasis, which plays a significant role in the therapeutic response of chemotherapies. We have developed an in vitro acquired chemotherapeutic resistance cell model by serial exposure of FOLFIRINOX components (5-Fluorouracil, Irinotecan, Oxaliplatin) to pancreatic cancer cell lines. We observed that therapy resistance cell lines exhibit reduced levels of ROS, and exposure of chemotherapeutic agents to these cells results in differential response to ROS alterations. We also observed an altered bioenergetic profile of therapy-resistant cells compared to wild-type cells. Further, we observed increased BACH1 expression in resistant cell lines compared to wild-type cells. BACH1 is a crucial transcription factor, a member of the Cap'n'Collar type of basic region leucine zipper transcription factor family, and plays a very important role in ROS regulation in different types of cells. Our results demonstrate that pharmacological or genetic targeting of BACH1 leads to improved sensitivity of pancreatic cancer cells toward the chemotherapeutic agents. Overall, our results demonstrate that altered ROS homeostasis in pancreatic cancer cells leads to poor sensitivity toward chemotherapeutic agents, and targeting key ROS regulator BACH1 can overcome therapeutic resistance.

336. Evan Falkenthal, University of Nevada Las Vegas. **Scholarly Impact of COBRE Publications Through Medical Subject Heading Analysis.** Co-Authors: Kristine Bragg Zizza, Hannah Williams, Jon Hilpert, Gwen Marchand. Co-Authors Institutional Affiliations: University of Nevada Las Vegas. COBRE
The Centers of Biomedical Research Excellence (CoBRE) award program supports the development of innovative biomedical research infrastructure in geographical areas that have traditionally received less

federal funding. Evaluating the scholarly output as a consequence of this program is a necessary part of ensuring continuing support. However, the literature indicates that evaluation of the CoBRE program has been neglected by researchers in several areas, including scholarly impact of funded research. The Entrez Programming Utilities (E-utilities) provide a stable access point into the Entrez database system, which includes access to the biomedical literature produced by CoBREs published in Pubmed. Bibliometric evaluation of CoBRE publications can be performed at scale by building tools to interact with E-utilities, and standard lexicons of keywords from the Medical Subject Headings (MeSH) applied to works in Pubmed allow for scholarly impact evaluation that could assist CoBREs in determining impactful topics. Our work has developed tools in the programming language R that allow for: 1. The ingestion of XML data output from the E-utilities system into a local, normalized data structure and 2. Analytical tools based on this data structure that allow for scholarly impact evaluation, such as MeSH term analysis. Visualizations of mean differences based on sets of keywords between CoBREs and the broader literature will be displayed.

337. Mona Batish, University of Delaware. **Identifying the regulation of circular RNA expression in human iPSC-derived cardiac fibroblasts.** Co-Authors: Brigette Romero, Trevor Burleigh, Visnu Pritom Chowdhury, Vijay Parashar, Chi Keung Lam. Co-Authors Institutional Affiliations: University of Delaware. COBRE

Cardiovascular disease (CVD) maintains its status as the leading global cause of mortality. Circular RNAs (circRNAs) have captured considerable attention due to their pivotal roles in both the physiological and pathological processes of various CVDs. Recent findings emphasize the essential role circRNAs may play in the context of cardiovascular injury and repair. CircRNAs possess inherent resistance to exonucleases and exhibit longer lifespans compared to their linear counterparts, making them promising candidates for disease biomarkers or targets for therapeutic interventions. Our objective is to identify changes in the expression of circular RNAs through the process of differentiation and when cardiac fibroblasts are treated with tyrosine kinase inhibitors (TKIs). TKIs operate by disrupting ATP (adenosine triphosphate) pathways, thereby inhibiting cell proliferation and growth. Cardiac fibroblasts were cultured and exposed to varying concentrations of TKIs. Subsequently, total RNA was extracted from both treated and untreated samples, and the expression levels of four circRNAs, circNFIX, circZNF609, circHIPK3, and circPVT1, were determined by qRT-PCR. All four circRNAs showed temporally dysregulated expression upon differentiation of human iPSCs. CircZNF609, circHIPK3, and circPVT1 showed increased enrichment into extracellular vesicles with increasing time of differentiation, indicating that these circRNAs may play a role in cell-cell communication. Additionally, we found that all four circRNAs exhibited dose-dependent differential expression patterns following treatment with TKI indicating their involvement in the pathways affected by the drugs. Future work is planned to understand the mechanism of action of these circRNAs to elucidate their role in the development and differentiation of cardiac cells.

338. Jonathan Hilpert, University of Nevada Las Vegas. **NIGMS COBRE Evaluation: Infrastructure development, mentorship of junior investigators, and scientific knowledge production.** Co-Authors: Judith Weber, Gwen Marchand, Kristine Bragg-Zizza. Co-Authors Institutional Affiliations: ACRI, UNLV. COBRE

The NIGMS COBRE funding initiative supports establishment of state-of-the-art biomedical and behavioral research centers in IDeA-eligible states. Evaluation of COBRE centers is critical because it provides information about the extent to which NIGMS funds have advanced the development of research infrastructure and knowledge production that can serve underfunded states and promote inclusion nationwide. The presentation will provide an overview of innovative COBRE evaluation methods based on five objectives derived from NIGMS aims and previous research and theory related to

the development of effective team science and supports. Our evaluation efforts utilize a multiphase mixed methods design to assess the research development efforts. The bulk of the conclusions draw upon existing data collected by the center administrative cores as well as interviews and surveys conducted by our evaluation team asking members about prior and current experiences. The presentation will discuss 1) the use of social network methods for examining infrastructure development and core sustainability within COBRE centers 2) the use of survey research methods to monitor and evaluate the quality of mentorship relationships developed by COBREs, and 3) bibliometric methods for evaluating scholarly productivity including coauthorship analysis and documenting impact. The findings will be examined from a team science lens and framed to support needs related to center renewal efforts and program improvement. The audience can expect to walk away with a high level understanding of our evaluation framework and our data collection and analysis methods.

339. Anna J. Ritter, Southeastern Oklahoma State University. **Analysis of DNA and Purification of Fluorescent Compounds Extracted from Redbud Trees.** Co-Authors: Reece A. Garcia, Kaisey L. Jones, Asuncion Eleazar Rubio, Cooper McKinney, Nancy L. Paiva. Co-Authors Institutional Affiliations: Not Listed. INBRE

Redbud (Cercis canadensis) seeds and flowers were eaten by Native American tribes in Oklahoma and across the US, and the bark or twigs were used to prepare medicinal drinks. Previous studies in our lab have analyzed some of the properties of the proteins in these tissues, and we would like to isolate and analyze either genomic or cDNA clones encoding key proteins identified earlier, such as seed storage proteins, lectins, and condensed tannin- or anthocyanin-related biosynthetic genes. Wood workers have used the yellowish fluorescence of redbud heartwood under UV light to identify the source of wood for small crafts, but the identity of the fluorescent compound or its properties has not been reported. We have isolated small samples of the main yellowish fluorescent compound and will report progress in determining its chemical structure and antimicrobial properties. In addition, we are preparing to isolate genes encoding various proteins from redbud, for comparison to other legumes (such as genes encoding seed storage proteins and lectins) or for biosynthetic studies. Cercis species have recently been identified by plant geneticists as possible close relatives to an ancient ancestor to many modern commercially-important legume crops, such as beans, peas, and soybean, although Cercis does not form the symbiotic nitrogen-fixing relationships with bacteria that commercial legumes do. Funding was provided by NIH/NIGMS award P20GM103447 for OKINBRE Summer Intern and SMaRT Interns, NASA Oklahoma Space Grant Consortium, and Ronald E. McNair Post-Baccalaureate Achievement Program at Southeastern Oklahoma State University.

340. Cristina Velazquez-Marrero, University of Puerto Rico - Institute of Neurobiology. **Contextual Extinction Learning Deficit After Single Binge-Like EtOH Exposure in Adolescent C57BL/6J Male Mice.** Co-Authors: Kiara M. Cardona Jordan, Xiany X. Lay Rivera, Eliezer Cartagena-Lopez, Dina L. Bracho Rincon, Ruth Gonzalez-Bermejo, Gerardo L. Alvarado Monefeldt, Christian J. Esquilin-Rodriguez. Co-Authors Institutional Affiliations: Not Listed. COBRE

Chronic heavy drinking and its relation to post-traumatic stress disorder (PTSD) has been well studied, but surprisingly the relationship between PTSD and more common drinking patterns, such as a one-time episode at the 0.09 g/dL BAC level (moderate intoxication), has not. The frequent co-occurrence of PTSD and alcohol misuse requires an understanding of the influence of biological and behavioral factors that lead to comorbidity. We hypothesize that alcohol's immediate sedative effect is accompanied by the development of a well-characterized form of persistent molecular alcohol tolerance that likely interferes with fear extinction learning. We used a single episode ethanol (SEE) in vivo exposure to model "binge-like" alcohol consumption during a 6-hour period, after contextual conditioning trials. This was followed

by extinction trials to test its effects on extinction learning 24 hours. Our results show a significant deficit in fear extinction learning in alcohol- vs. saline-treated male adolescent mice and no changes in female adolescent mice. This suggests non-chronic alcohol exposure is associated with the development of trauma and stressor-related disorders such as PTSD in males. Furthermore, histology indicates significant changes in FKBP5, ÃŸ-catenin, and GSK-3ÃŸ expression after extinction in alcohol-treated mice within the hippocampus, striatum, and basolateral amygdala. The information gathered within this study may substantially alter the view of possible risk factors leading to the development of PTSD and present new possibilities for the prevention and treatments targeting known molecular mechanisms that mediate alcohol tolerance.

341. Prajesh Shrestha, Louisiana State University. **SFTI-G5: An orally bioavailable peptide for HER2 specific non small cellular lung cancer.** Co-Authors: Prajesh Shrestha, Sitanshu S. Singh, Achyut Dahal, Vivitri Dewi Prasasty, Arpan Chowdhury, Debajyoti Majumdar, Seetharama D. Jois. Co-Authors Institutional Affiliations: Louisiana State University, University of Louisiana Monroe. INBRE
Human epidermal growth factor 2 receptors (HER2) are the members of Tyrosine kinase receptors. Although it lacks any known soluble ligand, its dimerization with other ligands bound to HER family receptors leads to its activation that prompts multiple signaling pathways. Furthermore, any genetic modifications such as mutation, amplification, or overexpression, may lead to its hyperactivation and autophosphorylation which has been associated with many diseases including cancer. Our research aims at developing novel orally bioavailable peptidomimetic compounds to target the HER2 receptor. We developed a novel peptidomimetic compound by grafting peptidomimetic compound 18 into a stable sunflower trypsin inhibitor (SFTI) framework. This novel compound is shown to bind domain IV of the HER2 receptor and demonstrates its action by preventing HER2 dimerization and subsequent activation. The compound showed antiproliferative activity and HER2 dimerization inhibition in both in vitro and in vivo studies. Similarly, the oral pharmacokinetic profile shows the oral bioavailability of the compound. Finally, the compound didn't show tumor suppression in HER2 deleted patient derived xenograft (PDX) model of cancer in mice in vivo indicating the importance of HER2 receptor for its activity. In summary, this study highlights the orally bioavailable peptidomimetic compound SFTI-G5 that reduces the tumor growth via inhibition of HER2 dimerization. This research was supported by funding from the National Cancer Institute of the National Institutes of Health, Grant/Award Number: 5R01CA255176-03 (SJ and DB) and Institutional Development Award from the National Institutes of General Medical Sciences of the national Institutes of health under the grant number P20 GM103424.

342. Adriana Verdezoto Alvarado, University of Delaware. **Associations between the Physical Home Food Environment, Cardiovascular Biomarkers, and Diet Quality in Children.** Co-Authors: Kaelyn Burns, Benjamin Brewer, Shannon Robson. Co-Authors Institutional Affiliations: University at Buffalo, University of Delaware. COBRE
Ecologically informed models suggest the home food environment (HFE) is a driver of individual dietary behaviors. This secondary analysis of a cross-sectional study aimed to explore the relationships between the physical HFE, cardiovascular biomarkers, and diet quality in children. Physical HFE was assessed using the obesogenic score (score range: 0-71; higher scores represent a more obesogenic environment) from the Home Food Inventory (HFI). Availability of fruits and vegetables (FVs), sweet and salty snack foods, and sugar-sweetened beverages were identified from food group scores of the HFI. Diet quality was measured using the Healthy Eating Index (HEI) based upon three-day diet records. HEI-2020 ranges from 0-100 (higher scores indicate higher diet quality). Height and weight were measured to calculate z-BMI. Fasted blood samples via venipuncture were analyzed for lipids, plasma glucose, and insulin. Children (n=44) from 29 households were 9.5Â±1.9y, 61.4% female, 59.1% White, 90.9% non-Hispanic.

Linear mixed model regressions found obesogenic score was not significantly associated with HEI-2020 (B=-0.51Â±0.26, F(1, 44)=3.90, p=0.054) or cardiovascular biomarkers, but was significantly associated with z-BMI (B=0.03Â±0.01, F(1, 44)=5.12, p=0.029). However, FV availability was positively associated with HEI-2020 (B=0.84Â±0.24, F(1, 44)=11.70, p=0.001) and inversely associated with total cholesterol (B=-1.54Â±0.59, F(1, 30)=6.88, p=0.014) and LDL-cholesterol (B=-1.31Â±0.47, F(1, 30)=7.63, p=0.010). Availability of sweet and salty snacks was positively associated with glucose (B=0.65Â±0.29, F(1, 30)=4.97, p=0.033), and sugar-sweetened beverages were associated with insulin (B=5.60Â±2.44, F(1, 17)=5.26, p=0.035). These findings suggest that specific food groups within the physical HFE may influence cardiovascular biomarkers and diet quality in children.

343. Katie Rose Ryan, University of Arkansas for Medical Science. **Rnd3 depletion in lung adenocarcinoma and patient derived lung to brain metastasis cell lines decreases cell invasion in a ROCK1 independent manner.** Co-Authors: Name: Noemi Garcia Garcia, Thanh Ha Vy Nguyen, Dane Richey, Cody Ashby, Analiz Rodriguez. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE

Lung cancer is the most common and among the deadliest cancer types in the US. Most lung cancers metastasize resulting poor prognosis, with lung to brain metastasis being the number one killer of lung cancer patients. Studying mechanisms that drive metastatic potential is key to unlocking new strategies for the treatment of this deadly form of cancer. Expression levels of the atypical Rho GTPase Rnd3 have been linked to several cancers and Rnd3 is involved in the regulation of several cellular processes which are commonly dysregulated in cancer. Our analysis of TCGA survival data of lung adenocarcinoma patients shows that patients expressing low levels of Rnd3 expression have significantly higher survival probability rates compared to patients expressing high levels of Rnd3. To gain insight into how low Rnd3 expression maybe beneficial to patient survival we performed IPA analysis on our proteomic generated global protein expression profiles of Rnd3 expressing (high) and Rnd3 knockdown (low) lung adenocarcinoma A549 cells, which predicted a decrease in cell invasion, a hallmark of metastasis. We validated these predictions in vitro by knocking down Rnd3 expression in A549 cells and two patient-derived lung to brain metastasis (PDLBM) cell lines (601 and 620), cell invasion was significantly decreased in all three cell lines. We also show that Rnd3 regulation of cell invasion is independent of ROCK1 signaling, a known regulator of Rnd3, indicating a novel pathway. Deciphering this novel mechanism may lead to identifying new therapeutic targets of lung cancer metastasis.

344. Kendrail Mouzon, Benedict College. **Effects of Polycyclic Aromatic Hydrocarbons on Human Breast Cancer Cells.** Co-Authors: None. INBRE

Polycyclic Aromatic Hydrocarbons (PAHs) are ubiquitous and persistent environmental contaminants. Some are suspected carcinogens and may affect the reproductive systems as potential endocrine disruptors. The purpose of this experiment was to examine the effects of two PAHs, Benzo(a)Pyrene (BaP) and Fluoranthene (FLA), on cellular protein production, lactate dehydrogenase (LDH) activity, or ROS production, which could be due to altered oxidative stress. Half a million MCF-7 or MDA-MB-231 cells were cultured in a 35-mm dish. We monitored the cells under a microscope, and on day 2, we added exposure media and media containing 0.01% DMSO, BaP, or FLA (both at 1 µg/ml or 500ng/ml). After 24 hours, the media was separated, and the conditioned media was saved in centrifuge tubes for the LDH assay using an ELISA plate reader to measure the absorbance of the samples at 490 nm. In MCF-7 cells, the protein level was decreased drastically with 1 µg/ml FLA, but we didn't see any noticeable changes in MDA-MB-231 cells. Regarding LDH release, we have observed some differences: FLA and BaP at 1 µg/ml decreased LDH in MCF-7, while in MDA-MB-231 cells FLA at both concentrations increased LDH levels. The results showed that BAP and FLA at both concentrations increased the level of ROS

production in MCF-7 cells when compared to the media and DMSO control groups. The increased level of ROS production in MCF-7 cells due to PAH exposure shows that the cells undergo oxidative stress, which may correlate with mitochondrial dysfunction. Additional experiments are underway to examine the potential changes in ROS production in PAH-exposed MDA-231 cells.

345. Zefeng Nie, Geisel School of Medicine at Dartmouth College. **Tunning Enantioselectivity of Epoxide Hydrolases by Engineering the Active- Site Cavity and Substrate-Entry Tunnel.** Co-Authors: Noor M. Taher, Adam R. Simard, Dean R. Madden. Co-Authors Institutional Affiliations: Dartmouth College. COBRE
Enantiopure vicinal diols produced by the hydrolysis of epoxides are ubiquitous synthons in many pharmaceuticals. We have recently characterized aCif, an epoxide hydrolase from A. nosocomialis, and found that aCif exhibits high enantioselectivity toward S-(+)-styrene oxide (SSO), while its homolog Cif from P. aeruginosa exhibits activity for SSO and an even higher activity toward R-(-)-styrene oxide (RSO). Structural analysis of aCif and Cif shows a C-alpha root mean square deviation of 1.0 Ã.... Such observations pose the question of how the high structural similarity confers such distinct enantioselectivity. To investigate the key structural elements that determine their enantioselectivities, we narrowed our search to the active-site cavity and the substrate-entry tunnel. Using mutagenesis and an activity assay, we found that mutation of aCif residues in the active-site cavity failed to elicit the activity for RSO while mutation of the substrate-entry tunnel of aCif causes complete loss of enzymatic activity. However, the combination of these mutations produced an engineered aCif variant with modest activity for RSO. Comparison of the crystal structures of the mutants with the wildtype structure shows that the integrity of the substrate entry-tunnel is linked to the structure of the active-site cavity. Together, our structure-function analyses revealed a key role of the substrate-entry tunnel in the enantioselectivity of aCif toward styrene oxide. Such knowledge will help expand the options in rational design of other enantioselective alpha/beta hydrolases.

346. Kimberly Canter, Nemours Children's Health. **Introducing the Intervention Methodology: Provision and Connection through Technology (IMPACT) Core: A Research Core supported by the Research Expanding Access to Child Health (REACH) Center.** Co-Authors: Michelle Goodreau, Melissa Alderfer, Anne Kazak. Co-Authors Institutional Affiliations: Nemours Children's Health. COBRE
The REACH Center is an NIH Center for Biomedical Research Excellence (COBRE P20GM144270) at Nemours Children's Hospital, Delaware. The IMPACT Core is supported by the REACH Center and is a resource for investigators interested in conducting innovative intervention research focused on reducing pediatric health disparities and improving child health. The first aim of the Core is to create a robust infrastructure to facilitate the development, delivery and implementation of scalable, innovative, technology enhanced interventions primed for delivery to patients and families impacted by health disparities and social inequities. A Core Internal Advisory Committee and a group of experts in various types of technology support the Core. An intake form was developed and disseminated to foster relationships and log results from ongoing consultations. The second aim of IMPACT is to prepare and support investigators in the conduct of intervention research using technology to address equity in pediatric health care. In addition to supporting research and pilot projects funded by the REACH Center, the Core Director and Core personnel consult with investigators. These consultations have been used to assist with the development of pilot and research projects, manuscripts, and an R21 application. Our final aim is to manage and sustain the IMPACT Core. This includes investments in training and incorporating cutting edge technological and methodological developments into interventions supported by REACH. We are tracking our progress with projects and consultations and having regular meetings with our collaborators. IMPACT also facilitated a workshop in partnership with The Center for Health Delivery Innovation at Nemours.

347. David Heinrichs, University of Arkansas. **Assessing the Effects of Senolytics on Mesenchymal Stem/Stromal Cell Functionality.** Co-Authors: None. COBRE
Cellular therapy and regenerative medicine are rapidly growing fields of research due to successes in clinical trials of stem cell therapy. Progressive in vitro aging, or replicative senescence, of mesenchymal stem/stromal cells (MSCs) is a major obstacle faced when trying to generate sufficient numbers of potent stem cells for use in therapies. Extensively passaged cells cease to divide and stop performing critical functions that contribute to their potency. It is not yet established how to reduce the number of non-viable MSCs in culture while leaving viable cells unharmed. We propose that clearing senescent populations with senolytics will reduce heterogeneity in MSC populations and yield improved potency for cellular functions and in vivo bone formation when transplanted into a bone defect. Our results using known senolytics dasatinib (D) and quercetin (Q) demonstrated significant changes in culture heterogeneity, cellular functions, differentiation abilities, and bone forming capacities. We will discuss the synergistic functions of D and Q in clearing senescent cells from culture while leaving behind healthy young cells to continue functioning to differentiate into new bone. Together, our results on functional assessments from the reduction of senescence to MSCs subjected to extensive culturing as well as our assessments of bone formation add new knowledge to the field of stem cell biology holding significance in development and optimization of MSC-based cellular therapies for treating degenerative disorders.

348. Denise L Daniello, University of Alaska Fairbanks. **Creating Opportunities for Community Dialogue.** Co-Authors: Kelly Drew. Co-Authors Institutional Affiliations: University of Alaska Fairbanks. COBRE
The Administrative Core of the UA Center for Transformative Research in Metabolism (TRiM) plays an important role in supporting administrative, fiscal, and scientific functions to facilitate the success of early stage investigators and sustain a diverse research program at UAF/UAA. The Center focuses on translational metabolic health research rooted in the study of hibernation, aiming to uncover innovative solutions for treating metabolic diseases. By leveraging insights from hibernation, the Center seeks to enhance healthy aging, reduce healthcare costs, and enhance quality of life in an aging population. In line with its mission, the Admin Core introduced the Community Advisory Panel (CAP) to establish stronger relationships with stakeholders through community engagement. The CAP comprises diverse stakeholders such as older adults, caregivers, healthcare providers, and concerned citizens who convene regularly to exchange insights. This outreach effort aims to bridge the gap between high-level scientific concepts and public understanding, particularly about metabolic-related diseases prevalent among older adults such as disuse muscle atrophy, sarcopenia, cardiovascular disease, and Alzheimer's disease. The goal is to create a platform for dialogue and mutual learning between community members and research scientists. This poster presentation will describe the CAP's endeavors in enhancing public awareness, gathering community feedback, sharing key learnings, and proposing an annual evaluation framework to increase participant engagement for better outcomes. This initiative underscores TRiM's commitment to fostering meaningful partnerships with the community for advancing metabolic health research, improving public understanding, and strengthening research outcomes.

349. Elizabeth Thompson, Rhode Island Hospital. **Psychosis-spectrum experiences, sleep difficulties, and suicidal ideation in youth: An exploration of findings across college counseling, adolescent inpatient, and juvenile legal system settings.** Co-Authors: None. COBRE
Sleep difficulties are prevalent among youth with psychosis-spectrum experiences (e.g., hallucinations, delusions), and both phenomena have been linked to increased suicidal ideation (SI). This set of studies explores the relations between psychosis-spectrum experiences, sleep difficulties, and SI in distinct groups of youth: 1) students at a university counseling center (n = 442; Mean age = 21.8; 59% female), 2)

a clinical sample of psychiatrically hospitalized adolescents (n = 617; Mean age = 15.0; 65% female), and 3) a sample of juvenile legal system (JLS) involved youth presenting for intake to a court-based diversion program (n = 1290; Mean age = 14.9; 37% female). Procedures included cross-sectional self-reports of psychosisspectrum experiences, sleep difficulties, and SI that were embedded in larger studies. Within all samples, linear regression results indicated that psychosis-spectrum experiences and sleep difficulties were positively associated with SI, even when controlling for other related clinical characteristics (e.g., depression, anxiety) and demographics in some samples. Within the college counseling and JLS samples, subsequent analyses identified sleep difficulties as a significant moderator of the association between psychosis-spectrum experiences and SI. Psychosis-spectrum scores were positively associated with SI at high and moderate, but not low, levels of sleep difficulties. This moderating effect was not observed in the inpatient sample. Findings indicate that psychosis-spectrum symptoms are associated with SI among youth across settings, and greater sleep quality may buffer this association for some youth. Interventions targeting sleep health may be particularly helpful for youth with psychosis-spectrum symptoms to mitigate suicide related risk.

350. Jingjie Hao, University of Nebraska-Lincoln. **Biomedical and Obesity Research Core (BORC).** Co-Authors: None. COBRE

The Biomedical and Obesity Research Core (BORC) within the Nebraska Center for the Prevention of Obesity Diseases (NPOD) is a pivotal research hub offering advanced biomedical research services to investigators in the University of Nebraska (UN) system and external users. The BORCs facility includes two offices and a 2,000 square feet laboratory in Ruth Leverton Hall and two animal rooms for in vivo studies in the Life Science Annex at the East Campus of University of Nebraska-Lincoln (UNL). BORC's overarching mission is to bolster biomedical research excellence within NPOD and UNL by providing a comprehensive suite of services. These include aiding in experimental design, executing experiments, offering training sessions, and facilitating access to state-of-the-art instruments crucial for cutting-edge research endeavors. The research services provided in BORC encompass molecular and cell biology, metabolite analysis, microbiome cultures, animal behavior research, small animal imaging, and services in experimental design and statistical analysis. Through collaborative efforts with biostatistics and bioinformatics coordinators, as well as Nebraska's supercomputing facility, Holland Computing Center (HCC), BORC ensures seamless coordination across all research stages - from initial experimental planning to data acquisition and comprehensive statistical analyses. This cohesive approach not only enhances the quality of research conducted within BORC but also fosters interdisciplinary collaborations, driving forward innovative discoveries in the realm of obesity-related diseases and dietary molecules.

351. Elizabeth Alberts, Creighton University. **Shape analysis of crassotrea gigas oaz-pk RNA.** Co-Authors: Juliane Soukup. Co-Authors Institutional Affiliations: Creighton University. INBRE

A riboswitch is a piece of non-coding RNA that functions in downstream gene expression when bound to a metabolite. When a riboswitch interacts with its metabolite, they will undergo a conformational change that will affect the expression of genes downstream to its binding site. The outcome of this pathway is a change in the production of the same metabolite it binds to. The Soukup lab is researching the potential eukaryotic riboswitch in the Ornithine Decarboxylase Antizyme pseudoknot (OAZ-PK) RNA segment. Known riboswitches in bacteria have a significant effect on various metabolic pathways, providing a way to develop new antibiotic treatments. Identification of a similar non-coding RNA in eukaryotic species may provide a possible way to develop novel antibiological agents. My project focuses on studying a potential riboswitch in Crassostrea Gigas, a species of oyster. Specifically, Selective 2-Hydroxyl Acylation analyzed by Primer Extension (SHAPE) experiments are being used to analyze structural changes of this non-coding RNA segment when it interacts with various natural and non-natural polyamines. Analyzing

these structural changes will aid in identifying this RNA segment as a riboswitch that could open the possibility of developing novel antibiological agents. The project described was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under Grant # 5P20GM103427.

352. Emily Gathright, The Miriam Hospital/Brown Medical School. **An Implementation Science-Informed Systematic Review and Meta-analysis of Stress Management for Cardiac Rehabilitation.** Co-Authors:
Laurie Storlazzi, Brittany Balletto, Traci Mancini. Co-Authors Institutional Affiliations: Not Listed. COBRE
Background: Cardiac rehabilitation (CR) is recommended to reduce risk of recurrent cardiovascular (CV) events and mortality following a qualifying CV event or diagnosis. Psychosocial stress is common among adults with CV disease and can undermine CR adherence. Increased incorporation of stress management in CR is needed. The goal of this research is to conduct a systematic review and meta-analysis to inform development of a comprehensive stress management implementation blueprint for CR programs. Methods: Comprehensive searches identified studies that evaluated a stress management, exercise, or CR intervention in adults with CV disease and measured psychological distress (e.g., depression, stress, anxiety). Independent raters coded study, sample, design, intervention, and methodological quality characteristics. Results: A qualitative summary is reported; final quantitative analyses will be available at the conference. Searches identified 13,233 unique records; as of February 2024, 39 eligible studies sampled a total of 4,494 participants (mean age=62; 39% women). Interventions included tai chi (k=14), mindfulness based stress reduction (k=8), cognitive behavioral approaches (k=5), meditation (k=4), biofeedback (k=3), coping skills training (k=2), progressive muscle relaxation (k=1), and a combination (k=2). Compared to controls, stress management interventions reduced depressive symptoms in 16/28 studies. Anxiety and perceived stress were reduced in studies 8/19 and 6/9 studies, respectively. Facilitators were predominately certified trainers (k=21). Interventions were most often conducted in person (vs online/tele-delivered). Conclusions: Quantitative meta-analytic assessments will summarize the effects of SMIs on CV outcomes and the role of important implementation-relevant moderators (e.g., delivery and facilitator characteristics, dose) of the effects.

353. Mojtaba Mohasel, Montana State University. **A Telehealth tool to Automate Mobility Testing for Lower Limb Amputees.** Co-Authors: Corey Pew. Co-Authors Institutional Affiliations: Montana State University. INBRE
Clinical mobility of individuals with lower limb amputation utilizes the 2-Minute Walk Test (2MWT) and Timed Up and Go (TUG) to evaluate functionality and prosthesis fit . Currently, no live telehealth tool enables individuals with LLA to conduct mobility testing at home with low-cost, real-time assessment. This study intends to create that tool. We utilized an Inertial Measurement Unit sensor as our hardware for data collection. In the software, we developed three methods for the 2MWT named Integration, step count, and machine learning (ML). The Integration method demonstrated the highest accuracy, while ML had the lowest variability. For the TUG, the Threshold method showed promise, however, more work is needed to increase reliability and current results fall within clinically relevant ranges of minimum detectable change. Future work includes improving accuracy and variability, and exploring sensor placement. This study took an initial step toward the long-term goal of creating a telehealth tool for LLA. This open-source tool will offer a cost effective solution for remote mobility assessment, enhancing healthcare access for individuals with LLA.

354. Vitali Victorovitch Maldonado, University of Arkansas. **Effects of Mechanical Stimulus on Bone-Marrow Derived Mesenchymal Stem Cells Osteogenic Differentiation.** Co-Authors: Neel Patel,

Rebekah Margaret Samsonraj. Co-Authors Institutional Affiliations: Georgia Institute of Technology, University of Arkansas. COBRE
The capacity of mesenchymal stem cells (MSCs) to differentiate into osteoblasts and self-renew is of special interest in the field of regenerative medicine. Multiple clinical trials show that MSCs can be potential candidates to treat bone-related diseases due to their osteogenic differentiation abilities. However, MSCs are heterogeneous by nature and not all donor-derived MSCs display similar osteogenic potencies. Consequently, there is a need to non-invasively improve the homogeneity of MSC preparations for applications in bone repair and regeneration. In this study, we research the effects of non-invasive mechanical stimulus (MS) on MSC bone regeneration potency. Since MSCs are mechanosensitive, daily MS delivery can bias the cells toward becoming osteoblasts without the need of exogenous growth factor supplementation. In vitro osteogenic differentiation and MS delivery was performed on MSCs isolated from multiple donors. Expression of key genes involved in osteogenesis, proteins involved in mechanotransduction, and in-vitro mineralization were assessed at different time points. The results from this study indicate that daily mechanical stimulation increases the expression of proteins involved in mechanotransduction as well as the expression of key osteogenic genes. The degree of in vitro mineralization also increased with LMV treatment. The techniques used in this study can be applied in MSC biomanufacturing to increase MSC bone healing potency useful for effective cell therapies.

355. Chenangnon Frederic Tovissode, University of Idaho. **A General Causal Network Inference Algorithm with Mendelian Randomization for Large Genomic Networks.** Co-Authors: Jarred Kvamme, Audrey Qiuyan Fu. Co-Authors Institutional Affiliations: University of Idaho. COBRE
Causal inference methods based on the Principle of Mendelian Randomization have become increasingly popular to learn potentially complex regulatory processes in biology from observational data. However, inferring causal relationships in a large network of molecular phenotypes remains a challenge, especially when multiple types of confounding variables are involved. We develop a method called Mendelian Randomization Genomic Network (MRGN) to learn large causal biological networks involving genotypes, molecular phenotypes, and confounding variables of different types: confounders, intermediate variables and common children. MRGN treats the latter two as regular nodes in the network to avoid adjustment bias, but potentially adjusts for a large number of confounders during inference. MRGN iteratively forms trios, each consisting of either one genetic variant and two phenotypes, or three phenotypes, performs causal analysis, accounting for confounders, and updates the network. In extensive simulations and the application to the Fifth Dialogue on Reverse Engineering Assessment and Methods (DREAM5) Systems Genetics Challenge data, MRGN appears to be conservative, favoring high precision over recall, and consistently outperforms popular competing methods. Future directions include evaluation in real datasets, and extension to improve the performance in networks including very dense hubs.

356. Kristen Rolen, Bluefield State University. **Active Hexose Correlated Compound Feeding to Stress Mice Alters Profiles of Cytokine Production during Chlamydia muridarum infection.** Co-Authors: Tesfaye Belay. Co-Authors Institutional Affiliations: Not Listed. INBRE
Active Hexose Correlated Compound (AHCC) is a nutritional diet extracted from mushrooms that may enhance immune cell functions but the mechanism(s) remain unexplored. We hypothesize that AHCC feeding to mice modulates the profile of cytokine secretion during chlamydial genital infection in stressed mice. Wildtype C57BL/6J mice were stressed and infected with C. muridarum intravaginally. After seven days, splenic and lymph node T cells bone marrow-derived dendritic cells (DCs), and macrophages (MÃ˜s) were purified, proliferated, and culture supernatants were collected to determine

cytokine production by ELISA. Phenotyping of surface markers of immune cells using flow cytometry is underway to be included in the poster. ELISA results show that AHCC increases the production of Th1 (IL-12 and IFN-ï•§) and Th2 (IL-10, IL-13, IL.23) cytokines compared to PBS-fed stressed mice. Increased production of TNF-Î±, IL-6, IL-1ï•¢, and IL-12 in LPS-treated DCs was observed. Overall, AHCC-feeding increases the production of protective and suppressive cytokines. The obtained preliminary data suggest that AHCC has immunomodulatory effects via immune cell activation, which could be useful for further studies in stressed physiological environments.

357. Xinggui Shen, Louisiana State University Health Sciences Center-Shreveport. **Glutathione Redox Regulation in Hyperglycemia-Induced Endothelial Dysfunction.** Co-Authors: Christopher B. Pattillo, A. Wayne Orr, Kevil G. Christopher. Co-Authors Institutional Affiliations: Not Listed. COBRE
Cardiovascular disease (CVD) remains a leading cause of mortality worldwide, with hyperglycemia emerging as a pivotal risk factor for its onset and progression. Hyperglycemia triggers augmented oxidative stress by inducing the production of reactive oxygen species (ROS), thereby compromising antioxidant defenses. Glutathione (GSH) plays a critical role as the predominant antioxidant, with its redox status intricately linked to cellular health. We explored the impact of hyperglycemia on glutathione-related redox regulation in Human Umbilical Vein Endothelial Cells (HUVECs). HUVECs were exposed to varying concentrations of Dglucose and mannitol for 16 hours, and cell viability was assessed via light microscopy. Superoxide and free thiol levels were quantified using HPLC with a fluorescence detector, while GSH-related proteins and GSH per/polysulfide levels were quantified using LC-MS/MS. Differential protein expression was analyzed using the PANTHER classification system and STRING interactome to elucidate functional roles and proteinprotein interaction networks. Our findings revealed hyperglycemia-induced cell death, concomitant with a significant increase in superoxide and oxidized GSH (GSSG) levels in HUVECs exposed to glucose concentrations exceeding 15 mM. However, no significant alterations were observed in GSH, cysteine, homocysteine, or total glutathione levels. Intriguingly, GSH per/polysulfide levels exhibited a marked elevation in hyperglycemic HUVECs. Furthermore, label-free quantitation (LFQ) of LC-MS/MS identified differential expressions of GSH-related proteins, with their biological functions elucidated through PANTHER and STRING analyses. Our findings shed light on the protective role of glutathione in mitigating endothelial dysfunction induced by hyperglycemia, offering potential therapeutic targets for CVD management.

358. Igor Koturbash, University of Arkansas for Medical Sciences. **Establishment of the Peer Mentoring and Work/Life Balance Committee as an Important Pillar in the Sustainability of Success of the Center Members.** Co-Authors: Taren Swindle, Craig Porter, Britni Ayers, Shannon Rose, Mallory Allred, Linda Larson-Prior, Judy Weber. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE
The importance of a work/life balance for sustainable success in academia has become increasingly recognized. Proper management of work commitments and leisure time is key to maintaining high-quality work and motivation, as well as to prevent burnouts and loss of productivity. In order to address these issues among junior faculty as well as their senior mentors, the Center for Childhood Obesity Prevention (CCOP) has established the Peer Mentoring and Work/Life Balance Committee. The Committee activities include bimonthly “Zoom coffee meetings”, during which both junior and senior faculty can discuss their concerns or needs either with the entire group of Committee members or one-on-one with a select Committee member in a private Zoom room. The Committee has also developed and successfully implemented a “Happy Faculty Seminar Series”, where established, nationally-recognized faculty share stories of their life outside academia from hobbies to physical fitness. Additionally, the Committee offers multiple career-advancing opportunities during regular Work-in-

Progress and Annual Retreat meetings. Such events span from short mindfulness and yoga exercises to day-long sessions that include career advice from established investigators outside the Center, as well as grant writing workshops. Importantly, in order to maintain an open dialogue with the Center's junior faculty and their needs, two current Project Leads serve as members of the Committee. Finally, the Committee actively collaborates with several other CCOP committees and participates in joint events to offer better opportunities for the professional growth of the Center's faculty and staff.

359. Negar Farhang Doost, West Virginia University. **Investigating the bioelectric signatures of Candida auris.** Co-Authors: Soumya K Srivastava, Tagbo H.R. Niepa. Co-Authors Institutional Affiliations: West Virginia University, Carnegie Mellon University.
The emergence of Candida auris has become a global health threat. Candida auris has spread in many states in the US and has demonstrated significant challenges in diagnosis. Current diagnostic methods, such as cell culture, are slow and insensitive. Moreover, molecular methods and MALDI-TOF are expensive and require advanced equipment. We propose a novel approach for diagnosis by utilizing an electrokinetic technique, dielectrophoresis (DEP). DEP involves the movement of a polarizable particle under a nonuniform electric field. Since different cell types exhibit different dielectric properties, DEP can provide a means of enriching and sorting them. C. auris cells are hypothesized to have a unique electrokinetic response based on their inherent properties and physiological state. To characterize the bioelectric signatures of C. auris, C. auris (CA1100) was cultivated and suspended in a buffer containing 8.5 grams of sucrose and 0.3 grams of dextrose with a conductivity of 80 Î¼S/cm. The dielectrophoretic crossover frequency principle was utilized to obtain the bioelectric signatures such as conductivity, permittivity, and membrane capacitance that correlate to the membrane morphology and cytoplasm contents. The cytoplasm conductivity, membrane conductivity, and membrane permittivity were 0.14 S/m, 117850.31 S/m, and 0.26 respectively. The bioelectric signatures are obtained by fitting the crossover frequency to a singleshell model. Our findings demonstrate DEP's potential for detecting Candida auris cells across different frequencies ranging from 0.5 kHz to 45 MHz at 20 Vpp. These bioelectric signatures will be utilized to design a diagnostic tool for Candidiasis and screen for drug resistance of these species.

360. Patrick Tomco, University of Alaska Anchorage. **Environmental health impact of oxidized hydrocarbons in high-latitude regions: non-target screening, aryl hydrocarbon receptor activity, and shellfish bioassays.** Co-Authors: Zachary Redman, Jason Burkhead. Co-Authors Institutional Affiliations: University of Alaska Anchorage. INBRE
As sea ice in the Arctic melts due to climate change, new developments of petroleum resources are occurring. At the same time, shipping activity in this remote, cold region is increasing. Both factors raise concerns over the likelihood of a petroleum spill in the Arctic that may persist for an extended period of time before responders can be present on-scene. The consumption of oil-contaminated food sources would pose an environmental health risk, both to humans and wildlife. Petroleum is a complex mixture known to contain polycyclic aromatic hydrocarbons (PAHs), a group of toxicants with long legacy of monitoring following a spill. Recent work has shown that PAHs can oxidize in the environment to oxidized PAHs (oPAHs), a poorly understood emerging contaminant class that is mobilized following sunlight exposure. The aims of this project are to (1) Assess the chemical composition of oPAHs following simulated oil spills exposed to simulated sunlight, (2) Define the aryl hydrocarbon receptor (AhR) activity along a time course of irradiation extent, and (3) Assess sublethal toxicological endpoints in shellfish. Non-target Liquid Chromatography Orbitrap mass spectrometry analysis identified 251 hydrocarbon oxidation products that were in greater abundance in light-exposed samples than dark controls, consistent with oPAHs that contained primarily 1-3 aromatic rings and 1-3 oxygens. AhR activity

correlated with oPAH formation, consistent with measurements of cytochrome P450 and heat shock protein. This project provides critical environmental health information related to the water-soluble fraction of oxidized petroleum-derived compounds.

361. Xiaopeng Ji, University of Delaware. **Chatbot-based sleep intervention for young Black/African American adults: a feasibility study.** Co-Authors: Sanaz Taherzadeh, Janeese A. Brownlow, Elizabeth Orsega-Smith, Jingwen Zhang, Freda Patterson. Co-Authors Institutional Affiliations: University of Delaware, Delaware State University, University of California Davis. COBRE INTRODUCTION: Unhealthy sleep, predicting cardiometabolic risk, disproportionately impacts young Black/African American (BAA) adults. This study tested the acceptability, usability, and feasibility of an artificial intelligence chatbot-delivered sleep intervention for short-or-poor sleepers among young BAA adults. METHODS: In this single-arm, pretest-posttest study, a 4-week transdiagnostic sleep intervention was delivered automatically through a chatbot with personalized algorithms via a mobile app. Feasibility, usability, and acceptability were measured using retention rates, questionnaires [e.g., Adapted System Usability Scale (SUS)], and interviews. Participants completed the Insomnia Severity Index (ISI), Pittsburgh Sleep Quality Index (PSQI), Sleep Self-efficacy (SSE), and Dysfunctional Beliefs and Attitudes about Sleep (DBAS-16) questionnaires, both pre-and post-intervention, and at the 4-week follow-up. RESULTS: Among seven participants (19.33Â±1.36 y.o., all females) who completed the end-of-intervention assessment, all completed 100% of dialogues for weekly sleep coaching and completed 70% of progress review dialogues. All rated chatbot as acceptable and the average SUS score (74) exceeded the favorable usability cutoff (68). In interviews, all found the chatbot user-friendly and time-flexible, improving sleep knowledge, and motivating behavioral changes, despite minor technical issues. They considered weekly goal setting, coaching dialogues, and sleep tracking most useful, and free-input Q&A less essential. Compared to baseline, participants showed decreased ISI, PSQI, and DBAS scores, and increased SSE scores post intervention and at the 4-week follow-up. CONCLUSION: Sleep chatbot intervention is feasible and acceptable, and has the potential to improve sleep health among young BAA adults. This study suggests an accessible, autonomous, and scalable approach to promoting sleep in this high-risk group.

362. Britni Ayers, University of Arkansas for Medical Sciences-Northwest. **Assessing the Acceptability of a Culturally Adapted Group-Based Well-Baby Intervention, Kokajjiriri, for Marshallese Mothers and Infants.** Co-Authors: Not Listed. Co-Authors Institutional Affiliations: Not Listed. COBRE Background: The prevalence of childhood obesity is significantly higher among racial and/or ethnic minority children in the United States, with Pacific Islanders disproportionately affected. Arkansas currently has the largest population of Marshallese Pacific Islanders living in the United States (~16,000 people). Despite the obesity rates experienced in this community, there are currently no childhood obesity interventions designed for Marshallese Pacific Islanders. The purpose of this study is to assess the acceptability and feasibility of a culturally adapted group-based well-baby intervention, Kokajjiriri, with Marshallese women to improve healthy infant growth and development. Methods: A multi-method design was used. In the first phase, (n=20) Marshallese women with children under 12 months completed three, telephone-administered 24-hour dietary recalls. Dietary data was applied to the healthy eating index (HEI)-2015. A food-level analysis identified top food groupings contributing to total calories and HEI-2015 nutrient components. In phase two, we culturally adapted the intervention based on dietary recalls, and implemented an abbreviated version of the intervention to assess acceptability and feasibility with (n=17) Marshallese women. Results: White rice was the top contributor to total calories; high seafood/plant protein and fatty acid HEI scores was influenced by high intakes of fish. Diet quality was low. Key adaptations include reducing rice portion sizes, while emphasizing lean proteins and

fruits/vegetables. Majority of the participants found the culturally adapted intervention helpful, feasible, and culturally acceptable. Conclusion: Cultural adaptation of nutrition education curriculum is essential to improve dietary patterns among communities with varying dietary practices.

363. Keyora Wharry, California State University- Fresno. **Development of reference genes for the study of chalcone-induced gene expression using qPCR in Caenorhabditis elegans.** Co-Authors: Alejandro Calderon-Urrea. Co-Authors Institutional Affiliations: Not Listed. Other
Plant-parasitic nematodes inflict harm and diminish agricultural yields, posing a significant obstacle to global farming endeavors. It's estimated that they incur estimated $157 billion in agricultural losses annually. Continuous research on these nematodes and endeavors to manage them persist, with a particular emphasis on devising sustainable and environmentally friendly remedies. Chalcones 17, 25, and 30, members of the flavonoid family, represent an environmentally sustainable organic compound known for their efficacy in eliminating nematodes when applied at a concentration of 10-4M. Chalcone 17, 25 and 30 induce death in C. elegans by targeting different, as of yet unknown molecular pathways , although we speculate controlling expression of a few genes belonging to the oxidative stress or neuropeptide signaling pathways of the nematode. My research uses Reverse Transcription-Quantitative Polymerase Chain Reaction (RT-qPCR) to monitor gene expression of genes involved in oxidative stress and the neuropeptide signaling pathway. Prior to that experimentation reference genes are needed for standardization. Suitable reference genes must meet several criteria: their threshold cycles should be similar to those of the gene of interest, indicating stable expression levels; they typically fulfill vital cellular functions involved in basic cellular processes, and their expression should remain relatively unaffected by experimental conditions. We selected three genes for testing to be used as reference genes for this project: actin-1, cdc-42, and 18SrRNA. RNA was extracted from C. elegans at various life stages to examine continual gene expression throughout their lifespan. Three trials propose that expression of these genes is relatively consistent at various concentrations of complementary DNA and unaffected at the different life stages of the nematodes, as well as sublethal concentrations of chalcones.

364. Justin Parent, Bradley Hospital. **Telehealth parenting program reduces epigenetic inflammation and aging in young children with delays: A randomized clinical trial.** Co-Authors: Sarah Merrill. Co-Authors Institutional Affiliations: Brown University. COBRE
Importance: Children with developmental delays are at a heightened risk of experiencing mental health challenges, and this risk is exacerbated among racially minoritized children who face disproportionate adversity. Understanding the impact of parenting interventions on biological markers associated with these risks is crucial for mitigating long-term health disparities.Objective: We examined the impact of 20 weeks of an internet-based Parent-Child Interaction Training (iPCIT) on biomarkers related to aging and chronic inflammation in predominantly Latino/a preschoolers with developmental delay at 12-month follow-up. Design: A randomized controlled trial was conducted to assess changes in salivary DNA methylation (DNAm)-derived biomarkers following iPCIT intervention. Intervention: iPCIT is a telehealth therapeutic intervention focused on enhancing the parent-child relationship and addressing behavioral challenges in young children. Results: Children (n = 71; mean age=36.3 months old, 71.8% male sex) who provided saliva in at least one study wave were analyzed. The iPCIT group had a slower pace of aging (DunedinPACE) (? = 0.26 [0.06, 0.50], p = .028) and less DNAm-derived CRP (? = 0.27 [0.05, 0.49], p = .015) relative to the control condition at the 12-month follow-up. These effects remained significant after accounting for baseline DNAm score, child demographics, and symptom severity, and were independent of predicted buccal epithelial cell proportion. Conclusions and Relevance: The findings suggest parenting interventions have the potential to modify aspects of biological embedding of stress, slowing the pace of

aging and reducing inflammation. Understanding the systemic biological impact of such interventions offers insights into addressing health disparities and promoting resilience.

365. Mary Kathryn Cancilliere, Rhode Island Hospital. **The Development of an Emergency Department Family Navigator Protocol to Reduce Risk of Suicide and Self-injurious Behavior.** Co-Authors: Lindsay Orchowski, Kathleen Donise, Kate Guthrie, Timmy Lin, Emely Arenas Lemus, Sheila Solarez, Anthony Spirito. Co-Authors Institutional Affiliations: Rhode Island Hospital, Bradley Hospital, The Miriam Hospital, Alpert Medical School at Brown University. COBRE
Suicide is the second leading cause of death for youth 10-18 years in the U.S. Over the last couple of years, youth 10-14 years rates of suicide and self-injurious behavior (SSIB) have doubled. This surge coincides with an increase in emergency department (ED) visits. 73% of youth with SSIB seen in the ED are discharged to the community, yet less than 40% receive subsequent MH care within 30 days. This study characterizes data from an open trial Family Navigator with technology-enhancements intervention for youth who were discharged from the ED for SSIB. This intervention aims to reduce SSIB risk, increase linkage to MH care, and reduce ED re-admission. We examined youth and caregiver report of demographic and behavioral data on youth MH symptoms, impairment, and knowledge, as well as caregivers' satisfaction. In the sample of youth (10-14yrs; M=12.67; SD=1.09) and caregiver dyads (N=17) recruited from a northeastern academic medical center's ED between November 2023 and March 2024, youth sex was 88.24% female, youth identified as 52.94% male, 23.53% female, 5.88% non-binary, 11.76% agender, 1% gender fluid, 29.41 Hispanic/Latinx, and 5.88% Black/African American, 64.71% White. Caregivers reported an average income of $50,000$74,999, ~68% had ï‚³ two-year degree. Roughly 88% of youth reported worse MH symptoms and impairment compared to caregivers' report. All youth endorsed above average MH literacy. About 79% of caregivers participated in the intervention and were highly satisfied (M=29; SD=3.61). Next steps include a pilot RCT to test the feasibility, accessibility, effectiveness, and implementation of the intervention.

366. Stassi DiMaggio, Xavier University of Louisiana. **Development of a Targeted Chemotherapeutic Drug Delivery System.** Co-Authors: Jayalakshmi Sridhar, Sri Hari Galla. Co-Authors Institutional Affiliations: Xavier University of Louisiana. INBRE
The present-day challenge of delivering anti-cancer agents selectively to tumor cells to mitigate systemic toxicity has led to greater focus on drug delivery research using nanoscale carriers. Despite progress, the therapeutic effects have not lived up to their expectations in the clinical setting. Though promising, these systems typically exploit passive delivery of a single therapeutic to the target tissue. Our current pilot project is addressing this issue through the design and synthesis of the 2 components of a Smart Dual Acting Drug Delivery System (SDADDS) consisting of bifunctional nanocarriers capable of synergistic targeting of multiple drivers of cancer thereby overcoming current limitations to treating cancers. The dual components consist of i) extracellular receptor targeting through polyvalent binding to increase selective binding to cancerous cells and ii) Intracellular targeting by delivering chemotherapeutics selectively through controlled photorelease. A designed bifunctional nanocarrier will have a targeting agent that binds to and inhibits a cell surface receptor highly overexpressed in tumor cells, coupled to a multiplexed anti-tumor drug that can be released locally by photolysis, affecting high spatiotemporal control for delivering the drug at high concentration. Triple negative breast cancer (TNBC) is a multi-driver disease with no selective actionable dominant target. As no targeted therapy has been approved for sporadic TNBC, this will serve as an excellent model to explore the efficacy of SDADDS as a potential new treatment of TNBC.

367. Tony W. Wilson, Boys Town National Research Hospital. **Functional Brain Development is Tightly Coupled to Hormone Levels during the Pubertal Transition Period.** Co-Authors: Giorgia Picci, Max J. Kurz, Elizabeth Heinrichs-Graham, Brittany K. Taylor. Co-Authors Institutional Affiliations: Boys Town National Research Hospital. COBRE
Dynamic cortical activity is known to undergo robust developmental changes during the pubertal transition period, but the trajectory and key mechanisms remain poorly understood. Our previous work has shown that such changes in both spontaneous (i.e., resting state) and task-related oscillatory neural activity predict improvements in sensory and cognitive function across multiple domains and are critical to the emergence of higher-order cognition during late childhood and adolescence. To help clarify the mechanisms, we have leveraged an advanced dynamic functional brain mapping method based on magnetoencephalographic (MEG) imaging, both hair- and saliva-based metrics of pubertal hormone levels, and high-level statistical modeling of the interrelationships in large samples of typically developing 6-15 year-old youth. These studies have shown that dynamic cortical activity serving multiple cognitive processes is tightly coupled to both pubertal testosterone and dehydroepiandrosterone (DHEA), after partially out age, during childhood through adolescence. The development of cortical dynamics in posterior occipital and parietal cortices appears to be closely linked to endogenous DHEA levels, while that in prefrontal cortices is more tightly aligned with testosterone levels. Taken together, these data suggest that puberty-related hormonal changes are strongly associated with developmental improvements in cognitive function and the underlying cortical dynamics in typically developing children and adolescents.

368. Rohan Gupta, University of South Carolina. **Prediction of putative diagnostic and therapeutic biomarkers for post-traumatic stress disorder and related comorbidities through machine learning.** Co-Authors: Mitzi Nagarkatti, Prakash Nagarkatti. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine, University of South Carolina. COBRE
Post traumatic stress disorder (PTSD), a condition with profound societal and individual impact, is often triggered by various factors like traumatic brain injury and mental health issues. Identifying biomarkers and genes linked to PTSD could transform treatment methods. Our study utilizes the Gene Expression Omnibus to analyze gene expression related to PTSD and associated disorders such as bipolar and schizophrenia. Employing techniques like Gene Set Enrichment Analysis and machine learning, we aim to decode the underlying mechanisms of these conditions. Our research also explores immune cell infiltration and the potential for drug repurposing to advance personalized PTSD treatments. This innovative approach is poised to enhance understanding and treatment of PTSD, offering more effective, customized interventions for those affected. Our findings highlight shared biological roots between PTSD and mental disorders. Functional enrichment and GSEA highlighted associations with immune response, inflammatory regulation, and cellular stress. Feature extraction methods pinpointed 11 critical signatures, namely HLA-DQA1, CD24, MMP8, DEFA4, TNFRSF9, TIMP1, TRPM3, TAPBP, IGFBP6, DEFA1, and OLFM4 associated with PTSD comorbidities, while ssGSEA revealed 7 types of immune cell infiltration (B cell, Macrophage, Regulatory T cell, CD4+ T cell, Eosinophil, Type 2 T helper cell, Central memory CD8 T cells) and 5 immune cells (Macrophage, B cells, CD4 T cell, CD8 T cell, and Dendritic Cells) that correlated with hub signatures. (Supported in part by NIH grants P20GM103641, R01ES030144, R01AI123947, and R01AI160896).

369. Yutong Liu, UNMC. **Preclinical MRI Core at the University of Nebraska Medical Center.** Co-Authors: None. COBRE
The Preclinical MRI Core at the University of Nebraska Medical Center (UNMC) in Omaha, Nebraska provides quantitative imaging capabilities using MRI for small animals. The core provides data

acquisition, analysis, user training, custom software development and RF coil building. Services ranges from providing raw images to scientific collaborations, including the development of imaging and image analysis methods, as well the preparation of manuscripts and grant applications. The Preclinical MRI Core has been in operation since 2001. It consists of 2 Bruker MRI systems (BioSpec 70/21 with AVANCE III and PharmaScan 70/16 with AVANCE III HD), 2 high performance workstations, and faculty devoted to the advancement of in vivo imaging methods. The MRI techniques provided include, but are not limited to, relaxometry, diffusion tensor imaging, perfusion-weighted imaging, functional MRI, cardiac imaging, manganese-enhanced MRI, chemical exchange saturation transfer MRI, and magnetic resonance spectroscopy. Image analysis methods include data visualization, registration, segmentation, and parametric map calculations. The facility has been involved in a broad number of successful NIH grant applications as the primary funding source for its operation, and continues to operate with the goal of complete funding by external sources.

370. Cody Casey, Coastal Carolina University. **Comparative analysis of Bicaudal C developmental regulator homologs in class Osteichthyes.** Co-Authors: Chiara Gamberi. Co-Authors Institutional Affiliations: Coastal Carolina University. INBRE

Bicaudal C (BicC) is an RNA binding protein first discovered in the fruit fly Drosophila melanogaster that has homologs in virtually all vertebrates. Within the fly germline, Bic functions in establishing the anteriorposterior polarity of the oocyte and the corresponding embryonic axis. Somatically, BicC functions in vertebrates by regulating cell fate and contributes to organ laterality. In both flies and vertebrates, BicC regulates renal cell function and profliferation. BicC loss-of-function (LOF) mutations in Drosophila lead to development of renal cysts, similar to human polycystic kidney disease. BicC has two canonical K Homology (KH) RNA binding domains, three noncanonical KH-Like Domains, and a Sterile Alpha Motif (SAM) Domain. The BicC SAM Domain resembles the RNA-binding SAM Domain of the fly protein Smaug. The evolutionary conservation of BicC implies it is a fundamental biological regulator for which specific targets and precise molecular functions have yet to be characterized. Our goal is to explore BicC structural and functional conservation in marine species, currently focusing on bony fish (Osteichthyes). Selected BicC homologs and isoforms sequences of chosen organisms were retrieved from Genebank in FASTA format and aligned with Drosophila and human BicC references using Clustal Omega. Resulting multiple sequence alignments were further annotated noting RNA binding domains and key residues. This research will expand understanding of RNA binding protein properties and allow for development of new hypotheses for BicC function in marine species germline and somatic tissues.

371. Robert T Wheeler, University of Maine. **Establishment of Super-resolution Confocal Microscopy CORE.** Co-Authors: None. COBRE

One of the crucial technological needs for the University of Maine COBRE is high-quality confocal fluorescence microscopy and image analysis. Our investigators have diverse technological requirements, from moderate super-resolution to high-speed live cell imaging. To provide this service for the COBRE, we worked closely with the COBRE investigators to choose the best microscope system and image analysis software for them. We have acquired this equipment and set it up within the first year of the grant, and have successfully trained several individual microscopists in each investigator's laboratory. This required navigating a number of obstacles, including purchasing constraints and difficulties in hiring a full-time microscopist. We have successfully vaulted these hurdles and have also received funding for capital improvements to the imaging suite that will improve the imaging and processing experience. Here, we will describe our experiences and discuss how it is important to work closely with the COBRE investigators to successfully navigate difficulties and develop a core facility that enhances the capabilities of the investigators.

372. Margaret C Walsh, The Miriam Hospital. **Community Collaborative Core.** Co-Authors: Ernestine Jennings, Stephanie Parade, Laura Stroud. Co-Authors Institutional Affiliations: The Miriam Hospital, Bradley Hospital. COBRE

The Community Collaborative (CC) Core supports the COBRE for Stress, Trauma, and Resilience (STAR) by facilitating relationships between community collaborators and STAR investigators to enhance the impact of the STAR COBRE at state and local levels. To achieve this aim, the CC Core has convened a Community Advisory Board to provide guidance on local community and government priorities and provide expertise, resources, and consultation to STAR COBRE Investigators related to developing community collaborations. The CC Core provides expertise, resources, seminars, and/or consultation to STAR investigators related to developing, maintaining, and enhancing community collaborations. The CC Core collaborates with community partners to identify ways the STAR COBRE can support their work by providing consultations and training on a variety of topics relevant to their goals, such as grant applications, program evaluation, data analysis, and interview training. The CC Core provides expertise, resources, seminars, and/or consultation focused on effective recruitment and retention of under-served and minoritized populations. Through this work, the Community Collaborative Core also supports STAR investigators in the ethical conduct of research with children and adults with stress and trauma histories and mental health symptoms/disorders. Finally, the CC Core aims to enhance community collaborations through increasing competence of STAR investigators regarding issues of diversity, equity, inclusion, and belongingness and in working with historically marginalized populations. This is achieved through trainings that focus on self-reflection and working with historically marginalized populations, and how diversity, equity, inclusion, and belongingness intersect with community collaborations and participant recruitment and retention.

373. Eva C. Diaz, University of Arkansas for Medical Sciences. **Wild blueberry volatile and phenolic fractions mitigate LPS induced inflammatory responses in whole blood of children.** Co-Authors: Sean H. Adams, Laura Felgus-Lavefve. Co-Authors Institutional Affiliations: University of California Davis School of Medicine, University of Arkansas. COBRE

Background: The anti-inflammatory effects of berries have been attributed to their polyphenol content. In vitro models of activated murine macrophages have shown that volatiles in berries exert anti-inflammatory effects as well. However, human data in this area are scarce. Objective: To evaluate effects of wild-blueberry phenolic (WBB-P) and WBB volatile (WBB-V) fractions in LPS-treated whole blood (WB) of children. Methods: Fasting WB was collected (n=19), and treated with high and low doses of either WBB-P (2 Î¼g/mL or 0.02 Î¼g/mL), WBB-V (2 ng/mL or 0.02 ng/mL), or culture medium (RPMI) as control. Interleukin (IL)-1Î², IL-6, IL-10 and TNF-Î± supernatant concentrations were measured by ELISA. One-factor ANOVA analysis was used to compare cytokine concentrations (ng/ml) of WBB fraction treatments against their respective RPMI + LPS controls. Results: Children (12.0Â±0.6 y/o) were predominantly white (79%), and with a BMI percentile of 51Â±35. At both LPS levels, IL-6 concentrations were lower in the high-dose WBB-P and WBB-V treatments compared to the control group. LPS-High: WBB-P: 22.2Â±6.7 vs. RPMI: 28.2Â±8.3 (p=0.005); WBB-V: 24.4Â±7.2 vs. RPMI: 28.2Â±8.3 (p=0.013). LPS-low: WBB-P: 20.4Â±5.5 vs. RPMI: 26.6Â±7.7 (p=0.001); WBB-V: 20.6Â±6.5 vs. RPMI: 26.6Â±7.7 (p

374. Abby Richardson, University of Delaware. **Optimization of HaloTag labeling for tracking Legionella pneumophila effector proteins.** Co-Authors: Jake Ellis, Summer Hackenburg, Ramona Neunuebel. Co-Authors Institutional Affiliations: University of Delaware. COBRE

Legionella pneumophila is a Gram-negative intracellular pathogen that infects and proliferates within human lung macrophages causing a severe pneumonia known as Legionnaires' disease. L. pneumophila

secretes >330 bacterial effector proteins into the host cytosol during infection which hijack the host cell's vesicular trafficking network to establish a replicative niche. However, the spatiotemporal distribution of the effectors remains largely unknown. A common approach to track the effectors during infection is immunostaining fixed cells. However, antibodies can produce non-specific signals and may not detect less abundant proteins. Instead, we can generate a fusion protein with the effector protein of interest and HaloTag which covalently binds to synthetic HaloLigands conjugated to a fluorophore. The covalent bond between the HaloTag and HaloLigand allows for visualization of the tagged effector within both live and fixed cells. HaloTag was previously shown to form an intramolecular disulfide bond between Cys61 and Cys262 residues under oxidizing conditions. This blocks the formation of the covalent bond between HaloTag and the HaloLigand, preventing visualization of L. pneumophila effectors. To maximize HaloTag's ability to label target effectors with HaloLigands, we can instead use a version of HaloTag where the cysteine residues are mutated. This version of HaloTag maintains its secondary structure and the ability to bind HaloLigands, but prevents disulfide bond formation. Here we will describe the contexts in which our lab is currently utilizing the HaloTag-HaloLigand system and how the Cysless HaloTag can benefit our future experiments.

375. Valeria C. Zarate, Ocean State Research Institute. **Mitochondrial Function and In Vivo Imaging (MF-II) Core Facilitates Basic and Translational Cardiopulmonary Vascular Biology Research in Rhode Island.** Co-Authors: Peng Zhang, Elizabeth O. Harrington, Gaurav Choudhary. Co-Authors Institutional Affiliations: Ocean State Research Institute. COBRE
The overall goal of the CardioPulmonary Vascular Biology (CPVB) COBRE program is to facilitate high impact vascular biology research. The CPVB COBRE has successfully supported numerous innovative studies for a better understanding of pathogenesis and the associated mechanisms of cardiopulmonary diseases. Over these years, there was increasing interest and requests to perform mitochondrial function assessments and high-resolution in vivo imaging in preclinical studies. The Mitochondrial Function and In Vivo Imaging (MF-II) Core evolved from the Respiratory Core that was established in 2021 as the 2nd technical core of the CPVB COBRE based on user needs. The mission of the MF-II Core is to develop a centralized system for mitochondrial function assessments and high-resolution in vivo imaging, with the goals to enhance productivity, promote interdisciplinary and inter-institutional collaborations, and increase research impact of the CPVB COBRE investigators and other investigators in Rhode Island. The Respiratory/MF-II Core has shown a steady growth of the deliverables and value of services over the years and has an excellent research pool for core usages. To date, the Respiratory/MF-II Core has served more than 30 unique users with over 4,500 services. There was a ~2.2-fold increase in yearly technical core services from Phase I to Phase II. In Phase III, the overall objective of the MF-II Core is to facilitate the scientific objectives and technical repertoire of the CPVB COBRE Pilot Project Investigators and other investigators by providing centralized cutting-edge technologies and essential services and to establish processes and procedures that lead to its sustainability.

376. Greer Porter, Creighton University. **Correlation of metabolic changes quantified by nadh phasor flim with P53 expression in uv-induced skin cancer.** Co-Authors: Alex Chen, Kennedy A. Haase, Reese Kolar , Jackson M. Laurent, Johnathan Li, Aidan O'Mara, Maimuna Olow Nagey, Jalen K. Ramos, Derek A. Remitar III, Abraham J. Saks, Hannah Schloman, Jinann A. Shoshara, Zachary J. Smith, Fiona Sun, Jacob A. Sweet, Jake S. Wakahiro, Laura A. Hansen, Michael G. Nichols. Co-Authors Institutional Affiliations: Creighton University. INBRE
Cancer causes significant alterations to cellular metabolism and tissue structure. While these changes occur early in the disease progression, they are not identified until much later due to limited screening. To investigate a more efficient, non-invasive method of diagnosing skin cancer, in vivo metabolic

changes of epidermal cells were quantified through fluorescence lifetime imaging microscopy (FLIM) of NADH and compared with immunofluorescence of tumor suppressor p53. We observed 18 UV-treated and 12 shamtreated SKH1 mice over 26 weeks. Epidermal images at varying depths were taken for each mouse every four weeks at several locations. Time-resolved NADH fluorescence decay was measured through FLIM, and the protein-bound: free ratio of NADH was calculated through phasor sine and cosine transformations. This ratio was used to monitor changes in metabolic activity. We found significant differences in this ratio for UVtreated mice compared to sham controls. P53 expression was also examined to correlate our findings with NADH FLIM. Preliminary data confirms an upregulation of p53 within the UV-treated mice in comparison to sham controls. This demonstrates the utility of NADH phasor FLIM for non-invasive, longitudinal monitoring of cellular metabolism. The project described was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under Grant # 5P20GM103427.

377. Asher Swan Adams, University of Montana. **Defining the role of pH regulatory proteins in neural stem cell development.** Co-Authors: Bernice C Lin, Isabella R Maag, Beverly J Piggott. Co-Authors Institutional Affiliations: University of Montana. INBRE
Electrolyte balance and maintaining physiological pH are vital for cell survival across the animal kingdom, especially in the brain where ionic distribution underlies neuronal function. While cellular pH is traditionally believed to remain tightly regulated (around 7.2 to 7.4), recent findings indicate significant variations over time and between cell types. pH levels, influenced by H+ ions, profoundly affect molecular interactions, impacting cellular activities. Despite the ability of cells to adjust pH for signaling and behaviors, little is known about its role in development. Major pH regulatory proteins like Na+/H+ exchangers (Nhe) play crucial roles in nervous system development. The human genome encodes 9 Nhe proteins and mutations in these genes cause Christianson syndrome and are linked to epilepsy and Autism Spectrum Disorders among others. Our research focuses on understanding pH regulation in neural development using the fruit fly, Drosophila melanogaster, as a model. Our preliminary work links distinct pH states to cell fate and identified a role for one of the three fly Nhe proteins, Nhe2, in neural stem cell proliferation. Nhe2 regulates cytosolic pH, but other family members are predicted to regulate organelle pH. We aim to elucidate how the other classes of Nhe proteins, Nhe1 (predicted Golgi localization) and Nhe3 (predicted endosomal localization) influence neural stem cell development. This research will provide fundamental insights into pH-sensitive processes crucial for nervous system formation that when disrupted can cause disease.

378. Marie-Rachelle Narcisse, Bradley Hospital. **Sleep Duration Moderates the Association between Bullying and Suicide Attempts Among U.S. Adolescents.** Co-Authors: David H. Barker, Jennifer Wolff, Mary A. Carskadon. Co-Authors Institutional Affiliations: Not Listed. COBRE
Suicide is a major public health issue among adolescents in the United States. Bullying is a significant risk factor for suicide attempts during adolescence, while sleep insufficiency is concurrently associated with bullying and suicide attempts. Research has not sufficiently investigated whether sleep duration might moderate the association between bullying and suicide attempts. Multivariable logistic regression based on 2021 Youth Risk Behavior Surveillance System data was used to evaluate the relationships among bullying (school/electronic), sleep duration, and past-year suicide attempts among 17,134 adolescents aged 12-18. An estimated 5% and 16% of adolescents were bullied at school or electronically; 10.2% had made â‰¥ 1 suicide attempt during the past year; 77.3% did not adhere to sleep duration recommendations; and 29.3% reported poor mental health either “most of the time” or “always”. Adolescents who were bullied in school or electronically were three times as likely to attempt suicide vs. those who were not bullied (OR:3.0, 95% CI:2.4â€“3.7). Adolescents with â‰¤4 hours of sleep (10.7%)

were twice (OR:2.6, 95% CI:1.5â€“3.0) as likely to attempt suicide. Sleep duration significantly moderated the association between bullying in schools and suicide attempts (F5,44=3.1;p=0.019), with those who were bullied showing a higher likelihood of suicide attempts with lower (â‰¤4-6 h) or higher (8-10+h) sleep duration. Those reporting no bullying showed reduced likelihood of suicide attempts as sleep duration increased to 7 hours, and the likelihood remained constant with more hours of sleep. Bullying (school/electronic) and short sleep duration increase odds of reported suicide attempts in teenagers.

379. Urmi Halder, University of South Carolina. **Cannabis component attenuates neurodegeneration through downregulation of microglial cell activation, astrocytosis and by reversing gut dysbiosis in GFAP-gp120 Tg Mice.** Co-Authors: Khadija Kakkar, Kiesha Wilson, Tayler Carter, Chloe Weyer, Amira Mohammed, Marcus Kaul, Prakash Nagarkatti, Mitzi Nagarkatti. Co-Authors Institutional Affiliations: University of South Carolina, University of California Riverside. COBRE
The GFAP-gp120Tg mice express soluble HIV-envelope protein, gp120, in astrocytes and share many neuropathological features observed in the CNS of HIV/AIDS patients. Here, we investigated the effect of a cannabinoid, âˆ†9-THC, on gp120-mediated neuroinflammation and progression of neurodegeneration. We treated groups of GFAP-gp120Tg and C57BL/6 WT mice with âˆ†9-THC or the vehicle. Immunofluorescence imaging, flow cytometry, Single-cell RNA-sequencing, and shotgun sequencing were performed to understand the cellular and molecular pathways involved. âˆ†9-THC reduced the neuroinflammation driven by gp120 by influencing the inflammatory chemokine receptors on immune cells that directly infiltrate the CNS. Pronounced astrocytosis and microglial activation seen in Tg mice were significantly reduced following treatment with âˆ†9-THC. Neuroglial gene expression was also reversed after âˆ†9-THC treatment. Tg mice exhibited significant gut microbiota dysbiosis which was reversed by âˆ†9-THC. Members of the genera Alistipes, Prevotella, Plasmodium, Helicobacter, Desulfovibrio had higher relative abundance in Tg mice but reduced after âˆ†9-THC treatment. Taken together, this study demonstrates that âˆ†9-THC treatment significantly improves HIV-gp120-mediated pathogenesis of neurodegeneration, neuroinflammation, and helps to reshape gut microbiota (This work was supported in part by NIH grants R01ES030144, P01AT003961, P20GM103641, and R01AI123947, R01AI160896).

380. Rama S. Gadepalli, University of Mississippi. **The University of Mississippi Drug Discovery Core Facility.** Co-Authors: Eliana Carter, Katie Heath, Soumyajit Majumdar, John M. Rimoldi. Co-Authors Institutional Affiliations: Not Listed. COBRE
Synthetic medicinal chemistry, pharmacokinetics, and animal studies are the three vital components of the iterative cycle of drug discovery. A majority of investigators are faced with significant hurdles in advancing their research programs mainly with compound acquisition and its early-stage pharmacological evaluation using animals and DMPK analysis. With twelve years of collective experience, our Drug Discovery Core of the NIH COBRE Natural Products Neuroscience (NPN) program at the University of Mississippi have bridged the gap by providing investigators services in all these three vital research areas within one facility on a fee-for service basis. Our Chemistry Team specializes in milligram to gram scale synthesis of small molecules including APIs, peptides, drug conjugates, reference standards, and natural product analogs. Our Neuropharmacology Core (NPC) has extensive expertise in various routes of drug administration and blood and tissue collection along with a variety of behavioral tests, including abuse potential, cannabinoid function, anti-nociception, anti-depressant, and ataxia assays. Our Drug Metabolism-Pharmacokinetics (DMPK) facility can then provide downstream bioanalysis using UPLC/MS-MS for various biological fluids (plasma and tissues homogenates).

Additionally, the DMPK Core provides in vitro metabolic stability evaluation, and identifies metabolites formed, in plasma, liver microsome and other tissue matrices, of the test compounds.

381. Daniel Blanchette, University of Idaho. **Segmentation analyses to identify and quantify microglia in 3D image stacks.** Co-Authors: Seth Long, Diana Mitchell. Co-Authors Institutional Affiliations: Not Listed. INBRE

Using time-lapse confocal microscopy to record and observe microglia behavior in living zebrafish embryos, the Mitchell lab investigates the molecular basis of dynamic migration and phagocytic behavior of microglia in the central nervous system. Microglial cells regulate brain development, maintain neuronal networks, and repair neural injuries. Timelapse imaging provides crucial insight into the behavior of these cells. Other methods, such as manual cell counting, are subject to human bias and are tedious, repetitive, and time consuming. The Long computer science lab utilizes Python and open-source modules to develop an automated pipeline as a programmatic solution. These methods aim to expedite and optimize the lab's manual processes. This research project seeks to segment microglia when applied to 3D time series image stacks. Computer segmentation of microglia imaging relies on pixel values to generate bitmasks. Microglia segmentation is challenging because the cell's irregular shape and size can be obscured, resulting in omitted pixel intensity values. Two programs were developed to test the viability of Otsu, multi-Otsu, and Yen automatic thresholding[2]. Both methods separate the raw image into two layers: the foreground and background. Numerical data is generated via histograms to predict optimal threshold values for each algorithm. Prototype implementations of these programs demonstrate viability for microglia counting. However, misclassification of microglia occurs when the predicted pixel threshold is outside the histogram's range. Further refinement of these programs is crucial as they will be foundational for future object classification methods and microglia tracking, optimizing the lab's data processing capabilities and time.

382. Marie Yarbrough, Furman University. **The impact of innocuous taste experience on long-term taste learning and memory persistence.** Co-Authors: Dallas Shuman, Kadence Alexander, Veronica Lee Flores. Co-Authors Institutional Affiliations: Furman University. INBRE

The five senses allow for the interpretation of experiences that are crucial for survival. For example, one wrong food choice can lead to detrimental repercussions-including death. Taste experiences are a risky process that pave the way for strong and robust taste learning. Rats can learn to associate a negative consequence, like malaise with a taste after only one negative experience. This type of learning is called conditioned taste aversion (CTA), and the strength of association between the taste and the consequence is known to be modulated by experience. For example, familiarity with a taste protects that taste from future associations with an aversion. Our lab has shown that animals who have had prior inconsequential experience with an array of tastes learn stronger aversions towards novel tastes. Here, we hypothesize that aversions formed after inconsequential taste experience are more adeptly stored in long term memory as compared to taste naÃ¯ve rats due to enhanced plasticity. Long Evans rats experienced inconsequential tastes (water, salty, and sour) followed by an conditioned taste aversion (CTA) to novel sucrose. Aversion memories were tested 24 hours, 1 week, or 2 weeks later. Our results show that experienced rats retain aversion memories longer than taste naÃ¯ve rats. We measured synaptic plasticity behind this retention through the immediate early gene Npas4. We hypothesize that incidental taste experience will enhance the expression of Npas4 within primary taste cortex. These results are the first to demonstrate the impact of inconsequential taste experience on synaptic plasticity and long-term memory retention.

383. Margaret Leonard, Presbyterian College. **Specific histone arginine methylation sites identified by histone proteomic profiling are depleted through dual p53 and PTEN deletion in metastasis-**

transformed MCF10A breast cells. Co-Authors: Charlotte B McGuinness, Megan A Wilson, Austin Shull. Co-Authors Institutional Affiliations: Presbyterian College. INBRE
Metastatic potential in basal-like breast cancers typically is initiated by genetic alterations that lead to a process known as epithelial-mesenchymal transition (EMT). However, the transition between these genetic alterations and the epigenetic switches that help drive the invasive EMT phenotypes in breast cancers is still not well defined. With this attempt to better connect epigenetic modifications in breast cancer invasiveness, we performed a DIA-based mass spectrometry of isolated histones from an isogenic panel of MCF10A breast cell lines where tumor suppressor genes TP53 and PTEN were silenced to induce EMT. From approximately 72 histone modifications identified and annotated from our mass spectrometry results, we identified 5 histone events differentially altered in our MCF10A cell line panel. Two events of note were histone H3 lysine14 acetylation (H3K14ac) significantly increasing and histone H4 arginine 55 dimethylation (H4R55me2) significantly decreasing in our EMT-transformed MCF10A p53-/PTEN- cell lines when compared to the parental, non-tumorigenic MCF10A cell line. Additionally, significant arginine demethylation of H4R55me2 & H3.1R83me in the EMT-transformed MCF10A p53-/PTEN- cell lines corresponded with JMJD6, an established histone arginine demethylase, being overexpressed in basal-like breast cancer cell lines as well as in basallike breast cancer patients from The Cancer Genome Atlas (TCGA) and METABRIC datasets. Through histone proteomic profiling of our isogenic EMT model, the loss of specific histone arginine methylation events corresponding with JMJD6 overexpression could highlight the potential for a targetable epigenetic mechanism in breast cancer metastasis.

384. Christopher A Pennington, Nemours Children's Health. **Facilitating Research Data Exchange among Delaware Healthcare Providers Using OMOP and FHIR.** Co-Authors: Claudine Jurkovitz, Bill Moyers, H. Timothy Bunnell. Co-Authors Institutional Affiliations: ChristianaCare Health Service, Inc., Nemours Children's Health. CTR
Sharing data extracted from electronic health records (EHRs) at multiple institutions is necessary to build the massive datasets required for emerging statistical and machine learning approaches to clinical translational research. Use of Common Data Models (CDMs) is a critical prerequisite for sharing EHR information. Within the Delaware Center for Translational Research (DE-CTR), Nemours Children's Health and ChristianaCare researchers have mapped their data to the Observational Medical Outcomes Partnership (OMOP) CDM. The Fast Healthcare Interoperability Resources (FHIR) standard offers an ideal solution to facilitate data exchange and the EHRs at Nemours and ChristianaCare are already FHIR-compliant. By creating an infrastructure for seamless data exchange, we will facilitate joint clinical research, expanding to additional Delaware healthcare organizations over time. We have implemented a FHIR resource server using the OMOPonFHIR platform containing fully deidentified pediatric data derived from Nemours' PEDSnet/OMOP database, which mirrors the contents of the Nemours EHR data warehouse. To demonstrate the use of FHIR data resources, we are developing a prototype SMART (Substitutable Medical Applications Reusable Technologies) on FHIR application to query the OMOP CDM and display aggregate results . For better performance, we are integrating the APIs of the OMOPonFHIR and SMART bulk data services. Additionally, we will support a patient-level Clinical Decision Support (CDS) tool aimed at obesity prevention and treatment being developed at the University of Delaware. Finally, we are in the process of collecting specifications and requirements from ChristianaCare and other institutions for the implementation of OMOPonFHIR at those sites.

385. Christian Potts, MaineHealth Institute for Research. **Establishing human vascular mural cells as novel adipocyte progenitors with in vivo transcriptomic insight and in vitro validation.** Co-Authors:

Xuehui Yang, Benjamin Tero, Lucy Liaw. Co-Authors Institutional Affiliations: MaineHealth Institute for Research. COBRE
Pericytes, situated alongside endothelial cells in microvessels, aid vessel development and maintenance. They have the capability to differentiate into diverse cell types, such as myofibroblasts, chondrocytes, vascular smooth muscle cells (vSMCs), and adipocytes, marking them as a distinct progenitor cell population. Collaborative efforts, using single-nuclei RNA sequencing strategies (scRNAseq), led to the discovery of a novel subset of smooth muscle-like cells expressing PPARg in human perivascular adipose tissue (PVAT). Utilizing informatic and traditional in vitro validation techniques, we molecularly characterized this cell population as pericytes. We reanalyzed scRNAseq data from human adipose tissues, encompassing aortic PVAT, subcutaneous and visceral adipose tissues (WAT), and deep neck brown adipose tissue (BAT). These efforts illuminated conservation of PPARg-expressing pericytes across multiple human adipose depots with consistent expression of COL25A1, MYO1B, and POSTN. We also found evidence of limited tissue-specific pericyte markers. Immunofluorescence staining of human adipose tissue was conducted to identify the spatial relationship of pericytes to tissue microvasculature. These experiments revealed presence of pericytes both distant from or adjacent to vasculature in PVAT. Additionally, we demonstrated the potential of human brain pericytes and aortic vSMCs to differentiate into adipocytes in vitro, based on intracellular lipid accumulation and expression of adipocyte markers. Given that vascular mural cells, including pericytes and vSMCs, can undergo adipogenesis, we postulate they are a novel source of adipocytes in the vascular microenvironment.

386. Chris Mantsounga, Providence VA Medical Center/OSRI. **Resistance to IL-1beta leads to reduced VEGF-A required for inflammatory angiogenesis in the setting of aging and chronic Diabetes mellitus.** Co-Authors: Sheila Sharma, Rachel Carley, Olivya Caballero, Crystal Perry, Saketh Uppuluri, Elizabeth Harrington, Gaurav Choudhary, Alan Morrison. Co-Authors Institutional Affiliations: Ocean State Research Institute Inc., Brown University, Providence VA Medical Center. COBRE
Background and objectives: Diabetes mellitus (DM) and DM-associated peripheral artery disease (PAD) cause impairments in angiogenesis-dependent wound healing, a major source of morbidity and mortality in the world. Critical ischemic limb and wound injury animal models have shown impact of monocytes/macrophages in new arterial growth and healing process. We have defined an IL-1betadependent transcriptional regulation of the VEGF-A. We hypothesized the disconnection of IL-1beta and VEGF-A signaling axis with consequent impairments in angio/arteriogenesis in the context of aging and Diabetes mellitus. Results: C57Bl6 mice at 52-weeks or mice with experimental type 2 diabetes (T2D, 10-weeks, Leptin receptor [Leprdb/db]) have reductions of angio/arteriogenesis, using a PAD model of femoral artery ligation that involves macrophage-directed blood flow recovery. Combined aging with chronic diabetes (52-weeks, Leprdb/db) led to further reductions in blood flow recovery consequent to impaired angiogenesis. On day 3 post-surgery, a peak of macrophage recruitment in ischemic limb, RNA and proteins data demonstrate reduced VEGF-A while IL-1beta was increased in 52-weeks T2D compared to Control 52-weeks. Moreover, immunofluorescence microscopy also showed decreased endothelial cells recruitment while macrophages was similar. Bone marrow-derived macrophages from 52-weeks diabetic mice demonstrated increased IL-1beta (4-5-fold) while VEGF-A was reduced. Uncoupled IL-1beta-VEGF-A expression was also associated with reduced IL-1 receptor (IL-1R) expression and IL-1R protein complex (MyD88; IRAK4). Lastly, macrophage-deleted IL-1R mice have shown impairment of blood flow recovery and reduced VEGF-A. Conclusion: Our studies will support diabetic macrophage resistance to generating IL-1R and IL-1R downstream effectors in response to elevated IL-1Î² leading to reduced VEGF-A.

387. Dagmawit Teka, University of Nevada, Las Vegas. **Career Advancement and Faculty Retention of Mountain West CTR-IN Pilot Grant Awardees.** Co-Authors: Beth Tigges, Rachel Boren, Francisco S. Sy. Co-Authors Institutional Affiliations: University of New Mexico, New Mexico State University, University of Nevada Las Vegas. CTR
Introduction: From 2013 -2022, the Mountain West Clinical and Translational Research Infrastructure Network (MW CTR-IN) has successfully nurtured a culture of transformative change and continuous improvement in Clinical and Translational Research. The Tracking and Evaluation Core tracks the career trajectory and faculty retention of our pilot grant (PG) awardees as key indicators of our program's impact, as awardees continue their research and leadership transitions after award completion. Methods: To examine the career progression of 122 faculty who received pilot grants between 2013-2022, we conducted a detailed career analysis of these PG awardees. Results: Of the 122 awardees from 2013 -2022, 89 (73%) were Early Stage Investigators and 27 (22%) were New Investigators. 66% of those who could advance in their tenure and promotion status did so by 2023. Of these, 65% were promoted to Associate Professor, 30% to Professor, and 6% to Deans or Associate deans. Career advancement is most prevalent in 51 of 66 (77%) pilot grantees from 2013-2018 when enough time has elapsed to be promoted. Almost all (93%) remained in academic settings. We also analyzed PG awardee faculty retention by assessing the annual number and percentage of grantees who remained at MW CTR-IN partner universities after their first grant application. Our grant kept 79% of PG awardees at their home university after ten years. Conclusions: These evaluation initiatives demonstrate the positive impact of MW CTR IN pilot awards on the grant awardees' career advancement and the high faculty retention of these PG awardees in our partner universities.

388. Juliane Strauss-Soukup, Creighton University. **Evolutionary conservation of ornithine decarboxylase antizyme pseudoknot RNA binding to spermine.** Co-Authors: Spencer Thompson, Rhiannon McCracken, Garrett Soukup. Co-Authors Institutional Affiliations: Creighton University. INBRE
Nearly all organisms possess the capability to synthesize polyamines, which are essential for cell growth and differentiation. Not surprisingly, the transport and metabolism of polyamines are highly regulated by complex feedback mechanisms. Ornithine decarboxylase (ODC) is the key regulatory enzyme in polyamine biosynthesis. Both ODC and cellular uptake of polyamines are inhibited by Ornithine Decarboxylase Antizyme (OAZ). Although the role of the OAZ pseudoknot RNA element (OAZ-PK) in polyamine biosynthesis has been investigated, it has not been examined as a distinct polyamine “sensor”. Riboswitches are elements within noncoding regions of mRNAs that directly bind to cellular metabolites and modulate gene expression. Many riboswitches provide a mechanism of feedback regulation for gene products within the biosynthetic pathway of the cognate metabolite. Although riboswitches are widespread among bacteria, no riboswitches have been found in animals. We propose that the highly conserved OAZ-PK RNA functions as a riboswitch. Utilizing in-line probing, equilibrium dialysis and gene expression assays, we have shown that mouse OAZ-PK RNA binds to spermine with greater affinity than to other polyamines, and spermine binding elicits conformational changes and modulates gene expression, all fundamental properties of riboswitches. Closely related spermine analogs (with identical or greater overall positive charge) have lesser affinity and specificity for the OAZ-PK RNA. Current work is focused on investigating OAZ-PK RNAs from other organisms. Preliminary results indicate specificity and affinity for spermine, as observed for the mouse OAZ-PK RNA. The function of OAZ-PK RNA as a spermine “sensor” suggests a substantially broader distribution of riboswitches among eukaryotes.

389. Loyda B. Mendez, Universidad Ana G. Mendez, Carolina. **Enhancing technical and research skills of the biomedical workforce in Puerto Rico.** Co-Authors: Sandra Charriez. Co-Authors Institutional Affiliations: University of Puerto Rico Medical Science Campus. INBRE
The Science and Technology Competency and Education (STCE) Core objective is to increase the research and technical skills of the biomedical workforce in Puerto Rico by encouraging a greater number of undergraduate and graduate students and postdoctoral associates to pursue careers in science and technology, and by providing hands-on research opportunities to increase their competitiveness when pursuing a career in the Biomedical field. To this extent, the STCE provides training through tuition support for specialized short courses and workshops, research experience for students through summer internships and the junior research associates (JRA) programs, support for visiting speakers through a seminar tours program, and professional development for student and faculty via travel support to scientific meetings. Our Mission is to strengthen the science, technology, community engagement, entrepreneurship, and data science competencies of the current and future STEM workforce through education and training programs. In addition, the STCE Core foster collaborations among investigators, entrepreneurs, and data scientists at network institutions, between INBRE researchers in Puerto Rico and other IDeA states.

390. Poorna Sai Vaddi, Louisiana State University. **Tamoxifen Regulation of the HIF Pathway mediated Angiogenesis and Tumor Aggressiveness in Glioblastoma.** Co-Authors: None. COBRE
Glioblastoma (GBM) is one of the most common and malignant primary brain tumors in adults. Approximately 49% of malignant brain tumors are glioblastomas. It has a poor prognosis of about 5-10%, with patients surviving no more than 5 years after the diagnosis. The intra- and intertumoral heterogeneity seen in GBM contributes to resistance and the eventual recurrence of the tumor. The rapid growth and invasiveness of GBM into surrounding tissue make it highly difficult to surgically remove. Recent studies show that GBM responds poorly to known standard treatments, so there's a pressing need for a more targeted approach. Upon diagnosis, GBM treatment starts with maximal surgical resection, followed by radiation and treatment with Temozolomide (TMZ), a DNA-alkylating agent. Although TMZ is part of the standard chemotherapeutic regimen for GBM, it has unintended effects and doesn't cure the condition alone. An alternate approach of targeted therapies might help reduce unintended effects and have a better prognosis for the patient. Tamoxifen (TAM) is a selective estrogen receptor modulator (SERM) that is primarily used in the treatment and prevention of estrogen receptor-positive breast cancer. It acts as an estrogen receptor alpha antagonist to block the negative effects of estrogen in the development and progression of cancer. Although GBM is a hormone-independent tumor, some studies have documented the role of estrogen in GBM's growth and advancement. Tumor hypoxia, or low oxygen levels within the cancerous tissues, is a very common feature of solid tumors, which contribute so much to tumor aggressiveness, angiogenesis, and metastasis through a key regulator called Hypoxia Inducible Factor (HIF). The aberrant dysregulation of HIF signaling has been implicated in various cancers and has been explored as a potential target for treatment for cancer. Based on the available evidence, we cultured mouse (GL261) and human glioblastoma cells (SNB19, U251) with 5ÂµM to 15ÂµM concentrations of TAM for 24 hours and 48 hours' time periods to establish and check the dosedependent effects of the drug. Consequently, we hypothesize that TAM's potential as a drug in regulating the HIF signaling pathway-mediated angiogenesis (Endothelial to mesenchymal transition (EndMT), P13k/Akt/mTOR pathway) and tumor aggressiveness (Epithelial to mesenchymal transition (EMT)). Our preliminary findings implicate and corroborate our hypothesis, suggesting TAM as an additional therapy along with a standard treatment regimen.

391. Lynne Dieckman, Creighton University. **Structural Basis for the Interaction Between Protein Complexes that Regulate Gene Silencing.** Co-Authors: Keely Orndorff, Grace Jaworski. Co-Authors Institutional Affiliations: Creighton University. INBRE
The eukaryotic genome must be accurately organized into nucleosomes immediately following DNA replication to maintain genomic and epigenetic integrity. This process, called replication-coupled nucleosome assembly, is mediated by two key factors: CAF-1, the protein complex that deposits histones onto the newly synthesized DNA, and PCNA, the ring-shaped sliding clamp that recruits and regulates the proteins that replicate DNA. Although the mechanism by which nucleosome assembly and DNA replication are coupled remains poorly understood, studies show that the interaction between CAF-1 and PCNA is essential for this process. Our goals are to understand this interaction at the kinetic, thermodynamic, and structural levels to determine the mechanism of CAF-1 recruitment to the replication fork and how PCNA distinguishes between CAF-1 and other PCNA-interacting proteins. We solved the 3D structure of PCNA bound to a motif of CAF-1 and performed binding studies with mutant forms of these two proteins. These results reveal the specific amino acids of CAF-1 required for binding PCNA, as well as residues that might interfere with a high affinity interaction. Together with previously determined structures of PCNA-bound complexes, our data suggest sequence-specific motifs are critical for PCNA to distinguish between binding partners at the replication fork during nucleosome assembly.

392. Tritia Yamasaki, University of Kentucky. **Metabolomic Assessment of Synucleinopathy Patients from Movement Disorder Clinic.** Co-Authors: Elena Ostrakhovitch, Bibi Broome, William Holden, Lance Johnson, Ramon Sun, Lei Wu, George Quintero, Craig van Horne, Tritia Yamasaki. Co-Authors Institutional Affiliations: University of Kentucky, University of Florida. COBRE
Parkinson's disease (PD) and multiple system atrophy (MSA) are neurodegenerative diseases with abnormal accumulation of pathologic alpha-synuclein. The similarity in symptoms between PD and MSA at early-stage can lead to misdiagnosis, incorrect prognosis, and erroneous clinical trial stratification. PD presents heterogeneously with different subtypes including tremor-predominant and rigid-akinetic forms which may have different progression rates. In this study we utilized metabolomic analysis of plasma from synucleinopathy patients to distinguish (1) PD from control, (2) subtypes of PD and (3) PD from MSA. Participants included MSA (9), PD (tremor predominant n=11, rigid akinetic n=8 and mixed n=10) and control (n=10) patients. Blood was processed, aliquoted and frozen at -80. Polar metabolites were extracted and analyzed by gas chromatography-mass spectroscopy. Data analysis was performed on MetaboAnalyst. Several metabolites had greater than 1.0-fold change between PD and control samples including pyruvic acid, oleic acid, lactic acid, palmitic acid, L-threonine and L-serine. Only one metabolite, 1,2-hydroxybutyrate, was significantly decreased in akinetic vs tremor-predominant PD. In PD vs MSA, arginine and proline metabolism was significantly different on impact analysis. Several metabolites were elevated (serine, threonine and proline). Glycolic acid, oxalic acid, 1,5-anhydro-D-glucitol, and phosphoric acid were all downregulated. These results confirm differences between plasma metabolites in PD vs control. Although less robust differences were seen in the plasma profile of patients with different clinical subtypes of PD, PD and MSA had distinct metabolite differences. We are expanding the number of tested samples and working to confirm differences via LC-MS.

393. Rori Schreiber, West Liberty University. **A molecular biology approach to identify Francisella tularensis proteins that interact with Band 3 of human erythrocytes.** Co-Authors: Josepha Horzempa, Luke D'Cunha. Co-Authors Institutional Affiliations: West Liberty University. INBRE
Francisella tularensis is a pathogenic gram-negative bacterium that causes the zoonotic disease Tularemia. In addition, F. tularensis is classified as a Class A Bioterrorism agent by the CDC due to the ease of aerosolization and the ability of this bacterium to cause fatal infection in low doses. Previous

studies suggest that invasion of mammalian erythrocytes by F. tularensis helps to increase colonization of ticks, an arthropod vector of this pathogen. Our laboratory previously found that the erythrocyte membrane glycoprotein, Band 3 is required by F. tularensis for invasion of red blood cells. Therefore, we predict that bacterial proteins interact with Band 3 to facilitate invasion. To identify these proteins, we will express codon-optimized Band 3 linked to a Glutathione-S transferase tag in F. tularensis LVS. Subsequent pull-down assays may reveal F. tularensis protein binding partners to Band 3 responsible for facilitating erythrocyte invasion. (NIH Grant R15HL147135 and P20GM103434 to the West Virginia IDeA Network for Biomedical Research Excellence.)

394. Eui Young So, Brown University/Rhode Island Hospital. **Myeloid Specific Ablation of SHIP1 Boosts Expansion and Regulatory Function of Myeloid-Derived Suppressor Cells in Inflammatory Arthritis.** Co-Authors: Olin D Liang. Co-Authors Institutional Affiliations: Brown University/Rhode Island Hospital. COBRE
Myeloid-derived suppressor cells (MDSCs) are a heterogeneous cell population and the immunosuppressive function of MDSCs has been well established in tumor microenvironment. Recent studies show that adoptive transfer of MDSCs can ameliorate collagen-induced inflammatory arthritis (CIA), a mouse model of human rheumatoid arthritis (RA). Src homology 2 domain-containing inositol polyphosphate 5-phosphatase 1 (SHIP1) was previously shown to regulate MDSC differentiation. Here, we aimed to generate immunosuppressive MDSCs from mouse bone marrow (BM) through genetic modification combined with cytokine treatments, and to investigate the ability of these ex vivo induced BM-MDSCs to suppress inflammatory responses in the CIA mouse model of RA. We found that myeloid specific ablation of SHIP1 increased the ratio of MDSCs and enhanced their regulatory functions in cytokine induced BM culture. MDSCs from LysMcre:SHIP1flox/flox mouse BM culture demonstrated stronger inhibitory effect on T cell proliferation than from control mouse BM. Ex vivo induced MDSCs from either control mice or mice with myeloid specific ablation of SHIP1 were administered to the CIA mice as a cell-based therapy to treat inflammatory arthritis. Adoptive transfer of either BM-MDSCs significantly reduced disease incidence and severity, but SHIP1 deficient BMMDSCs exhibited even higher efficacy compared to control BM-MDSCs. In conclusion, myeloid specific ablation of SHIP1 boosts ex vivo expansion and regulatory function of MDSCs in experimental inflammatory arthritis. These ex vivo generated BM-MDSCs may provide novel therapeutic opportunities for the treatment of RA and other inflammatory diseases.

395. Jo Sevier, Montana State University - Billings. **The Rise and Decline of Pain Clinics in the United States.** Co-Authors: Joshua Hill. Co-Authors Institutional Affiliations: Not Listed. INBRE
This paper establishes baseline data on the rise and more recent decline in pain clinics as a means of managing patient pain. Obviously, finding the balance between minimizing the experience of physical and psychic pain in society and the negative impacts of dependency on pain medication is difficult to find. Pain clinics (and their concomitant strategies for pain management) came to the fore following the return and reintegration of veterans into civilian life in the early 1940s. In the 1950s and into the 1960s, there was a recognized lack of collaboration between specialists. Doctors started to advocate for consolidated treatment plans and introduced the concept of multidisciplinary pain clinics. Positive patient outcomes within pain clinics led to a push for pain clinics as central to pain management. However, in recent years a lack of insurance coverage, liability concerns, and overall negative net revenue have led these clinics to cease operation in many jurisdictions, with direct patient-provider treatment plans filling the gap left. There is little established research about the impact of the change in pain treatment structure on patient outcomes. However, antecedent to that research, there is also a paucity of research upon the prevalence of, or contraction in, the use of pain clinics for treatment. This

paper establishes a baseline for, and explanation of, the rise and decline of pain clinics in the United States and draws lessons to inform policy and regulatory change going forward.

396. Bahaa Jabali, University of Arkansas for Medical Sciences. **Discovery of Non-Covalent pan EGFR Inhibitors for the Treatment of Non-Small Cell Lung Cancer.** Co-Authors: Baku Acharya, Maha Hanafi, Brendan Frett. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences. COBRE Background: Non-small cell lung cancer (NSCLC) remains a significant health concern, with a high mortality rate despite advancements in treatment. Epidermal Growth Factor Receptor (EGFR) mutations drive NSCLC progression in about 30% of cases, making EGFR a key therapeutic target. However, resistance and toxicity to existing EGFR inhibitors pose a challenge for long-term efficacy, necessitating the development of novel therapies. Methods: Using computational screening and fragment-based drug discovery, we propose developing pan-EGFR inhibitors capable of binding within the ATP pocket targeting EGFR mutations. We will then evaluate the biological activity and toxicity of compounds through biochemical screenings and in vitro testing in NSCLC cell lines with clinically relevant mutations. Results: Our findings indicate the successful development of an EGFR inhibitor with efficacy against wild-type EGFR and mutated variants, encompassing L858R, T790M, L858R/T790M, E746-A750del, and L747-S752del. This preliminary compound displays strong binding affinity towards wild-type EGFR as well as diverse mutated isoforms, exhibiting dissociation constants ranging from 0.22 to 7.3 nM. Further refinement has led to the generation of additional analogs exhibiting substantial inhibitory effects on NSCLC lines with EGFR mutations. One analog, BJ-1-86, effectively suppresses mutated forms of EGFR such as E746-A750del (IC50 = 0.032 ÂµM) and L858R/T750M (IC50 = 1.802 ÂµM) while exhibiting selectivity against wild-type EGFR (IC50 = 7.71 ÂµM). Moreover, this analog subsequently blocks downstream pathways that are activated by EGFR. Conclusion: Our research aims to develop novel non-covalent EGFR inhibitors for NSCLC. These inhibitors exhibit the potential to overcome resistance mechanisms and improve patient outcomes.

397. Jacob Ellis, University of Delaware. **Legionella pneumophila effector Lpg2409 interacts with mitochondrial contact site and cristae organizing system (MICOS) subunit Mic60 and alters host mitochondrial structure.** Co-Authors: Marina Grossi, Ramona Neunuebel. Co-Authors Institutional Affiliations: University of Delaware. COBRE
Mitochondria are dynamic organelles, both in their constant energy turnover and in their structural selfregulation via elongation, fission, and mitophagy. A growing number of effector proteins of the intracellular pathogen L. pneumophila are known to target mitochondrial structure and function within host cells. Here we present evidence that a previously uncharacterized effector, Lpg2409, targets mitochondrial components. mCherry-Lpg2409 was found to not only localize to mitochondria in HEK293T cells but to also be transported inside mitochondria via Proteinase K protection assays. Live cell confocal microscopy also revealed that EmGFP- Lpg2409 localized around the mitochondria of HeLa cells. Infections in RAW 264.7 macrophages with L. pneumophila strains expressing 4xHA-Lpg2409 demonstrated that this effector accumulates in host cells late during infection, and subcellular fractionation confirmed localization to mitochondria. HEK293T lysate pulldowns to identify potential host interaction partners with mCherryLpg2409 were enriched in Mic60/Mitofilin, a protein that regulates mitochondrial structure, and was ubiquitinated in the presence of Lpg2409. In vitro pulldown assays further revealed that Lpg2409 and Mic60 can directly interact in the absence of other host proteins. Additionally, Lpg2409 can bind the phosphoinositide PI(3)P in vitro and in cellulo, which is present on endosomes and early autophagosomes. Thus, we hypothesize that Lpg2409 may localize to structures either on or adjacent to mitochondria using its PI(3)P- binding activity, where it targets Mic60.

398. Angel Mayor, Universidad Central del Caribe. **Machine learning for mortality evaluation in Hispanic Persons With HIV.** Co-Authors: Abiel Roche Lima. Co-Authors Institutional Affiliations: University of Puerto Rico. CTR
Background: Significant life expectancy and outcomes improvements had been reported in person with HIV (PVH) after antiretroviral therapy availability. Chronic diseases, and other factors began to play an important role in PVH prognosis. This study evaluates the association between HIV and non-HIV related factors among PVH mortality using machine learning (ML). Methods: The study used a cohort of adult PWH followed since 2000 at Bayamon, Puerto Rico (PR) matched with the PR Heath Department Mortality Registry. Data were analyzed using ML algorithms logistic regression (LR), linear discriminant analysis (LDA), and support vector classifier (SVC). Models were trained using 80% and validated with the remaining 20%. Cross validation ensures high-quality performance. Additional analyses were performed by gender. Results: A total of 1,929 PWH was evaluated, 67.9% male, 67.1% injected drugs (IDs), 38.7% man-sex-with-man, and 32.2% was death by 12/31/2022. In the cohort the best performing model was LDA with an estimated 0.78 mortality probability. By gender, an 0.83 mortality probability was obtained with SVC for men and 0.86 with LR for women. Cancer, anemia, and HCV infection were the predominant mortality predictors in the group and in men. In addition, liver conditions, IDs, and alcohol consumption in men. In women liver condition and HBV were relevant predictors. Conclusions: Using innovative ML models, we found important preventable factors associated with mortality among highly vulnerable Hispanic PWH. These findings highlight the gaps and necessity of preventive interventions strategies beside the ounces for HIV. Further studies are recommended. Acknowledgments: Sponsored grants: U54MD007600-G12MD007583-U54GM133807-U01AI069918-S21MD001830 and NPCR-CDC-5-NU58DP006318.

399. Anupam Kotwal, University of Nebraska Medical Center. **Tumor immune infiltrate in differentiated thyroid cancer.** Co-Authors: Kemal Hajric, Krysten Vance, Ernesto Martinez-Duarte, Ana Yuil-Valdes, Melissa Holzapfel, Salma Elhag, Madelyn Fitch, Oleg Shats, Whitney Goldner, Apar Ganti, Hamid Band, Benjamin Swanson. Co-Authors Institutional Affiliations: Not Listed.
Differentiated thyroid cancer (DTC) accounts for 3.8% of all cancers in the U.S., with roughly 10% of cases progressing to distant metastatic DTC, which is associated with a poor 5-year survival outcome despite conventional management, including surgery and radioactive iodine ablation. While immunotherapies have been proposed as a means of slowing tumor progression, response to them remains poor and unpredictable. In this translational study, we aimed to identify tumor-infiltrating immune markers amongst 15 adult patients with DTC with samples containing tumor and stromal regions collected at initial thyroidectomy. The samples were analyzed using multiplex immunofluorescence with antibodies against cell-surface molecules PD-1, PD-L1, FOXP3, CD3, CD8, CD4, CD68, CD163, and iNOS. Specimens were analyzed via machine learning algorithms and a positive threshold was assigned based on review by a pathologist. A classifier was developed to distinguish auto-fluorescent blood from tissue. Mean expression of immune markers between the tumor and adjacent thyroid tissue were compared by paired t-test. Immune checkpoints PD-1 and PD-L1 were highly expressed within the tumor, despite variability in lymphocyte infiltration. A discernable trend toward increased M2 macrophages and CD4+ T cells along the tumor interface and within the tumor core were observed (p

400. Jennifer Wolff, Alpert Medical School of Brown University. **Bradley Hospital COBRE Center for Sleep and Circadian Rhythms in Child and Adolescent Mental Health: A Pediatric Biopsychology Research Core in a Child Psychiatry Hospital.** Co-Authors: John McGeary, Ella Diab, Micaela Maron, Brynn Chouinard, Mary Carskadon. Co-Authors Institutional Affiliations: Brown University. COBRE

Introduction: The objective of the Pediatric Biopsychology Research Core (PBRC) is to support pediatric mental health assessment, provide consultation for collection, maintenance, and analysis of such data, including use of technology-based resources; and provide resources and consultation for collection, storage, and processing biospecimens. Methods: The aims of the PBRC are 1) select, mentor, and provide career advancement to junior investigators, 2) sustain the infrastructure required to build a Center of Biomedical Excellence in sleep, circadian rhythms, and pediatric mental health, 3) recruit faculty with expertise in sleep and circadian science in the context of pediatric mental health. Results: The PBRC has provided 76 consultations, including project design and setup, inpatient data statistics, measure selection, and data collection, management, and cleaning. Additional activities include training workshops related to the DIAMOND assessment tool, IRB procedures, REDCap, and DNA acquisition, preparation, analysis, and storage. Conclusions: The PBRC works to integrate pediatric biopsychology into the Bradley Hospital clinical and research infrastructure. Our future goals include developing protocols for biospecimen equipment, offering ELISA assays for saliva samples, and providing ongoing consultation and workshops as part of our resources to support research. Clinical Implications: Improving youth mental health care through the integration of sleep and mental health research.

401. Alia Tereza Sadek, University of South Carolina School of Medicine Greenville. **Resistance and Intracellular Survival of Atypical Acinetobacter baumannii Isolates from a Fatal Case of Necrotizing Fasciitis.** Co-Authors: Elias M. Wheibe, Kyleigh Connolly, Christine Liu, Chelsea R. Gutierrez, Brock A. Arivett, Ryan F. Relich, Luis A. Actis, Steven Fiester, Maria Soledad Ramirez, Jennifer T. Grier. Co-Authors Institutional Affiliations: Not Listed. INBRE
Acinetobacter baumannii is one of the most rapidly-evolving pathogens in the world. Although previously a common cause of nosocomial respiratory and bloodstream infections, atypical strains of A. baumannii have been increasingly isolated from fatal cases of necrotizing fasciitis (NF), or flesh-eating disease, over the past decade. Unlike type strains, these NF A. baumannii (NFAb) strains display distinct genomes and enhanced antibiotic resistance, resulting in limited efficacy of current therapeutics and increased patient mortality. In the present study, we sought to elucidate how two NFAb isolates (NFAb-1 and NFAb-2) obtained from a fatal case of NF respond to environmental stressors, and behave in the host-immune cell niche. To determine environmental resistance, desiccation and transformation assays were performed. To assess host-immune cell entry, isolates were co-incubated with human-derived THP-1 macrophages with or without pre-treatment with Cytochalasin D, an inhibitor of phagocytosis. A colistin-protection assay was performed, allowing for isolation of viable intracellular bacteria and quantification after 24 hours. Intracellular and cell-free bacterial samples were also collected for total RNA sequencing analysis. No significant differences were seen in transformation, but NFAb-1 displayed greater resistance to desiccation. All isolates primarily entered macrophages via macrophage-driven phagocytosis; however, NFAb isolates displayed greater intracellular entry and survival in host cells, and altered expression of potential virulence factors in the intracellular compartment. Collectively, these results suggest NFAb isolates have the ability to survive across environments, potentially due to mechanisms conferred by altered gene expression.

402. Rona Scott, Louisiana State University Health Sciences Center-Shreveport. **Empowering Research: The Evolution of the Bioinformatics and Modeling Core in the COBRE Center for Applied Immunology and Pathological Processes.** Co-Authors: Jian Wang, Xiaolu Zhang, Marcin Sypniewski, Ricky Wiggins Jr., Rona S. Scott, Andrew D. Yurochko. Co-Authors Institutional Affiliations: Not Listed. COBRE
The COBRE Center for Applied Immunology and Pathological Processes (CAIPP) established a fee-for-service Bioinformatics and Modeling core to support research, training and education in various aspects of data science. The Bioinformatics and Modeling Core has rapidly expanded to meet the research needs

and capable of analyzing any annotated species from microbes to humans. Over 80 projects have been supported, encompassing bulk and single cell transcriptomics, weighted correlation gene network analysis, variant calling analysis, ChIP-seq, ATAC-seq, Alphafold protein structure prediction, proteomics, and metabolomics. Many profiling approaches rely on the exploration of share functions among genes to extract biological knowledge. For this purpose, we have employed clusterProfiler and 3PodR to evaluate ontological classification and enrichment drawing from multiple biological databases (GO, KEGG, REACTOME, and NIH LINCS). clusterProfiler offers visualization capabilities for gene classification and enrichment analyses, while 3PodR integrates GSEA, targeted gene pathway analysis, and perturbagen analysis into an automated pipeline. Comparison of input gene profiles to perturbagen signatures in the LINCS database identifies perturbagens/regulators that mimic or reverse effects of the input treatment. Our core also provides handson training opportunities to undergraduate and master's students to build infrastructure that assists with FAIR data practices. Our trainees have created databases and user interfaces for project tracking/ordering and antibody inventory systems, as well as engaged in research using deep learning to morphologically identify cell death mechanisms in monolayer culture. Through such short-term internships the CAIPP Bioinformatics and Modeling Core will continue to build infrastructure to support research at LSU Health Shreveport.

403. Eduardo Enrique Romero Camacho, University of Nebraska-Lincoln. **LEMC NCIBC Core (CryoEM) A New CryoEM facility in the State of Nebraska.** Co-Authors: None. COBRE

Cryo-electron microscopy (CryoEM) is a versatile and straightforward tool for studying cellular and structural biology. In recent years, CryoEM has experienced significant growth in the structural biology field, producing near-atomic resolution structures that rival and, in some cases, surpass X-ray crystallography. Furthermore, despite the availability of multiple regional and national CryoEM facilities in the US, the Midwest requires new CryoEM facilities with state-of-the-art instrumentation to conduct high-quality research at low cost and reasonable timelines. In this conference, we present the capabilities, current workflows, and instrumentation of our recently open CryoEM facility at the University of Nebraska-Lincoln with the support of the Nebraska Center for Integrated Biomolecular Communication (CIBC) and the Nebraska Center for Biotechnology. The facility aims to serve the needs of CryoEM researchers in Nebraska and neighboring states and act as a point of contact for national CryoEM centers. NCIBC supports this work under the COBRE-funded grant P20 GM113126, NIGMS.

404. Gangqqing "Michael" Hu, West Virginia University. **Scientific Figures Interpreted by ChatGPT: Strengths in Plot Recognition and Limits in Color Perception.** Co-Authors: Jinge Wang, Qing Ye, Li Liu, Guo Nancy Lan. Co-Authors Institutional Affiliations: West Virginia University, Arizona State University. CTR

Emerging studies underscore the promising capabilities of large language model-based chatbots in conducting basic bioinformatics data analyses. The recent feature of accepting image inputs by ChatGPT, also known as GPT-4V(ision), motivated us to explore its efficacy in deciphering bioinformatics scientific figures. Our evaluation with examples in cancer research, including sequencing data analysis, multimodal network-based drug repositioning, and tumor clonal evolution, revealed that ChatGPT can proficiently explain different plot types and apply biological knowledge to enrich interpretations. However, it struggled to provide accurate interpretations when color perception and quantitative analysis of visual elements were involved. Furthermore, while the chatbot can draft figure legends and summarize findings from the figures, stringent proofreading is imperative to ensure the accuracy and reliability of the content.

405. Anuradha Roy, University of Kansas. **Infectious Disease Assay Development Core: High Throughput Screening Laboratory at the University of Kansas.** Co-Authors: Peter McDonald. Co-Authors Institutional Affiliations: Not Listed. COBRE
The overall goal of the IDAD Core is to provide expertise, facilities, services, and training in the area of HTS assay design, development, validation, small and large-scale screening for whole cell based or biochemical infectious disease targets. The IDAD core is an extension of the University of Kansas High Throughput Screening Laboratory which is a fee-for-service, state-of-the-art facility dedicated to providing academia, not-for-profit institutions, biotech, and pharmaceutical industries with exceptional assay development, high throughput screening and data mining services at economical rates. The staff has experience in executing cell-based, biochemical, siRNA as well as high content screening campaigns against a plethora of target classes. The laboratories are equipped with cutting-edge liquid handling and signal detection instrumentation for increasing throughput and precision of screening campaigns. Clients have the option of using our collection of 395,000 compounds and/or a client's own chemical library. KU-IDAD/HTS lab further leverages the strengths of the medicinal chemistry/ computational modeling cores under CoBRE Chemical Biology of Infectious diseases (CBID) program to support your tool/lead discovery research.

406. Hongwei Yao, Providence VA Medical Center. **Cell isolation and organ function (CIOF) core enhances cardiopulmonary vascular biology research in Rhode Island.** Co-Authors: Amy Princiotto, Valeria Zarate, Peng Zhang, Elizabeth O. Harrington, Gaurav Choudhary. Co-Authors Institutional Affiliations: Providence VA Medical Center. COBRE
The mission of the CardioPulmonary Vascular Biology (CPVB)/COBRE program is to develop novel therapeutic strategies for blood vessel diseases that impact the pulmonary and cardiovascular systems. The Cell Isolation/Organ Function core (CIOF) of the CPVB/COBRE was established ten years ago, which facilitated the scientific objectives and technical repertoire of the Project and Pilot Project Investigators and other Rhode Island or IDeA researchers by providing essential services. The latter includes 1) technical services by offering effective and reproducible services in cell isolation and ex vivo organ function; 2) technical development by acquiring, establishing, and disseminating technologies and instrument capabilities to provide state of the art research tools for the scientific community; 3) collaboration through work with IDeA programs to foster scientific networks and collaborations by providing technical services to enhance research productivity; 4) core sustainability via maintenance of a robust line of services that meet the research needs of the scientific community. The CIOF core has provided approximately 2000 and 3200 times of services during Phases I and II of the CPVB/COBRE program, respectively. In Phase III, the CIOF core will continue to support and enhance vascular biology research, including the new pilot project investigators and scientific community, in developing, facilitating, implementing, and performing technical services to impact the research productivity of our IDeA colleagues and collaborators. This will build the sustainability of the CIOF core.

407. Luis Vazquez, University of Oklahoma. **Using Machine Learning to Automatically Classify Pericyte and Endothelial Cells in Diabetic Mouse Models.** Co-Authors: Anne Martin, Lauren Wilcox, Rui Zhang, Joshua Butcher, Cammi Valdez. Co-Authors Institutional Affiliations: Northeastern State University, Oklahoma State University. INBRE
Diabetic retinopathy, a complication of Type 1 and Type 2 diabetes, stems from elevated blood sugar and blood pressure levels, resulting in microvascular degradation in the retina. This degradation alters the ratio of pericytes to endothelial cells within retinal capillaries, which is typically 1:1 but shifts to 1:4 in diabetic retinas. Traditional manual counting of these cell types is time-consuming, prompting the development of a machine learning model to automate cell classification. We explored four machine

learning algorithms (decision tree classifier, random forest classifier, support vector machine, k-nearest neighbor) to classify pericytes and endothelial cells. We fine-tuned each model's hyperparameters and assessed their performance based on training, validation, and testing set accuracies. The dataset used was composed of 2775 instances with each instance being composed of 4 features (perimeter, eccentricity, aspect ratio, and extent). The most effective model was further optimized to enhance its performance. Among the tested models, the random forest classifier emerged as the most promising, achieving an accuracy of 91.57% on the testing set. Additionally, manually classifying 10 images took 54.28 minutes, while the model accomplished the same task in just 2.57 minutes. The success of the random forest classifier suggests a potential shift away from manual classification, offering a more efficient approach to categorizing cell types.

408. Rosalyn Hill, West Virginia University. **Sign-tracking is associated with self-reported impulsivity but not risky decision making in human participants.** Co-Authors: Krom P, Potts M, Brodie H, Russell B, Stoessl AJ, Barton JJS, Clark L, Winstanley CA, Cherkasova MV. Co-Authors Institutional Affiliations: West Virginia University, University of British Columbia. INBRE
Sign-tracking (ST), which is the attribution of incentive salience to reward cues, has been linked to addiction vulnerability. This phenomenon has been demonstrated with animal models, and data has begun to emerge supporting this in humans. Addictive disorders have also been linked to impulsivity and risky decision making. ST has been linked to impulsivity in both rodents and humans, but associations with risky decision making have been inconsistent in rodents and scarcely examined in humans. This study examined the relationship between ST propensity with self-reported impulsivity and risky choices across three studies with 250 human participants. ST was measured by quantifying gaze fixation on reward-predictive cues during Pavolvian conditioning, risky decision making was measured using a behavioral economic task, and impulsivity was measured by the UPPS-P Impulsive Behavior Scale. In light of previously reported sex differences on these measures, we considered sex a moderator of these associations. We found that males and females did not differ in ST propensity. ST was associated with higher scores on the negative and positive urgency UPPS-P scales, and males scored higher on positive urgency and sensation seeking. ST did not significantly predict risky choices on its own or in interaction with sex. Relative to females, risky choices in males were more determined by the expected values of the prospects. Our results support the previous association between ST and impulsivity, however, ST appears to have little overlap with risky decision making.

409. David Ruiz Bolivar, University of Puerto Rico Medical Health Science Campus. **Boosting Memory Potential: How Exercise-Induced Metabolic Transformations in the Hippocampus Can Fuel Neurogenesis.** Co-Authors: Nicole Rodriguez Trujillo, Alejandra Vazquez Medina, Patricia Morales Iglesias, Karina Marin Hernandez, Danniela Rivera Ortiz, Briana Bello Rivera, Francisco Vizcarrondo Fornaris, Filipa Godoy Vitorino, Nataliya Chorna. Co-Authors Institutional Affiliations: University of Puerto Rico Rio Piedras Campus, University of Puerto Rico School of Medicine. INBRE
The hippocampus, a central hub for learning and memory, undergoes neurogenesis, or the creation of new neurons, throughout one’s lifespan’s process significantly enhanced by running exercise. However, our understanding of how exercise induces metabolic transformations that enable adult neural stem cells to undergo neurogenesis is still unknown. This study aims to delve into the intricate relationship between exercise and hippocampal metabolism, seeking to uncover how this interplay of metabolites enriches the neurobiological foundation, providing valuable insights into exercise-induced cognitive improvement. We used 20-week-old male C57BL/6J mice (Jackson Lab) randomized into sedentary (SED) and running (RUN) groups in a study approved by IACUC. The metabolic extracts obtained from the hippocampus after 8 weeks of running exercise were analyzed via GC/MS, followed by Univariate,

Chemometric, and Enrichment analyses. In the RUN group, we observed a significant increase in key metabolites essential for energy metabolism in the hippocampus, including oxidative phosphorylation, the tricarboxylic acid cycle, fatty acid, nitrogen metabolism, and CoA biosynthesis. These processes are crucial for neurogenesis and neuronal integration into existing circuits. Enhanced CoA biosynthesis and folate/methionine cycles indicate improved epigenetic regulation, essential for supplying acetyl and methyl groups for histone modifications, critical in gene expression and neuronal differentiation. Taken together, our study unveils the impact of running exercise on hippocampal metabolic pathways crucial for neurogenesis and spatial memory enhancement. It highlights the interplay between exercise, metabolism, and brain health, offering insights for therapeutic interventions in memory, learning, and neurodegenerative disorders. This research was supported by the NIH/NIGMS-PRINBRE Grant 5P20GM103475.

410. Jagdish Patel, University of Idaho. **Computational modeling of opsin function in visual pigments.** Co-Authors: Jonathan E. Barnes. Co-Authors Institutional Affiliations: University of Idaho. COBRE
While crucial for human health, the significant impact of single missense mutations in the opsin component of a visual pigment and the resulting anomalies remains unclear due to a lack of molecular-level data. Elucidating the precise structural changes caused by these mutations; and their functional consequences on the visual pigment is essential. This knowledge holds immense potential for developing targeted therapies for various visual disorders like color blindness and night blindness. Human vision requires that these visual pigments, consisting of a chromophore and associated opsin protein, have distinct peak spectral sensitivities in separate rod and cone photoreceptor populations. Peak spectral sensitivity is determined by the chromophore type and the amino acid sequence of the opsin. Even minor differences in opsin sequence can result in large differences in peak spectral sensitivity and/or result in anomalous visual function and disease. We seek to accurately predict changes in peak spectral sensitivity due to changes in opsin amino acid sequence and reveal the underlying mechanisms of the spectral shift in visual photopigments. In our preliminary work, we built upon our previous research and developed an automated modeling pipeline that predicts peak spectral sensitivity and offers mechanistic insights into spectral shift as a byproduct. We then applied this pipeline to predict peak spectral sensitivity of opsin sequences and elucidated mechanism underlying important mutations leading to shift in spectral sensitivities. This preliminary work will help further understanding of sequence-structure-function relationship for opsin protein and aid in understanding eye disease mechanisms, and to develop molecular-level therapeutic strategies.

411. Elio Frank Delatore III, West Liberty University. **Utilization of Double-Immunofluorescence Microscopy to determine the role of FTL_1199 in erythrocyte invasion by Francisella tularensis.** Co-Authors: Joseph Horzempa. Co-Authors Institutional Affiliations: West Liberty University. INBRE
Francisella tularensis is an intracellular bacterium that is the causative agent of the zoonotic disease, tularemia. F. tularensis invades host erythrocytes during infection, a phenomenon that leads to increased colonization of ticks after a blood meal. To better understand the mechanism of erythrocyte invasion, an RNA-seq analysis was conducted to identify genes whose transcription was affected by the presence of erythrocytes. A putative transcriptional regulator, FTL_1199 was determined to be modulated in the presence of erythrocytes. We hypothesized that this gene may therefore play a role in erythrocyte invasion. Deletion of FTL_1199 resulted in a significant reduction in the invasion of rabbit erythrocytes, and complementation of FTL_1199 restored this strain's ability to acquire the cytoplasmic space of erythrocytes. These findings were determined by a gentamicin protection assay to quantify erythrocyte invasion. To validate these findings, we conducted double-immunofluorescence microscopy. F. tularensis strains incubated with rabbit erythrocytes to allow for invasion. Cells were probed with anti-

F. tularensis antibodies followed by red fluorescent secondary antibodies. Cells were washed and erythrocytes were permeabilized. Bacteria were probed a second time utilizing a green fluorescent secondary antibody. Therefore, intracellular bacteria were only labeled with a singular secondary antibody, while extracellular bacteria were tagged with two secondary antibodies. Intracellular bacterial enumeration showed that deletion of FTL_1199 resulted in a significant reduction of invasion ($p = 0.0253$), while FTL_1199 complementation to the deletion mutant restored invasion to that of wild type ($p = 0.3258$). These data demonstrate that FTL_1199 plays an important role in erythrocyte invasion.

412. Zhejia Dong, Department of Biostatistics, Brown University. **Towards Valid Statistical Inference under Network Dependence.** Co-Authors: Youjin Lee. Co-Authors Institutional Affiliations: Brown University. COBRE
Network dependence -- a statistical dependence within a variable due to network ties -- presents intricate challenges in statistical and causal inferences. In particular, when the exposure and the outcome variables of interest exhibit network dependence on similar or identical underlying networks, estimates of their association may be spurious. To address this issue, we propose a novel approach to disentangle dependence within each variable by adapting pre-whitening methods used in time-series data. We incorporate more complex dependence structures using the known network information, e.g., adjacency matrix, compared to those considered in time-series settings and then leverage those to construct nearly independent variables. We empirically investigate the performance of our proposed dependence-adjusted method under different transmission processes that generate network dependence within the same variable. Our empirical evidence suggests that our method effectively reduces the problems of spurious associations due to network dependence.

413. Raymond Anan Otoo, University of Arkansas at Little Rock. **Impact of Simulated Microgravity and Radiation on the Gut Microbiome.** Co-Authors: None. INBRE
Space travel exposes astronauts to unique challenges, including microgravity and ionizing radiation. These factors may alter the gut microbiome, a complex ecosystem of microbes crucial for human health. Our study aimed to investigate how simulated microgravity and exposure to Â¹â•¶O (Oxygen-16) radiation affect the gut microbiome composition in mice. We employed hind limb unloading to mimic microgravity and whole-body irradiation with Â¹â•¶O to simulate space radiation. Mice were divided into four groups: sham (control), hind limb unloading (HLU), Â¹â•¶O irradiation (IR), and combined HLU and IR (IR+HLU). Fecal samples were collected, and 16S rRNA amplicon sequencing targeting the V3-V4 hypervariable regions was used to analyze the gut microbiome composition. The sequencing data was processed using the QIIME 2 bioinformatics pipeline to characterize the microbial communities. Our results revealed that both simulated microgravity and exposure to Â¹â•¶O radiation significantly altered the gut microbiome composition in mice. These changes suggest that certain microorganisms may be more adaptable to these harsh conditions, while others may be less favored. Understanding the impact of spaceflight on the gut microbiome and identifying resilient microbial communities is critical for developing protective measures to mitigate health risks associated with long-term space missions and ensure astronaut well-being.

414. Carl J Rorstrom, Washburn University. **Exploring Protein-Protein Docking of Sox2 and HDAC1 Proteins.** Co-Authors: Allan Ayella. Co-Authors Institutional Affiliations: Washburn University. INBRE
The Sox2 protein has been shown to associate with a multitude of proteins such as HDAC1 protein to produce large-scale genomic epigenetic changes such as cancer cells. From previous literature, we know the Sox2 123-180 destabilized loop region (DLR) associates with HDAC1 protein, and the Sox2 HMG box is inhibitory to DLR association. Thus, we first hypothesized, the binding sites for the Sox2 HMG and DLR

regions may be at the same HDAC1 region. To analyze this, we used InterEvDock3 predictive computer modeling for prediction of the Sox2 HMG region-HDAC1 protein docking site. This predicted a site of interaction at the HDAC1 325-343 complexing turn region (CTR). Thus, with these predicted regions of docking, three different oligopeptides from the unknown Sox2 DLR region were synthesized and tested for association with the HDAC1 CTR. Native tris-tricine PAGE gel electrophoresis testing showed negative results with unclear aggregation when the Sox2 DLR oligos were run with the HDAC1 CTR oligo. However, circular dichroism testing showed a positive shift in absorbance with all the Sox2 DLR oligos and the HDAC1 oligo when combined. Combining these results with further large complex computational modeling, this shows the Sox2 DLR region may bind with the HDAC1 CTR as well as other regions to participate in transient interactions. This verifies our hypothesis that the Sox2 DLR region binds with the HDAC1 protein. Further, this alludes to the fact that protein binding and interaction might involve disordered regions with no apparent structure.

415. Chamani Perera, University of Kansas. **The Synthetic Chemical Biology Core (SCB): A Resource for Research in Chemical Biology.** Co-Authors: None. COBRE

The Synthetic Chemical Biology Core strives to provide comprehensive synthetic chemistry capabilities to investigators under one roof. The synthetic expertise of the core includes, but is not limited to, novel and commercially unavailable small molecules, fluorescent molecules and custom peptides. The core assists in identifying hits for medicinal chemistry optimization in infectious disease targets and provides synthesis capabilities for structure activity studies of said hits. The core staff will work with investigators to design and synthesis novel molecular probes to facilitate their research. SCB core encompasses the Purification and Analysis Laboratory (PAL) that provides purification, analysis and quality control of compounds via LC/MS. The SCB core also provides MALDI-TOF analysis of biomolecules.

416. Dev Majumdar, University of Vermont**. Hallmarks of mRNA/LNP Immunogenicity for the Rational Design of Vaccines and Therapeutics.** Co-Authors: William Dowell, Jacob Dearborn, Sylvester Languon, Zachary Miller, Tylar Kirch, Olivia Garvin, Lily Kjendal, Ethan Harby, Adam Zuchowski, Emily Clark, Carlos Lescieur Garcia, Jesse Vix, Amy Schumer, Somen K Mistri, Kalev Freeman, Deena B. Snoke, Michael J. Toth, Matthew E. Poynter, Jonathan E. Boyson, Devdoot Majumdar. Co-Authors Institutional Affiliations: University of Vermont. COBRE

Developments in mRNA/LNP technologies have heralded a new era of both vaccines and therapeutics, raising questions about muscle tissue-defined mechanisms of immunogenicity of both mRNA payload and LNP delivery strategies. While some mRNA/LNPs generate a singular immunogenic environment in muscle tissue for a long-lasting humoral immune response, other mRNA/LNPs are distinct in their capacity for multiple rounds of therapeutic nucleic acid delivery. This conundrum led us to define the hallmarks of mRNA/LNP-induced muscle tissue immunogenicity, to define which stromal and immune cells are transduced, which soluble immune mediators are generated, and whether specific gene expression programs inform downstream immunogenicity. We hypothesize that these pillars of muscle immunogenicity can be used to distinguish “immunogenic” and “non-immunogenic” mRNA therapeutics. Here, we evaluate the adjuvancy of component parts of mRNA/LNP by phenotyping cellular infiltrate at the site of their injection, tracking their uptake by immune cells, and analyzing the inflammatory states they induce. We find that intramuscular injection with SM-102 but not DLin-KC2-DMA or TCL-053, containing empty lipid nanoparticles (eLNP) induce robust neutrophil infiltration into the site of injection within 2 hours, and a diverse myeloid population within 24 hours. Surprisingly, we found direct transduction of muscle infiltrating myeloid cells and splenocytes 24 hours after intramuscular mRNA/LNP administration. Transduced myeloid cells within the muscle exhibit an activated phenotype 24 hours after injection. Similarly, directly transduced splenic lymphocytes and dendritic cells are

robustly activated by SM-102 containing mRNA/LNP. Within the splenic dendritic cell compartment, cDC2s are directly transduced and activated by mRNA/LNP. Delivery of 9 common, but chemically distinct, LNPs to muscle revealed broad classes of inflammatory gene expression programs induced by ionizable lipids. Similarly, single cell RNA sequencing revealed SM-102 mediated expression of inflammatory cytokines by myeloid infiltrates within muscle within 1 day of injection. Together, we show that mRNA and LNPs work synergistically to provide the necessary innate immune stimuli needed for effective vaccines within hours of injection. Importantly, this work provides a design framework for mRNA/LNP vaccines and therapeutics alike.

417. Abigail G Weatherford, Presbyterian College. **Open chromatin regions identified by ATACseq correspond with overexpression of metastatic drivers in dual p53/PTEN-deleted metastasis-transformed MCF10A breast cells.** Co-Authors: Margaret V Leonard, Charlotte B McGuinness, Megan A Wilson, Austin Shull. Co-Authors Institutional Affiliations: Presbyterian College. INBRE
Metastatic potential in basal-like breast cancers typically correspond with increased enrichment of aggressive progenitor-like populations called cancer stem cells (CSCs), typically identified by the loss of epithelial markers EpCAM and CD49f. In our MCF10A breast cell line model, deletion of p53 and PTEN lead to tumorigenic transformation and cancer stem cell expansion. With these observations that reflect cell dedifferentiation as a mechanism of oncogenic transformation, it was important to better detail the epigenetic events that correspond with breast CSC progression. With this in mind, we performed Assay for Transposase-Accessible Chromatin sequencing (ATACseq) on our isogenic panel of MCF10A breast cell lines where tumor suppressor genes TP53 and PTEN were silenced to drive breast CSC expansion. Furthermore, we performed gene expression analysis of isolated EpCAM-/CD49f- CSCs from MCF10A p53-/PTEN- cells to determine which genes differentially upregulated in CSCs corresponded with open chromatin in our ATACseq data. Based on this analysis, we identified 96 genes with open chromatin that were also significantly overexpressed in our isolated CSCs. Such examples of transcripts include cell markers like PECAM1 (i.e. CD31), NCAM1, and IL6R, protein kinases like FYN and ROR2, and transcription factors like NPAS2 and KLF15. Additionally, several identified transcripts are also significantly upregulated in basal-like breast cancers from The Cancer Genome Atlas (TCGA) breast cancer dataset. Collectively, this work provides an overview of open chromatin sites that contribute to oncogene overexpression in breast cancer and provide rationale for targeting these transcripts via chromatin targeting-based therapies (ex: BET bromodomain inhibition).

418. Edu B Suarez Martinez, University of Puerto Rico in Ponce. **Asthma and Persistent Allergic Rhinitis Cytokine-Specific Profile in Puerto Ricans: Step Closer to Biologically-Based Diagnostic Tool.** Co-Authors: Guillermo Armaiz, Camilo Mora, Lisandro Cunci. Co-Authors Institutional Affiliations: Ponce Heath Sciences University, University of Puerto Rico Mayaguez, University of Puerto Rico Rio Piedras. INBRE
Asthma and persistent allergic rhinitis are complex, chronic inflammatory airway disorders with overlapping pathologies and prevalence in Puerto Rico (19% and 17%, respectively), which make it challenging a differential diagnosis when present alone combined. Current differential diagnoses pose accessibility limitations, mostly related to the dearth of Board-Certified physicians in Allergy or Pulmonary Medicine. This study seeks to define a cytokine -specific profile for the clinical phenotypes: Asthmatic/Allergic, Asthmatic/Non-Allergic, and Non-Asthmatic/Allergic (NAA) using as base line Non-Asthmatic/Non-Allergic cytokine levels. We hypothesized that cytokine-specific profiles with allow advancement for biologically based diagnostic tools for achieving a differential diagnosis in the clinical settings of these diseases. We started working with a 105-cytokine dot blot in 10 participants' serum samples (2 replicas of 5) matched by phenotype and age. We identified 23 cytokines significantly

differing at each clinical phenotype. We validated candidate cytokines using ELISA for 34 participants' serum samples followed by a 27-Plex-cytokine multiplex-assay. Up to date, the results showed significant differences in 12 molecules compared to controls: IFN-y,IL-1ra,IL-2,IL-4, IL-8,IL-12,IL-17,MIP-1b,bFGF,GM-CSF,G-CSF, and MCP1. Furthermore, IL-4 was validated by the three experimental protocols as a major maker for NAA. We still validating the candidate cytokines and in parallel, we are currently developing a custom ELISA to determine the minimum detection levels of these cytokines. This step will allow us to translate this biological data by integrating it as a proof of concept for developing electrode-based biosensor. An accurate diagnosis is essential for providing appropriate standard of care to individuals with these diseases. The proposed approach will overcome the difficult accessibility to specialized physicians and the limitations that current diagnostic tests showed at the population level such as the Puerto Rican.

419. Joelle Hannam, North Dakota State University. **Sociodemographic factors and sleep: An intersectional framework.** Co-Authors: Odalis G. Garcia, Jeremy M. Hamm, Matthew Pierce, Laura Klepacz, Katherine A. Duggan. Co-Authors Institutional Affiliations: North Dakota State University. INBRE
Understanding the impact of multiple demographic factors on sleep is an important consideration for health interventions and health equity. Although disparities in sleep associated with sociodemographic factors are well-documented, most studies do not use intersectional frameworks. This study uses data from the NDSU National COVID Study, which has followed 300 American adults since April 2020. The current analysis includes data from Wave 1 (April 2020) in 263 participants (51% male, 25% people of color, 12% LGBTQ, Mage = 44, MSES = 5 on a 10-point scale). Regression interactions were used to test whether consideration of intersectional identities enhanced the prediction of sleep, over and above linear effects. Sociodemographic factors best predicted bedtime procrastination (~18% of the variance), followed by insomnia (15%), sleep disturbance (14%), sleep-related impairment (14%), sleep health (8%) and sleepiness (not significant). Across sleep outcomes, age was the strongest predictor of sleep (MB = 0.28), followed by sex (MB = 0.18), socioeconomic status (MB = 0.17), race/ethnicity (MB = 0.10), and LGBTQ status (MB = 0.03). Interactions between sociodemographic factors were not statistically significant; thus, associations were additive. These results are consistent with the socioecological model of sleep. Although there were not statistically significant interactions within the sociodemographic level, interactions may still be present across levels. Sleep researchers may want to focus on linking sociodemographic factors with individual, interpersonal, community, and policy-level factors, consistent with the socioecological model of sleep.

420. Margarita Echeverri, Xavier University of Louisiana. **LACaTS's Community Scholars Program (LaCoSP).** Co-Authors: LaKeisha Williams, Stephanie Broyles, Jennifer Caldwell, D'Andra Odom. Co-Authors Institutional Affiliations: Xavier University of Louisiana, Pennington Biomedical Research Center. CTR
The Louisiana Clinical and Translational Science Center (LACaTS)'s Community Scholars Program (LaCoSP) is a research opportunity that was developed by the LACaTS's Community Engagement Core. LaCoSP's primary goal is to increase the capacity of community-academic partnerships to conduct community engaged research (CEnR) with the ultimate goal of improving the health of Louisianans and the nation. LaCoSP is divided into three components: 1) Funding of pilot CEnR projects, 2) Training and mentorship to community-researcher teams during the development of successful CEnR research proposals, and 3) Training and mentorship to awarded teams during the conduction of the research activities. Since 2016, the Program has had five cohorts, received 24 full-proposals, trained 29 community partners and 25 academic-researchers, and awarded 12 projects. Currently, the Program is providing training and mentorship to four new teams who are preparing their proposals. LACoSP pilot projects are intended to inform future grant applications for external funding considerations.

421. Debarshi Roy, Alcorn State University. **Environmental factors playing a crucial role in triggering cancer in the "cancer alley" in Louisiana.** Co-Authors: Subhajit Chakrabarty, Priyadarshini Dasgupta. Co-Authors Institutional Affiliations: Louisiana State University - Shreveport, Southeastern Louisiana University. INBRE

Poor quality of air, soil and water consisting of industrial and agricultural waste products are of a critical concern in respect to the health and safety of the surrounding population. Purpose: "Cancer Alley" (85 mile stretch between Baton Rouge and New Orleans) in Louisiana is surrounded by small to mid to large size factories producing abundant number of industrial wastes in the region. These wastes are potential carcinogens and are associated with cancers of lung, skin, thyroid, and mouth. Our research focusses on the impact of different types of industrial emissions from petrochemical industries, associated air quality index of that area and types of cancers that are prevalent. Methods: We have performed our preliminary analysis based on the publicly available datasets on environmental pollutants, air quality index, socio economic indicators and cancer incidences and mortality from EJScreen: Environmental Justice Screening and Mapping Tool, airnow.gov and CDC. We performed statistical data analysis to find correlations among the various parameters. Results: Our analysis demonstrates increased cancer cases and mortality along with lower socio-economic index in the "cancer alley" region. Most of the factory workers as well as the residents of that area are constantly exposed to the toxic release by these industries and making them vulnerable to respiratory disorders and cancer development. Our preliminary data shows that Cancer Alley parishes have been correlated with lung fatalities including lung cancer. This is an ongoing work.

422. Oxana Gorbatenko, Black Hills State University. **The Western South Dakota Genetics and Genomics Core Facility.** Co-Authors: Cynthia Anderson. Co-Authors Institutional Affiliations: Not Listed. INBRE

The Western South Dakota Genetics & Genomics core facility is located at Black Hills State University (BHSU). WestCore provides access to comprehensive genomic services from pre-experimental consultation through sample processing and data analysis. WestCore also provides faculty and students access to specialized equipment, training in genetic and genomics research techniques, and technical assistance in support of their research endeavors. WestCore is equipped with the latest available Next Generation Sequencing instrument Illumina NextSeq 2000, as well as instrumentation to support qPCR (QuantStudio 3), dPCR (QuantStudio Absolute Q), Sanger Sequencing (AB model 3500 genetic analyzer) and other instruments. This provides faculty and students with opportunities to access a wide range of genetic, epigenetic and gene expression applications for organisms from viruses and microorganisms to plants, animals, and humans. WestCore's highly experienced staff provide cost-effective and timely services, assist with experiment design, training and data analysis utilizing variety of bioinformatics tools, including established and customized data analysis pipelines. WestCore provides unique opportunities for researchers, undergraduate and graduate students to explore variety of genomics applications and receive hands-on training and experience using state-of-the-art instruments.

423. Angel Mayor, Universidad Central del Caribe. **Trends in neoplasm incidence among a Hispanic cohort of Person with HIV in the Caribbean.** Co-Authors: Diana Fernandez. Co-Authors Institutional Affiliations: Universidad Central del Caribe. CTR

Background: Introduction of antiretroviral therapy (ART) dramatically improves immunological function and life expectancy among people with HIV (PWH). However, late outcomes, including malignant conditions, often curtail PWH's healthiness. Method: The study used a prospective cohort of adult PWH followed at Bayamon, Puerto Rico (PR) matched with the PR Central Cancer Registry to evaluate the neoplasm's incidence trend among Hispanic PWH. Total and specifics cancer incidence rates (per 10.000)

were calculated and compared between three follow-up periods, 2005-2009, 2010-2014 and 2015-2019. Fisher exact test was used to evaluate incidence differences. Results: A total of 2,796 PWH were evaluated. Of them, 67.9% male, 34.9% man-sex-man, and 77.0% received ART. The total cancer incidence increases through time periods (252, 318 and 333). AIDS defining neoplasm incidence decreased over the time periods, however, Kaposi's Sarcoma and cervical cancer remained high. Kaposi's Sarcoma was exclusively diagnosed in men, especially in man-sex-man. Non-AIDS defining neoplasms increased over time; oral-pharynx, anus-rectum, lung, colon, and prostate. Non-Hodgkin's lymphoma and liver remained stable. Oral-pharynx and liver cancers increment were more prevalent in males, and anus-rectal and colon cancer in females. Lung cancer incidence trends were similar in both genders. Conclusion: The study found a raise in cancer incidences among this Hispanic PWH through the time, principally non-AIDS neoplasm more associated with other viral diseases (HPV-HCV-HBV), tobacco used and alcohol consumption. These findings highlight the needs of more effective Ca preventive interventions, beside the adequate HIV prevention and treatment among this vulnerable population. Acknowledgments: Sponsored by grants: G12MD007583-U54GM133807-U01-AI069918-S21MD001830 and NPCR-CDC-5-NU58DP006318

424. Md Imran Hossain, Louisiana State University. **Regulation of Dynein-dependent HSV-1 Virion Retrograde Transport by Viral and Cellular Kinases.** Co-Authors: Brent Stanfield, Vladimir Chouljenko, Harikrishnan Mohan, Christella J Nelson, Ojasvi Dutta, Konstantin Gus Kousoulas. Co-Authors Institutional Affiliations: Not Listed. COBRE
Herpes simplex virus 1 (HSV-1) navigates the complex neuronal network with remarkable efficiency, hijacking cellular machinery to propagate and establish latency. A critical step in this journey is retrograde axonal transport, where the virus moves from peripheral nerve to the neuronal cell body. While several viral factors have been implicated in this process, the precise mechanisms still remain unknown. Retrograde transport of virions in all types of cells and especially in neurons is mediated by the dynein motor complex. Previous studies from this laboratory showed that that the virion tegument protein UL37 interacted with the dynein intermediate chain while the major capsid protein VP5 interacted with dynactin, a dynein cofactor (Musarrat et al., J. Virol. 2021). Dynein retrograde transport is regulated by multiple cofactors and phosphorylation events. The hypothesis of this study is that the viral kinase US3 is directly or indirectly involved in phosphorylation events that regulate virion retrograde transport. Furthermore, we hypothesize that the US3 kinase acts in a synergistic or antagonistic manner with the cellular kinase GSK-3b which is known to regulate dynein-dependent intracellular transport. To address the US3 kinase function, we generated the mutant HSV-1 strain HSV1Î"US3 lacking the US3 gene and compared its retrograde transport efficiency to that of a wild-type virus. Time-dependent fluorescence microcopy for viral capsid imaging in African green Monkey (Vero) cells revealed a reduction in retrograde transport of HSV1Î"US3 capsids compared to wildtype virus. Additional experiments are planned for neuronal cells in cell culture and in vivo mouse infections to fully ascertain the role of US3 in retrograde transport. The potential interaction between US3 and GSK-3b is being explored through computational docking experiments and immunoprecipitation studies using transient transfection of US3 and GSK-3b genes, in combination with the dynein intermediate chain. This approach seeks to elucidate the synergistic or antagonistic relationship between these kinases in regulating retrograde transport. Ultimately, these investigations not only deepen our understanding of HSV-1 neuronal propagation but also hold promise for identifying novel antiviral targets that could potentially impede virus infection by disrupting crucial transport mechanisms.

425. Sierra Grace Keele, University of Idaho. **Transcriptional investigations into neonatal gut development related to early feeding.** Co-Authors: Laurel Nunez, Jordan Richter, Yimin Chen, Mataya

Fox, Bethaney Fehrenkamp. Co-Authors Institutional Affiliations: University of Idaho, Idaho WWAMI Medical Education University of Washington School of Medicine. INBRE
Introduction: While numerous correlational studies suggest human milk optimizes infant gut development1, little is known about the physiological process. The recommended time to exclusively breastfeed an infant is six months2, which is equivalent to one month in a piglet's development. To study the mechanisms by which human milk is protective for intestinal development, we used the piglet model. Methods: We reared littermate Yorkshire-duroc piglets for 28 days and randomly assigned them to different feeding groups, human milk fed (n=3) and infant formula fed (n=3). Two controls reared on sow's milk at the farm (n=2) were also collected. Following euthanasia and tissue collection, we extracted RNA from intestinal tissues, purified them of DNA contaminates, synthesized complementary DNA (cDNA), and performed quantitative PCR (qPCR). Inflammatory cytokines and gap junctional proteins Claudin 1 (CLDN1), Tight Junction Protein 1 (ZO1), Tight Junction Protein 2 (ZO2), and Interleukin 1 Beta (IL-1B), were examined and normalized to reference gene expression within individuals and averaged across feeding groups. These proteins are primarily involved in regulating the intestinal semi-permeable barrier and inflammatory responses3. Results: ANOVA, analysis of variance, with multiple comparisons, was used to determine differences between feeding groups. Currently, there is not enough data to produce statistically significant results. However, prospects for this project, which include collecting a larger sample size, validating more primers, and quantifying expression of more genes, should produce more significant results.

426. Zaina Punter, Delaware Technical Community College. **Development of a CRISPR-cas12a Gene Editing System to Mutate GFP Gene to Produce BFP and CFP.** Co-Authors: Naiesha Brown, John McDowell. Co-Authors Institutional Affiliations: Not Listed. INBRE
GFP is commonly used in molecular biology for reporter assays, cellular localization studies, fluorescence microscopy, FRET, and biosensors among other applications. Directed mutations in the primary amino acid sequence, particularly to the amino acids which form the central chromophore, result in proteins with different fluorescence characteristics. While educators have employed various techniques to mutate the GFP gene in an educational laboratory setting, this project uniquely modifies the GFP gene utilizing an in vitro CRISPR/cas12a based procedure. Given the higher success rate of cas12a compared to cas9 in previous experiments, we hypothesized a greater editing success rate of GFP with cas12a. A different altered GFP gene (fGFP) was selected which allows for the use of cas12a-induced editing. A site-directed mutation of the fGFP gene was produced to introduce a cas12a PAM site. sgRNA was designed to allow for the directed editing of fGFP using cas12a to produce Y66H and Y66W mutants (CRISPR-produced BFP and CFP; crBFP, crCFP). A protocol was developed to sequence the mutated plasmids using the Oxford Nanopore MinION and further sequence analysis was performed using Biomix, a High Performance Computer [HPC] cluster. The newly developed crBFP and crCFP were analyzed for fluorescent characteristics by fluorescence spectroscopy. This analysis revealed unique excitation and emission spectra that do not correspond to any spectra listed in fluorescent protein databases. This process touches upon genotype-phenotype associations, CRISPR gene editing, cloning, analytical analysis of proteins, and other fundamental concepts of genetics, molecular biology, biochemistry, and analytical chemistry.

427. Bethany McManus, Presbyterian College. **Assessing the Impact of the N185D Mutation on NPC1 Through In-Silico Analysis.** Co-Authors: Marharyta Petukh. Co-Authors Institutional Affiliations: Presbyterian College. INBRE
The Niemann-Pick Type C1 Protein (NPC1) is a large multidomain transmembrane protein playing a vital role in transporting cholesterol (CLR) from late endosomes/lysosomes to the endoplasmic reticulum and

other cellular compartments in humans. Mutations in NPC1 are commonly linked to Niemann-Pick Disease Type C (NP-C), a rare progressive genetic disorder characterized by the buildup of CLR and lipids in organs such as the liver, brain, and spleen. Recently discovered N185D mutation in NPC1 (allele frequency of 8.13e-5) is found to disrupt protein function and potentially lead to NP-C. Per evolutionary analysis, N185 is a well conserved residue among orthologous sequences, indicating its high structural/functional importance for the protein. Dynamical analysis of NPC1 in various states(apo-state, with bound CLR, and while binding its native partner, NPC2, involved in CLR transfer) indicate that the mutation impacts a) the stability and flexibility of the protein in its apo-state, b) the positioning of CLR within the protein's binding pocket and c) the interaction between the protein and NPC2, likely leading to a disruption in recognition and the subsequent transfer of CLR across the membrane. To investigate the plausibility of rescuing the effect of mutation on the protein function with the small molecule (drug) binding, we performed a virtual screening using the FDA-approved drug database. We identified a subset of molecules with a high binding affinity near the mutation site. However, the efficacy of these molecules in restoring NPC1 functionality requires further evaluation.

428. Katherine Martin, University of Delaware. **University of Delaware Mass Spectrometry Core Facility.** Co-Authors: Papa Nii Asare-Okai, Yanbao Yu. Co-Authors Institutional Affiliations: University of Delaware. COBRE

The University of Delaware Mass Spectrometry Core Facility provides internal and external academic researchers and public agency and industry professionals access to advanced mass spectrometry instrumentation, offering sample preparation and analysis of proteins and peptides, and analysis of other biomolecules, polymers, metabolites, and small molecules. The lab has 9 mass spectrometers in operation, covering gas chromatography (GC-MS), liquid chromatography (LC-MS), tandem MS (LC-MS/MS), and high resolution (HRMS) systems, as well as a prep LC coupled system for fraction collection. Certain instruments are available as walk-up, open-access instruments after training. The facility is overseen by three dedicated PhD-level staff members with diverse expertise in sample preparation covering biological and environmental matrices, targeted and non-targeted method development, analysis, and data processing. Our mission is to provide high quality service as well as training and education on how mass spectrometry can help address your unique research and analysis needs.

429. Michael Moore, Delaware State University. **OSCAR Imaging Facility at Delaware State University.** Co-Authors: Hacene Boukari. Co-Authors Institutional Affiliations: Not Listed. INBRE

The Imaging Facility at Delaware State University is a multi- user core facility that offers advanced imaging and spectroscopy instruments with scientific and technical expertise in optical microscopy, spectroscopy and computation image analysis. The mission is to advance transformative excellence in research, innovation and education and to provide a vital support structure to the faculty and students in specialized facilities. The core facility houses state of the art optical and electron imaging instruments. Currently the facility has two confocal microscopes, a Zeiss LSM 780 and, and a Crest Optics Xlight V3 Spinning disk confocal. We recently added the DeepSIM structured illumination Super Resolution microscopes by Crest Optics and a Raman Confocal Microscope by Horiba. The facility has several advanced bright field and widefiled microscopes with extended contrast techniques (e.g. Polarized light, Dark-Field, Phase Contrast, DIC, Fluorescence). In addition, we have a Bruker Innova AFM a Bruker Anasys nanoIR2-s AFM system, and a FEI Quanta FEG 250 scanning electron microscope with EDS, STEM, and ESEM. The imaging facility also hosts a uv-vis spectrophotometer, FTIR, and an ISS-K2 spectro-fluorimeter. Furthermore, the data collected is archived on a server housed with-in the facility and the data is analyzed on our power workstations in our Image Analysis room. We have several commercial software packages, ImagePRO 11, Huygens Deconvolution, Topo Maps 3D, Imaris, Avizo, Velocity, and

more. The OSCAR imaging facility hosts several middle school and high school workshops throughout the year. The facility has hosted several of these workshops for INBRE summer internship students. We coordinate with the multitude of summer science based programs on campus providing tours and workshops. These workshops are part of our mission to educated the next generation of scientist.

430. Rachel Veri, Coastal Carolina University. **Molecular Characterization of the Mycobacteriophage Refuge.** Co-Authors: Brannon LaFrancis, Daniel C. Williams. Co-Authors Institutional Affiliations: Coastal Carolina University. INBRE

Treatment of many bacterial diseases, such as tuberculosis, is burdened by increased prevalence of antibiotic resistance. An alternative to chemical antibiotics is bacteriophages, which are viruses that specifically infect bacteria and lead to cellular death by lysis. Temperate phages have the ability to also integrate into the host genome, and replicate without inducing lysis. Development of phages for therapeutic use requires understanding molecular mechanisms of phage lifecycles and cellular processes within host cells during infection. Work in our lab is focused on phages that infect Mycobacterium smegmatis, which is in the same genus as the causative agent of tuberculosis. We have taken a systematic approach to examine the functional significance of individual phage gene products in vivo. The genome of phage Refuge contains 92 predicted protein encoding genes, many of which lack functional characterization based on bioinformatic analysis. We are in the process of generating an expression plasmid library that consists of all Refuge genes and have successfully cloned 53% of them. Individual plasmids are transformed into M. smegmatis and the effect of phage gene expression on growth of host cells is analyzed. The majority of temperate phages have a specific integration cassette to allow integration and excision within the host genome. Refuge however, has a Par-ABS partitioning domain cassette in place of the integration cassette. Expression of Refuge gene product 38, which encodes a ParA-like DNA partitioning domain protein, strongly inhibited cell growth, indicating this gene product is very cytotoxic. Current work is in progress to generate a complete Refuge library and perform cytotoxic assays using individual genes in an effort to increase understanding of phage gene function.

431. Abhishek Pandit, Louisiana State University. **Unraveling Tamoxifen's Impact: Autophagy, MAPK Signaling, and ER Expression in Endometrial Cancer.** Co-Authors: A. Pandit, S. Thota, R. Begum, , B. Sapkota, N. Chintala, CA. Simintiras, J. Francis. Co-Authors Institutional Affiliations: Louisiana State University and A&M College. COBRE

Endometrial cancer ranks as the fourth most prevalent cancer among women globally, primarily characterized by endometrioid adenocarcinoma, designated as type 1 endometrial cancer. Tamoxifen, a commonly prescribed selective estrogen receptor modulator for estrogen receptor-positive breast cancer, paradoxically poses a substantial clinical challenge due to its linked elevated risk of endometrial cancer development. Increasing evidence indicates that tamoxifen can trigger autophagy, an evolutionarily conserved cellular mechanism recognized as pivotal in cancer pathogenesis, potentially fostering tumor advancement and resistance to therapy in endometrial cells. The activation of mitogen-activated protein kinase (MAPK) signaling cascades has been implicated in regulating autophagy in various cellular contexts. Based on this evidence, we cultured human endometrial cancer cells (HEC-1-A) and subjected them to tamoxifen treatment at concentrations of 2.5ÂµM and 5ÂµM for 48 hours. We established our concentrations through MTT assay analysis. Our preliminary investigations revealed heightened production of cytokines/chemokines (IL-6, IL-8), induction of autophagy (LC3B, Beclin1), and perturbations in the MAPK cascade following tamoxifen exposure. Alterations in estrogen receptor expression (ERÎ± and ERÎ²) were observed. Consequently, we hypothesized that targeting specific components of the autophagy machinery or MAPK signaling pathways could hold promise in overcoming tamoxifen resistance and enhancing clinical outcomes in endometrial cancer patients. Additionally, we

conducted in vivo experiments to corroborate our in vitro findings, which yielded concordant results. Further exploration of the molecular mechanisms driving these phenomena is imperative to validate our hypothesis and unearth novel therapeutic targets for managing tamoxifen-induced endometrial cancer.

432. Xuyi (Kevin) Yue, Nemours Children's Health. **Design and Synthesis of PET Imaging Probes for the Brain Lymphatic System by Targeting Vascular Endothelial Growth Factor Receptor-3.** Co-Authors: Wenqi Xu, David K. Johnson, Sigrid A. Langhans, Erik Stauff, Vinay V.R. Kandula, Heidi H. Kecskemethy, Thomas H. Shaffer, Lauren W. Averill, Xuyi Yue. Co-Authors Institutional Affiliations: Nemours Children's Hospital, University of Kansas. INBRE

Dysfunctions of the recently discovered glymphatic-lymphatic system have been reported in neuropathological conditions such as traumatic brain injury, epilepsy, and autism. Current optical imaging methods for the brain lymphatic system are destructive or invasive and do not apply to clinical care. The vascular endothelial growth factor receptor 3 (VEGFR3), a tyrosine kinase receptor, is expressed exclusively by the lymphatic endothelium and is a potential target for imaging agent development. Positron emission tomography (PET) is a sensitive and noninvasive imaging modality to assess molecular-level metabolic rates, receptors, and transporters. We aim to rationally design, synthesize, and characterize VEGFR3-specific PET imaging agents with favorable physicochemical properties, enhanced binding profiles, and readily available fluorine-18 incorporation. A series of VEGFR3-specific binding compounds were designed based on a known VEGFR3 inhibitor SAR131675 (IC50 = 23 nM) using bioisosteric rationale. SAR131675 was docked into the adenosine triphosphate (ATP) binding groove of a model of VEGFR3 generated by AlphaFold using Glide by Schrodinger. The new compounds were synthesized in five steps. The target compounds were characterized by high-resolution mass spectrometry (HRMS), proton nuclear magnetic resonance (1H NMR), carbon-13 NMR (13C NMR), fluorine-19 NMR (19F NMR), and analytical high-performance liquid chromatography (HPLC). Twenty new VEGFR3 targeting compounds containing one fluorine-19 atom were designed. SAR131675 was docked into VEGFR3 with two hydrogen bonds and good packing interactions. Twelve of the newly developed compounds had better docking scores than SAR131675. We streamlined the synthetic pathway for VEGFR3 targeting compounds. Three representative target compounds were obtained with over 95% purity.

433. Shirin Ghods, University of Louisville. **Crucial Role of Cobalamin (Vitamin B12) in Stress Response Mechanisms of Porphyromonas gingivalis.** Co-Authors: Saba Tohidkhah, Mozhgan Mousavi. Co-Authors Institutional Affiliations: Not Listed. COBRE

Periodontitis, characterized by gum tissue infection and inflammation, is linked to an imbalanced microbiome in the dental plaque and the development of a virulent community of anaerobic bacteria known as periodontopathogens. These pathogens have been found to extensively utilize cobalamin (vitamin B12) transporters during disease progression, suggesting a potential role of cobalamin in their pathogenesis. However, the specific biological significance of cobalamin utilization in the pathogenesis of these pathogens and the progression of the disease remains largely unknown. In this study, we employed Porphyromonas gingivalis, a model pathobiont, and a defined biologically relevant medium to examine the role of cobalamin transportation in its pathogenesis. The supplementation of the medium with cobalamin led to prolonged exponential growth, suggesting that cobalamin enhances the survival of P. gingivalis. Our findings demonstrate that cobalamin utilization significantly enhances the survival potential of P. gingivalis under biologically relevant stress conditions such as the presence of hydrogen peroxide and lactate. Moreover, cobalamin utilization positively correlates with P. gingivalis' ability to form biofilms in the presence of stress conditions. These findings suggest that cobalamin significantly

contributes to stress response mechanisms in P. gingivalis, thereby enhancing the survival and pathogenic potential of this species during disease progression.

434. Savannah Noblitt, University of South Carolina. **The Creation and Implementation of a Novel Database for Medical School Research Tracking and Student Research Opportunities.** Co-Authors: Savannah Noblitt, Sabrina Carrel, Kirby Allen, Victoria Lawhun Costello, Anna V. Blenda, Homayoun Valafar. Co-Authors Institutional Affiliations: University of South Carolina, University of South Carolina School of Medicine. INBRE
Introduction: In medical education, research plays a pivotal role in refining critical thinking skills, fostering mentorship opportunities, and laying the foundation for evidence-based medical practice. However, medical schools often lack a centralized system to promote and track research opportunities for students. Hypothesis: Implementing a unified database will enhance student satisfaction and productivity, foster better communication between mentors and students, and increase institutional funding based on measurable research outcomes. Methods and Results: To address this gap, we developed the Database of Projects and Experiences. The Database of Projects and Experiences is a MySQL Relational Database Management System (RDBMS) paired with a Flask web application via SQLAlchemy. The database is divided into two parts: A Faculty portal and Student portal. From this division each portal has a unique set of fields that were created to address medical school research needs. Currently the database and web application pairing are being utilized to match students with research mentors and report research outcomes for medical students between their first (M1) and second (M2) year. Conclusions: A centralized database is imperative for tracking and facilitating research activities for numerous medical schools. Grant Support: This research received funding from the University of South Carolina School of Medicine Greenville.

435. Patience Okoto, University of Arkansas. **Bioenergetics Core at the Arkansas Integrative Metabolic Research Center at the University of Arkansas.** Co-Authors: Suresh Thallapuranam. Co-Authors Institutional Affiliations: Not Listed. COBRE
Bioenergetics focuses on how energy is transferred in cells, tissues, and organisms. Cells transform energy often by producing, storing, or consuming adenosine triphosphate (ATP). The way the body regulates energy transfer pathways and processes has a fundamental influence on human health. Many disorders such as mitochondrial encephalomyopathies, neurodegenerative diseases, and cancer feature bioenergetic dysfunction. The Bioenergetic core uses cutting-edge equipment to study various aspects of cellular respiration and real-time metabolic analysis The Bioenergetic core's instrumentation involving real-time cell measurements provides a clear understanding of the critical functions driving cell signaling, proliferation, activation, toxicity, and biosynthesis. Promethion animal cage system allows for tight synchronization of metabolic data with behavioral events. The system provides highest resolution oxygen and carbon dioxide gas analyzers, comprehensive activity measurements including running, eating, and drinking. There is also a real-time system monitoring and experiment analysis using Promethion Live software. Seahorse Xfpro, XFe24 and XFp mini-Analyzer investigates the key cellular functions such as mitochondrial respiration and glycolysis by measuring the oxygen consumption rate and the extracellular acidification rate of live cells. Biotek Cytation 5 is both an automated digital widefield microscope and a conventional multi-mode microplate reader. Oroboros delivers the O2k-technology for high-resolution respirometry in mitochondria and cell research. The O2k allows the measurement of respiration at controlled oxygen levels, combined with ROS production, mitochondrial membrane potential and ATP. The Tecan Spark instrument is a cell imaging module built directly into a reader, enabling automated cell counting, viability analysis, bright field imaging, and automated confluence assessment in microplates.

436. Claudine T. Jurkovitz, ChristianaCare Health Services, Inc. **BERD: A Biostatistics Epidemiology Research Design core for the Delaware IDeA Network.** Co-Authors: None. CTR

The Biostatistics, Epidemiology Research Design (BERD) core of the Delaware ACCEL Center for Translational Research (CTR) was created in 2013 and has matured into a large, stable yet dynamic core with skills and resources that enable quality clinical and translational (C&T) research. The BERD core includes biostatisticians, epidemiologists, data scientists, qualitative researchers and bioinformaticians with a wide range of expertise from all four ACCEL partner institutions: University of Delaware, Nemours Children's Health system, ChristianaCare Health Services Inc., and Delaware State University. Through the BERD, investigators find collaborators to assist on research design, data extraction and statistical, geospatial and qualitative analysis, to explore cohorts and train on approaches ranging from basic statistics to cloud-based large scale genomic analyses. To expand its reach to all IDeA network researchers, BERD also serves as an INBRE affiliated core and is a resource for several COBREs. BERD scientists are focusing on several objectives: 1) Expand the consultative services for C&T research; 2) Promote virtual self-paced synchronous and asynchronous learning opportunities; 3) Develop innovative methods in biostatistics; 4) Expand the biomedical informatics research infrastructure. We will accomplish these goals by leveraging expertise and skills across Delaware institutions to establish an integrated network of resources and develop teams that include clinicians with content knowledge and BERD scientists with expertise ranging from qualitative analysis to advanced statistics and artificial intelligence. In conclusion, BERD assembles a diverse core of skilled scientists from each Delaware Institution who have the common goal of advancing translational science and assist C&T investigators.

437. Balqees Ara, CAMC Institute for Academic Medicine. **Database Determination of Relative Risk of Neuropathy with SARS-CoV-2 Infection, Type 2 Diabetes Mellitus, and Associated Predictive Biomarkers.** Co-Authors: Sonya Dunlap, James Russell. Co-Authors Institutional Affiliations: CAMC Neurology Research Center, WVU.

A retrospective cohort study using TriNetX and N3C databases analyzed patients with confirmed diagnoses of SARS-CoV-2, type 2 diabetes mellitus (T2DM), and neuropathy based on ICD-10 coding. Propensity score matching ensured demographic comparability. Analyses assessed neuropathy outcomes over 24 months at intervals, revealing a progressively increased risk of neuropathy and mortality in patients with pre-existing T2DM and concurrent SARS-CoV-2 infection. In Cohort A (T2DM/Pre-DM with COVID-19) versus Cohort B (Without T2DM/Pre-DM with COVID-19), the relative risk (RR) for neuropathy was 1.674 (95% CI 1.653-1.697) and for mortality was 1.407 (95% CI 1.390-1.425) at 2 years. Within Cohort A, compared to Cohort B (T2DM/Pre-DM without COVID-19), consistently higher risks of neuropathy (RR 1.207, 95% CI 1.203-1.211) and mortality (RR 2.067, 95% CI 2.038-2.096) were observed at 2 years. Comorbidity analysis showed significantly increased RR of neuropathy associated with ischemic heart diseases, sleep disorders(obstructive sleep apnea), chronic kidney diseases, and high obesity levels. Biomarker assessment indicated elevated risks linked to relative hyperglycemia, higher CRP, triglycerides, ESR, cholesterol, TSH, and VitB12 levels below 200 pg/dL. SARS-CoV-2, especially in conjunction with T2DM, escalates the RR of neuropathy and mortality. Specific biomarkers, notably CRP, emerge as early indicators of heightened neuropathy risk. This study underscores the need for early intervention in individuals with both COVID-19 and T2DM, offering insights for targeted healthcare strategies.

438. Jason Landen, University of Wyoming. **Huddling substates in mice dynamically control body temperature and are modulated by Shank3b and Trpm8 mutation.** Co-Authors: Morgane

Vandendoren, Samantha Killmer, Nicole Bedford, Adam Nelson. Co-Authors Institutional Affiliations: University of Wyoming. COBRE
Social thermoregulation is a means of maintaining homeostatic body temperature. While mice are a model organism for studying both social behavior and energy regulation, how huddling regulates body temperature (Tb) is poorly understood. We developed a behavioral paradigm and computational tools to identify activehuddling and quiescent-huddling as distinct thermal substates. We find that huddling is a thermoregulatory strategy in female but not male groups and that at room temperature, but not thermoneutrality, huddling is associated with very low Tb and Tb-variance. Notably, active-huddling has a bidirectional effect on Tb: it is cooling prior to, but warming after, bouts of quiescent-huddling. Further, group-housed animals lacking the synaptic scaffolding gene Shank3b have hyperthermic Tb and spend less time huddling. In contrast, individuals lacking the cold-sensing gene Trpm8 have hypothermic Tb a deficit that is rescued by increased huddling time. These results reveal how huddling behavior acutely adjusts Tb in a state-dependent manner. This paradigm helps to establish a system capable of identifying the neural circuitry and genetic components that coordinate social and thermoregulatory behaviors.

439. Karina Kapusta, Tougaloo College. **Unraveling Immune Evasion: In Silico Investigation of Novel SARSCoV-2 Variants Dynamics Complexed with Neutralizing Antibodies.** Co-Authors: Allyson McGowan, Jordhan Booth, Jerzy Leszczynski. Co-Authors Institutional Affiliations: Tougaloo College, Jackson State University. INBRE
The rapid emergence and global spread of SARS-CoV-2 variants, particularly those belonging to the Omicron lineage, potentially may pose significant challenges to current vaccine efficacy and antibody therapeutic strategies. With a record number of mutations in the receptor-binding domain (RBD) of the spike protein, Omicron mutants evade the immune response developed by previous infection or vaccination. Though there are many high-quality experimental and computational works being published up to date in this area still many knowledge gaps exist. Mainly one lacks uniform big data related to the neutralization of various mutants by human-neutralizing antibodies, as the majority of published works consider only several mutants in their investigations. By bridging existing gaps, one could be able to extend knowledge of the various mutations' influence on a viral immune escape, and possibly develop quantitative predictive models based on as little data as the sequence of newly emerging variants. We present the application of an In Silico approach, which employs molecular dynamics (MD) simulations to investigate the interactions between the RBDs of various SARS-CoV-2 variants and a wide array of neutralizing antibodies. Given the lack of crystallographic structures for the novel clades of Omicron, the generation of reliable, high-quality homology models based on the closest available structural analogs is crucial. As a benchmark for this approach, we used experimental data depicting the neutralizing power of murine antibody 2B04 against the RBDs of wildtype, Alpha, Beta, Gamma, and Epsilon variants of SARS-CoV-2. Complexes' stability was evaluated through calculations involving a total of 300 ns MD simulations. A strong correlation was observed between experimental data and the computationally predicted number of protein-protein interactions formed by complexes. Successful benchmark enabled us to use a proposed approach for further elucidation of interactions between various SARS-CoV-2 variants (specifically novel Omicron mutants, such as JN.1) and an array of human neutralizing antibodies. RBD-antibody complexes undergo extensive Molecular Dynamics simulation under physiological conditions to explore their dynamic behavior. This approach allows us to predict alterations in antibody-neutralizing power and identify potential mechanisms of viral immune escape. This study aims to shed light on the molecular underpinnings of immune escape and to establish a framework for the rapid assessment of future SARS-CoV-2 variants. Acknowledgments: This work was supported by the Mississippi INBRE, funded by an Institutional Development Award (IDeA) from the National Institute of

General Medical Sciences of the National Institutes of Health under grant number P20GM103476. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of General Medical Sciences or the National Institutes of Health.

440. Vinicius Magalhaes Borges, Marshall University. **ACOX1-CAT Multimeric Chain Formation: Implications for Ethanol Metabolism.** Co-Authors: Natalia Fagundes Borges Teruel, Anna Mazur, W. Christopher Risher, James Denvir, Yongke Lu, Alejandro Q. Nato, Jr. Co-Authors Institutional Affiliations: Universite de Montreal, Marshall University. INBRE

Peroxisomes, like mitochondria, facilitate fatty acid oxidation (FAO) by processing very long chain fatty acids before they undergo further oxidation in the mitochondria. Acyl-CoA oxidase 1(ACOX1) is a rate-limiting enzyme for peroxisomal FAO. Unlike mitochondria, peroxisomes generate hydrogen peroxide (H2O2) through ACOX1 during FAO. Fortunately, another peroxisomal enzyme, catalase (CAT), decomposes H2O2 into H2O. Interestingly, when ethanol is present, CAT not only degrades H2O2 to H2O, but also metabolizes ethanol into acetaldehyde simultaneously. Ethanol metabolism primarily involves alcohol dehydrogenase and the microsomal ethanol oxidizing system, and CAT is thought to play a minor role. However, under peroxisome proliferation conditions, ACOX1 collaborates with CAT to enhance ethanol metabolism, emphasizing the intricate interplay between these enzymes. Here, by leveraging computational resources and available experimental data, we deduced the potential formation of an ACOX1-CAT complex, facilitating the delivery of ACOX1-generated H2O2 to CAT for ethanol metabolism. Utilizing experimentally solved structures of human erythrocyte CAT (1DGH) and peroxisomal ACOX1 (7Q84), we performed docking using web-based servers HDOCK and LZerD. We evaluated the top 10 docking poses from each tool using Surfaces to standardize and compare binding metrics, revealing HDOCK's proposed interfaces as significantly more favorable, with a top binding Î”Î”G of -29.1 kcal/mol compared to -11.2 kcal/mol from LZerD. HDOCK top results offered a larger docking interface and suggest a chain of docking complexes exploiting the symmetric nature of CAT and ACOX1 multimers. We validated ACOX1-CAT binding by co-immunoprecipitation assay. This study highlights the pivotal role of peroxisomal FAO in ethanol metabolism.

441. Wesley Kimble, West Virginia Clinical and Translational Institute. **Necessity Driven Clinical Data Architecture: Building a Scalable COVID-19 Research and Operations Registry.** Co-Authors: Emily Morgan, Matthew Armistead. Co-Authors Institutional Affiliations: West Virginia Clinical and Translational Science Institute. CTR

West Virginia (WV) received its first confirmed case of COVID-19 on March 17, 2020. Prior to the first confirmed case in WV, the Bioinformatics, Epidemiology and Research Design Core (BERD) of the West Virginia Clinical and Translational Science institute (WVCTSI) began building the data architecture to collect clinical data related to COVID-19 for research purposes in almost real time. This database was architected so that clinical information could be pulled from the West Virginia University Healthcare System (WVUHS) which has 23 sites and over 2.5 million patients. To design the database, clinician input was sought to ensure the capture of specific relevant data elements. From WVUHS, encounters, demographics, lab results, and vitals were obtained, including elements that were not previously recorded for research purposes, such as continuous ventilator data. Later, through a relationship with the West Virginia Department of Health and Human Resources (WVDHHR), we obtained datasets on COVID-19 vaccinations, COVID-19 laboratory tests, and detailed death data including cause of death. Finally, we were able to work with Marshall University to access COVID-19 genomic sequences that included FASTA files and Pangolin lineages. These five disparate datasets were matched and linked using probabilistic entity resolution methods and validated. Presently, the COVID-19 registry contains over 3.5 million patients, 23,000 viral sequences, 9 million lab results, 1.4 million vaccinations, and 8,000 deaths.

The creation of this database was the impetus for the WVCTSI to become the lead hub for 13 Clinical and Translational Research (CTR) sites for the National Covid Cohort Collaborative (N3C).

442. Benjamin Tero, MaineHealth Institute for Research. **A Human Abdominal Aortic Aneurysm-Derived Smooth Muscle Cell 3D Ring Model.** Co-Authors: Larisa Ryzhova, Abigail Kaija, Anne Harrington, Kimberly Malka, William DeMaria, Marsha Rolle, Lucy Liaw. Co-Authors Institutional Affiliations: MaineHealth Institute for Research, Worcester Polytechnic Institute, Roux Institute at Northeastern University. COBRE
Abdominal aortic aneurysms (AAA) occur when significant proteolysis of structural protein in the vessel wall leads to aortic dilation with chronic inflammation and potential rupture of the vessel wall. Mechanisms behind AAA onset are currently unknown, and it is hypothesized that surrounding tissues play a role in the disruption in normal signaling pathways. Our work is aimed at establishing 3D cell culture models that can be used to study molecular and functional attributes of vascular smooth muscle cells derived from human aneurysms, as well as the impact of cells from perivascular adipose tissue (PVAT). We are adapting prior stem cell models for primary vascular smooth muscle cells from donors undergoing surgical repair of abdominal aortic aneurysm. Our goal is to establish an in vitro model of the cellular environment found in human AAA. We successfully derived primary cell cultures of human aortic vascular smooth muscle cells, and optimized growth conditions to promote contractile protein production in 3D ring-shaped models. Differentiation of human aortic cells using inhibitors of the MEK signaling pathway and stimulation of the TGF-b signaling pathway increased smooth muscle cell makers ACTA2, MYH11, and transgelin. When differentiated, cell orientation in the ring configuration showed greater alignment, with similarities to previous mesenchymal stem cell models and native vascular tissue. These results indicate this as a viable model for future investigation of molecular mechanisms behind aneurysm onset. Future work will focus on co-culture with primary PVAT adipocytes to study cellular communication and potential impact in the setting of AAA.

OPTIONAL POSTER PRESENTATIONS

Poster Numbers Organized by Author First Name

Attendees selected for Short Research Presentations and Flash Talks were provided with an option to present a poster during NISBRE2024. The abstract for optional poster presenters is listed under the Short Research Presentations and Flash Talk section (earlier in this document) according to the presentation type noted at the end of their citation. As a reminder, odd numbered posters will be presented on Monday, June 17, 2024 from 5:15 - 6:30PM ET and even numbered posters will be presented on Tuesday, June 18, 2024 from 5:15 - 6:30PM ET. All posters will be displayed in the International Ballroom.

443. Adam C. Nelson, University of Wyoming. **The role of oxytocin neurons of the paraventricular hypothalamic nucleus in social thermoregulation.** Co-Authors: Joe Rogers, Morgane Vandendoren, Jason Landen, Samantha Killmer, Baizar Alamiri, Nicole Bedford. Co-Authors Institutional Affiliations: University of Wyoming. COBRE, Flash Talk

444. Adriana Aponte Ramos, Inter American University of Puerto Rico, Bayamon Campus. **Exploring Ergosterol Peroxide's Mechanism of Action on the VCP / ANKZF1 Complex in Triple Negative Breast Cancer Models.** Co-Authors: Michelle Martinez Montemayor. Co-Authors Institutional Affiliations: UCC School of Medicine. CTR, Flash Talk

445. Akash J. Vaidya, University of Delaware. **Repurposing Barley-Stripe Mosaic Virus for Cancer Immunotherapy.** Co-Authors: Mruthula Rammohan, Jesal Patel, Evan Gillen, Robyn Logue, Kevin V.

Solomon. Co-Authors Institutional Affiliations: University of Delaware. INBRE, Flash Talk

446. Alexa Bostic, West Virginia University. **Dielectric Characterization of HL-60 Cells under Microgravity.** Co-Authors: Soumya Srivastava. Co-Authors Institutional Affiliations: Not Listed. Flash Talk

447. Alexei G. Basnakian, University of Arkansas for Medical Sciences. **Modification of the TUNEL assay with increased sensitivity to nanoparticles.** Co-Authors: Olena Levurdiak, Shenyang Li, Zach McGowan, Fidaus Razak, Randal S. Shelton, Qinglong Jiang. Co-Authors Institutional Affiliations: University of Arkansas for Medical Sciences, Central Arkansas Veterans Healthcare System, University of Arkansas in Pine Bluff. COBRE, Short Research Presentation

448. Alia Tereza Sadek, University of South Carolina School of Medicine Greenville. **Resistance and Intracellular Survival of Atypical Acinetobacter baumannii Isolates from a Fatal Case of Necrotizing Fasciitis.** Co-Authors: Elias M. Wheibe, Kyleigh Connolly, Christine Liu, Chelsea R. Gutierrez, Brock A. Arivett, Ryan F. Relich, Luis A. Actis, Steven Fiester, Maria Soledad Ramirez, Jennifer T. Grier. Co-Authors Institutional Affiliations: INBRE, Flash Talk

449. Ana-Maria Dragoi, LSUHSC Shreveport. **Interaction of human macrophages with Neisseria gonorrhoeae.** Co-Authors: Maria Dolores Juarez Rodriguez, Stanimir Ivanov. Co-Authors Institutional Affiliations: LSUHSC-Shreveport. COBRE, Short Research Presentation

450. Anastacia Kudinova, Alpert Medical School of Brown University. **Quadratic association between ecologically assessed sleep duration and next-day suicidal ideation in youth.** Co-Authors: Jacqueline Nesi, Sarah K. Ryan, Ella Diab, Mary A. Carskadon. Co-Authors Institutional Affiliations: Alpert Medical School of Brown University. COBRE, Short Research Presentations

451. Avishek Mitra, Oklahoma State University (OSU). **A Novel Class of Channel Forming Membrane Proteins Mediate Heme Iron Acquisition in Mycobacterium tuberculosis.** Co-Authors: Padam Singh. Co-Authors Institutional Affiliations: Oklahoma State University. COBRE, Short Research Presentation

452. Bao Vu, University of Oklahoma Health Sciences. **Upc2A: A Key Regulator of Triazole Resistance and Hypoxic Fitness in Candida glabrata.** Co-Authors: None. COBRE, Flash Talk

453. Bedia Akosman, Rhode Island Hospital. **Deciphering the Role of the SOX17/Runx1 Axis in Endothelial Dysfunction and Pulmonary Arterial Hypertension Pathogenesis.** Co-Authors: Eui Young So, Mandy Pereira, Moon-Jung Choi, Euy-Myoung Jeong, James Klinger, Olin Liang. Co-Authors Institutional Affiliations: Rhode Island Hospital, Warren Alpert Medical School of Brown University. COBRE, Flash Talk

454. Belinda Joyce Petri, University of Louisville. **Differential m6A modification identified by direct mRNA sequencing in endocrine- resistant and sensitive breast cancer cells.** Co-Authors: Kellianne M. Piell, Eric C. Rouchka, Carolyn M. Klinge. Co-Authors Institutional Affiliations: University of Louisville School of Medicine. INBRE, Short Research Presentation

455. Benjamin King, University of Maine. **Inhibition of NADPH Oxidase 2 Improves Survival in Zebrafish Infected with Influenza A Virus.** Co-Authors: Brandy-Lee Soos, Alec Ballinger, Mykayla Weinstein, Julianna Grampone. Co-Authors Institutional Affiliations: University of Maine. COBRE, Flash Talk

456. Bhaswati Kashyap, University of Delaware. **Elevated Mitochondrial CD36 and Superoxide Production in Endothelial Cells Exposed to Prolonged High Glucose and Fatty Acids In-vitro.** Co-Authors: Thanh Nguyen, Erica Johnson, Ibra S Fancher. Co-Authors Institutional Affiliations: Not Listed. COBRE, Short Research Presentation

457. Bikram Subedi, Murray State University. **Wastewater Analysis - Near Real Time Approach of Estimating Substance Use.** Co-Authors: Anita Sapkota, Durga P. Kodati, Landon Jones, Jusdin Kamuf. Co-Authors Institutional Affiliations: Murray State University, INBRE, Short Research Presentation

458. Brigitte E Martin, University of Mississippi Medical Center. **Temporal dynamics of cardiovascular response to influenza infection in mice.** Co-Authors: Kurt C Showmaker, Austin A Medders, Jacqueline B Starrett, Lavanya Challagundla, Michael R Garrett. Co-Authors Institutional Affiliations: The Jackson

Laboratory for Genomic Medicine, University of Mississippi Medical Center. COBRE, Short Research Presentation

459. Cammi Valdez, Northeastern State University. **Characterizing a New Longitudinal Mouse Model of Diabetic Retinopathy.** Co-Authors: Cammi Valdez, Erica Dotson, Joshua Butcher, Phillip Coburn. Co-Authors Institutional Affiliations: Northeastern State University, Harold Hamm Diabetes Center, The University of Oklahoma Health Sciences Center, Oklahoma State University, The University of Oklahoma Health Sciences Center. INBRE, Short Research Presentation

460. Carly Michelle Goldstein, PhD, FAACVPR, The Miriam Hospital/Alpert Medical School of Brown University. **Using the Multiphase Optimization Strategy and an Electronic Health Record Review to Refine, Finalize, and Prepare Trauma-Informed Interventions to Increase Phase II Cardiac Rehabilitation Initiation in a Full Factorial Experiment.** Co-Authors: J. Graham Thomas, Benjamin T. Ladd, Wen-Chih Wu. Co-Authors Institutional Affiliations: The Miriam Hospital/Alpert Medical School of Brown University, Providence VA Medical Center. COBRE, Flash Talk

461. Caroline de Carvalho Picoli, MaineHealth Institute for Research. **The Gut-Bone Connection: Gastric X/A-like Cells and Skeletal Homeostasis.** Co-Authors: Caroline de Carvalho Picoli, Jeyrie Ramos Aponte, Tiange Feng, Clifford J Rosen, Ziru Li. Co-Authors Institutional Affiliations: MaineHealth Research Institute, MMC Medical School. COBRE, Short Research Presentation

462. Christopher Johansen PhD, MPH, University of Nevada, Las Vegas. **Parental acculturation and its association with preschool-aged child's health behaviors among Latinos in Southern Nevada.** Co-Authors: Miguel Fudolig, Liliana Davalos, Brisa Rodriguez, Marissa Martinez. Co-Authors Institutional Affiliations: University of Nevada Las Vegas. INBRE, Short Research Presentation

463. Daysha Marie Isaac, Langston University. **Stalk Cell Movement in Drosophila: a model to understand how migrating cells shape tissues and organs.** Co-Authors: Sally Horne-Badovinac, Jocelyn A. Mcdonald. Co-Authors Institutional Affiliations: University of Chicago, Kansas State University. INBRE, Flash Talk

464. Debora Kamin Mukaz, University of Vermont Larner College of Medicine. **Residential Segregation and Thrombo-inflammatory Biomarkers Related to Hypertension in Black and White Americans.** Co-Authors: Andrew D. Sparks, Ryan Packer, Suzanne E. Judd, Virginia J. Howard, April P. Carson, Timothy B. Plante, D Leann Long, Katharine Cheung, Mary Cushman. Co-Authors Institutional Affiliations: University of Vermont Larner College of Medicine, University of Alabama at Birmingham, University of Mississippi Medical Center, Wake Forest University. COBRE, Short Research Presentation

465. Devin M. Drown, University of Alaska Fairbanks. **Impact of Arctic Thaw on Soil Microbial Communities and Emerging Environmental Health Risks.** Co-Authors: Bevyn Cover. Co-Authors Institutional Affiliations: University of Alaska Fairbanks. INBRE, Short Research Presentation

466. Dionysios Patriarcheas, West Virginia University. **Deciphering Glyphosate Resistance Mechanisms: Insights from S. cerevisiae into Mitochondrial Function and Human Glutamate Transport.** Co-Authors: Jennifer E. G. Gallagher. Co-Authors Institutional Affiliations: West Virginia University. CTR, Short Research Presentation

467. Dylan Feist, Kansas State University. **Fine-tuning of Cell-ECM Assembly by Transglutaminase.** Co-Authors: Erika R. Geisbrecht, Nicole Green. Co-Authors Institutional Affiliations: Kansas State University, Cornell College. INBRE, Short Research Presentation

468. Elizabeth B. Quigley, University of Wyoming. **Sexually Dimorphic JNK Signaling in the Gonadotrope is Important for Female Fertility Regulation.** Co-Authors: Alexandra Verosky, Brian S. Edwards, Shaihla A. Khan, Ulrich Boehm, Roger J. Davis,Amy M. Navratil. Co-Authors Institutional Affiliations: University of Wyoming, Laramie, University of Colorado, Mayo Clinic, Genus PLC, Saarland University School of Medicine, University of Massachusetts Medical School, Howard Hughes Medical Institute. INBRE, Short Research Presentation

469. Emily E. Schmitt, University of Wyoming. **The aging mouse as a novel model of nocturia.** Co-Authors: Danielle R. Bruns, Nicole L. Bedford. Co-Authors Institutional Affiliations: University of Wyoming. INBRE, Short Research Presentation

470. Emily Tolbert, Kansas State University. **cHPV E6 reduces innate immune signaling.** Co-Authors: Dalton Dacus, Rose Pollina, Nicholas A. Wallace. Co-Authors Institutional Affiliations: Enliven Therapeutics, Kansas State University. COBRE, Flash Talk

471. Emily Zeitler, Dartmouth Health. **Experience of Remote Monitoring of Cardiac Implantable Electronic Devices in Rural New England.** Co-Authors: Laure Bernstein, Jennifer Wenner, Nichole Rogovoy, Mark Creager, Karen Schifferdecker. Co-Authors Institutional Affiliations: Dartmouth Health. COBRE, Flash Talk

472. Erica J. Johnson, University of Delaware. **Subcutaneous adipose arteries exhibit significantly less fatty acid uptake in obesity.** Co-Authors: Thanh Nguyen, Sabita Rokka, Caitlin Halbert, Ibra S. Fancher. Co-Authors Institutional Affiliations: University of Delaware. COBRE, Flash Talk

473. Erica Sood, Nemours Children's Health. HEARTPrep: **A digital health psychosocial intervention for mothers expecting a baby with congenital heart disease.** Co-Authors: Kimberly Canter, Anne E. Kazak, Angel Munoz-Osorio, Alejandra Perez Ramirez. Co-Authors Institutional Affiliations: Nemours Children's Health. COBRE, Short Research Presentation

474. Gary ZeRuth, Murray State University. **Gli-similar 3 is essential for proper pancreatic and kidney development in zebrafish.** Co-Authors: None. INBRE, Flash Talk

475. Hamed Fayyaz, University of Delaware. **An Interoperable ML Pipeline for Pediatric Obesity Risk Prediction using Commonly Available EHR Data.** Co-Authors: Mehak Gupta, H. Timothy Bunnell, Claudine Jurkovitz Thao-Ly, Thao-Ly Phan, Rahmatollah Beheshti. Co-Authors Institutional Affiliations: Southern Methodist University, Nemours Children's Health, ChristianaCare, University of Delaware. CTR, Flash Talk

476. Hannah Ladwig, Creighton University. **Structural Analysis of Crassostrea gigas OAZ-PK RNA.** Co-Authors: Rhiannon McCracken, Juliane Soukup. Co-Authors Institutional Affiliations: Creighton University. INBRE, Flash Talk

477. Harilaos Filippakis, University of New England. **Therapeutic targeting of Tryptophan-mediated macropinocytosis in Tuberous Sclerosis Complex.** Co-Authors: Sarah Lafleur, Windrie Cox, Aidan McGrath-Conwell, Elizabeth P. Henske, Harilaos Filippakis. Co-Authors Institutional Affiliations: University of New England. COBRE, Short Research Presentation

478. Heather Drummond, University of Mississippi Medical Center. **Acid sensing ion channel 2 (ASIC2) deficiency increases light cycle ambulatory activity in mice.** Co-Authors: Kylie M. Larson, Emily Hildebrandt, Jussara do Carmo. Co-Authors Institutional Affiliations: University of Mississippi Medical Center. COBRE, Short Research Presentation

479. Janeese A Brownlow, PhD, Delaware State University. **An Examination of Neighborhood Disadvantage and Stress on Objective Sleep and Sleep-Related Fears.** Co-Authors: None. INBRE, Short Research Presentation

480. Jared C Talbot, University of Maine. **Fast-twitch myofibrils grow in proportion with Mylpf dosage.** Co-Authors: Adekeye TE, Teets EM, Tomak E, Sprague K, Waterman S, Varga S, Austin J, Rodriguez-Medio C, Hupper T, Shepherd SJ, Amacher SL, Kelley JB, Talbot JC. Co-Authors Institutional Affiliations: University of Maine, Ohio State University. COBRE, Short Research Presentation

481. Karthik Swaminathan, University of Wyoming. **Ribosomal Heterogeneity in Stress Neurobiology.** Co-Authors: Rammohan Shukla. Co-Authors Institutional Affiliations: University of Wyoming. COBRE, Flash Talk

482. Katherine A. Berry, University of Wyoming. **Anxiety on the rocks: College students' anticipatory and compensatory urges to drink in response to a laboratory-based social stressor task.** Co-Authors:

Alison Looby. Co-Authors Institutional Affiliations: University of Wyoming. INBRE, Flash Talk

483. Kevin Michael Brown, University of Oklahoma Health Sciences Center. **Elucidation of TgPKG kinase substrates required for Toxoplasma motility.** Co-Authors: Gabriel Cabral, Bingjian Ren, Sebastian Nasamu. Co-Authors Institutional Affiliations: University of Oklahoma Health Sciences Center, University of Geneva. COBRE, Short Research Presentation

484. Khadija Kakar, University of South Carolina School of Medicine. **Protective Effects of Delta-8-THC Against EAE-Induced Enteric Neuropathy and Neuroinflammation through Regulation of miRNA-Mediated Signaling Networks.** Co-Authors: Urmi Halder, Manikandan Palrasu. Co-Authors Institutional Affiliations: Not Listed. COBRE, Flash Talk

485. Lauren Covington, University of Delaware. **Socio-ecological Stressors Among Mothers Experiencing Socioeconomic Disadvantage.** Co-Authors: Destiny Mahmood, Kiara Shay, Emma Archer, Freda Patterson, Emily Hauenstein. Co-Authors Institutional Affiliations: University of Delaware, University of Virginia. CTR, Flash Talk

486. Leela V. Thomas, Delaware State University. **Influence of social determinants on maternal and infant complications of gestational diabetes mellitus.** Co-Authors: Zugui Zhang, Claudine T. Jurkovitz, Mitchell R. Fawcett, M. James Lenhard. Co-Authors Institutional Affiliations: ChristianaCare Health Services Inc., Sidney Kimmel Medical College. CTR, Short Research Presentation

487. Leya Givvines, West Virginia School of Osteopathic Medicine. **Ovariectomy exacerbates plasma IgE and lung eosinophilia, but is not associated with greater vascular endothelial dysfunction in asthmatic mice.** Co-Authors: Abigail R. Patterson, Marina Diioia, Dovenia S. Ponnoth, Shinichi Asano. Co-Authors Institutional Affiliations: West Virginia Wesleyan College, West Virginia School of Osteopathic Medicine. INBRE, Flash Talk

488. Lisa T. Jansen, University of Arkansas for Medical Sciences - Arkansas Children's Nutrition Center. **Impact of Physical Activity Intervention on Longitudinal Glycemic Patterns in Pregnant Women with Obesity: A CGM Pilot Study.** Co-Authors: Scott Stewart, Lilian Cheak, Precious Jeffrey, Aline Andres. Co-Authors Institutional Affiliations: Arkansas for Medical Sciences, Arkansas Children's Nutrition Center, Arkansas Children's Research Institute. COBRE, Short Research Presentation

489. Lydia Ostmo, Northeastern State University. **Unraveling the functions of Polymerase Epsilon complex in DNA replication and DNA damage.** Co-Authors: Brandy Fultz, Sapna Das-Bradoo. Co-Authors Institutional Affiliations: Northeastern State University. INBRE

490. Luz Maria Deardorff, University of Hawai'i Maui College. **Environmental Microbes as Indicators of Human Health Risk After the Lahaina Wildfires.** Co-Authors: Tara Zamani, Michelle Gould, Sally Irwin, Junnie June, Rachel Wilsey, Jennifer Honda. Co-Authors Institutional Affiliations: University of Hawai'i Maui College, University of Texas Health Science Center. INBRE, Short Research Presentation

491. Mabruka Alfaidi, LSHSC**. Interleukin-1 Receptor Activation in Vascular Remodeling and Early Atherosclerosis**. Co-Authors: Siddhartha Gangopadhyay, Evan Kidder, Meleah Pea, Quartina Henderson, Siyuan Cheng, Matthew Woolard, Xiuping Yu, Mabruka Alfaidi. Co-Authors Institutional Affiliations: Feist-Weiller Cancer Center, Center for Cardiovascular Diseases and Science (CCDS), Louisiana State University Health Sciences Center. COBRE, Short Research Presentation

492. Manikandan Palrasu, Dept of Pathology, Microbiology and Immunology, School of Medicine, University of South Carolina. **Aryl hydrocarbon receptor transcriptionally regulates beta-defensin-1 and consequently suppresses colonic inflammation during colitis.** Co-Authors: Khadija Kakar, FNU Hamida, Amarnath Satheesh Marudamuthu, Tayler Carter, Kiesha Maria Wilson, Archana Saxena, Xiaoming Yang, Narendra P. Singh, Philip Brandon Busbee, Prakash Nagarkatti, Mitzi Nagarkatti. Co-Authors Institutional Affiliations: University of South Carolina School of Medicine. COBRE, Flash Talk

493. Manisha Thakur, Southern University and A&M college. **Unraveling the Interplay: Carbon Nanotubes, Inflammation, and Environmental Stressors.** Co-Authors: Sanjay Batra. Co-Authors Institutional

Affiliations: Southern University and A&M college. Short Research Presentation

494. Martha Rojo, University of Arkansas for Medical Sciences. **Hispanic Faith-based leaders' perspectives on healthy eating interventions in the Hispanic community.** Co-Authors: Hannah Aston, Johnathan Rodriguez, Erickson Feliciano, Carson Guatemala, Janet Lopez. Co-Authors Institutional Affiliations: Not Listed. COBRE, Flash Talk

495. Maria Jesus Ruiz Echevarria, Oklahoma University Health Sciences, Faculty. **Towards Identifying Novel Therapies for Prostate Cancer.** Co-Authors: Joshua M. Corbin. Co-Authors Institutional Affiliations: Duke University. INBRE, Short Research Presentation

496. Matthew D Lynes, MaineHealth Institute for Research. **Peroxiredoxin 2 protects Trpv1+ derived fat cells from excessive reactive oxygen species induced cell death.** Co-Authors: Breanna Morrill, Carolina Cora, Wadak Harbi, Caitlin Ellis, Benjamin Tero, Kimberly Malka, Lucy Liaw. Co-Authors Institutional Affiliations: MaineHealth Institute for Research, University of Southern Maine. COBRE, Short Research Presentation

497. Md Jobayer Hossain, Nemours Chindren's Health, Wilmington. **Precision Race-Ethnic Disparity in Mortality Risk in Pediatric Cancers: A Study Using SEER Data.** Co-Authors: Zhaoying Lu, Araf Hossain Jahin. Co-Authors Institutional Affiliations: Nemours Children's Health, University of Delaware. CTR, Short Research Presentation

498. Mehtap Haktanir Abul, Alpert Medical School Brown University, Rhode Island Hospital. **Asthma and Sleep-Related Environmental Factors Contributing to Sleep Awakenings in Urban Children with Asthma.** Co-Authors: Sheryl J. Kopel, Shira Dunsiger, Luiz Guzman, Carly Mattice, Sidney Kirchhof, Caroline Gredvig-Ardito, M. Carskadon. Co-Authors Institutional Affiliations: Rhode Island Hospital, Alpert Medical School of Brown University, Bradley-Hasbro Research Center, EP Bradley Hospital Sleep Research Laboratory. CTR, Flash Talk

499. Michael Robichaux, West Virginia University. **Misfolded rhodopsin disrupts the ER secretory pathway to the presynaptic terminals of rod photoreceptors in a retinitis pigmentosa mouse model with retinal neurodegeneration.** Co-Authors: Samantha Thompson, Sophie Crowder, Emily Sechrest, Wen-Tao Deng. Co-Authors Institutional Affiliations: West Virginia University. COBRE, Short Research Presentation

500. Michayla Moore, MaineHealth Institute for Research (MHIR). **BMP9/ALK1 Signaling is Required for Transcription and Secretion of Mesenchymal Stem Cell Marker, ISLR (Meflin), in Human Cardiac Progenitor Cells.** Co-Authors: Calvin Vary, Douglas Sawyer. Co-Authors Institutional Affiliations: MaineHealth Institute for Research. COBRE, Short Research Presentation

501. Motoki Takaku, University of North Dakota. **Dissecting cellular reprogramming by genomics and machine learning.** Co-Authors: Mika Saotome, Aerica Nagornyuk, Jill Goodman. Co-Authors Institutional Affiliations: University of North Dakota School of Medicine. COBRE, Flash Talk

502. Prateek Verma, University of Arkansas. **Evaluation of Large Vision Language Models on Scientific Images.** Co-Authors: Minh-Hao Van, Xintao Wu. Co-Authors Institutional Affiliations: University of Arkansas. COBRE, Short Research Presentation

503. Raphael Oladokun, West Virginia University. **Dielectrophoretic Characterization and COMSOL Analysis of Late Carcinoma Using PBMCs from MMTV-PyMT (PyMT) and MMTV-WT (WT) Mammary Carcinoma Models.** Co-Authors: Soumya Srivastava. Co-Authors Institutional Affiliations: West Virginia University. INBRE, Flash Talk

504. Russell McCulloh, University of Nebraska Medical Center. **Outlining a vision for a learning research system.** Co-Authors: Ellen Kerns, Jerrod Anzalone, Matthew Rizzo. Co-Authors Institutional Affiliations: University of Nebraska Medical Center. CTR, Short Research Presentation

505. Sabrina Duran, West Virginia University School of Medicine. **Comparing Readability of American Academy of Dermatology and AI-generated Patient Education Materials.** Co-Authors: Jenna Foster,

Andrea Medina Gonzalez, John Nguyen, Diane Wang, Zachary Zinn. Co-Authors Institutional Affiliations: West Virginia University. Flash Talk

506. Sahil Lohana, North Dakota State University. **Validation of novel histone deacetylases (HDAC) specific nanoparticles using HDACs overexpressed human embryonic kidney cells.** Co-Authors: Yogaraj S Ramakrishnan, Premanand Balraj, Md Rakib Hasan Khan, Sanku Mallik, Venkatachalem Sathish, Quadir Mohiuddin. Co-Authors Institutional Affiliations: Not Listed. INBRE, Flash Talk

507. Sai Prashanthi Gumpili, University of Delaware. **Risk factors for cardiac events in children and young adults within 6 months following a COVID-19 infection.** Co-Authors: Sai Prashanthi Gumpili, Shubhika Srivastava, Carol Prospero, Ran Zhang, Jobayer Hossain, Suzanne McCahan, Chuming Chen, Julie Cowart, Cathy Wu, H. Timothy Bunnell, Robert Akins, Claudine Jurkovitz. Co-Authors Institutional Affiliations: Nemours Children's Health, University of Delaware, Christiana Care Health Services, Inc. INBRE, Flash Talk

508. Shyanna Larocque, Turtle Mountain Community College. **Fetal C-Reactive Protein rs1205 Genotype Is Not Associated with Maternal Pre-eclampsia.** Co-Authors: Crystal Azure, Hailey Davis, Craig Poitra, Jackie Poitra, Shayden Standish, Tyler J Parisien, Lyle G. Best. Co-Authors Institutional Affiliations: Turtle Mountain Community College. INBRE, Flash Talk

509. Steven Ionov, Dartmouth College. **Molecular Analysis of SARS-CoV-2 Vaccine Serum Antibody Repertoires in Individuals with Cystic Fibrosis.** Co-Authors: Seungmin Shin, Ruth Connor, Jiwon Lee. Co-Authors Institutional Affiliations: Dartmouth College, Dartmouth-Hitchcock Medical Center. COBRE, Flash Talk

510. Tasnim Imran, Alpert Medical School of Brown University, Providence VA Medical Center. **Characterizing cardiac microstructure in heart failure with preserved ejection fraction using cardiac magnetic resonance diffusion tensor imaging.** Co-Authors: Daniel Arcuri, Christopher Nguyen, Reza Avazmohammadi, Michael Atalay, Wen-Chih Wu, Gaurav Choudhary. Co-Authors Institutional Affiliations: Providence VA Medical Center, Rhode Island Hospital, Cleveland Clinic Foundation, Texas A&M University. COBRE, Short Research Presentation

511. Thomas Huckaba, Xavier University of Louisiana. **Development and Testing of Proteolysis-Targeting Chimeras (PROTACs) as Therapeutics for Non-Small Cell Lung Cancer.** Co-Authors: Fasial Abedin, Cecily DeFreece, Xianyou Peng, Guangdi Wang. Co-Authors Institutional Affiliations: INBRE, Short Research Presentation

512. Tirumalai Rangasamy, Louisiana State University. **Development of Small Molecule-based Intervention to Combat the Infection Caused by the Superbug Carbapenem-resistant Klebsiella pneumoniae.** Co-Authors: Kennedy Trahan, Duane Jeansonne, Allyson Mohanty-Aldana, John Le, Amit Sharma, Basel Abuaita, Samithamby Jeyaseelan. Co-Authors Institutional Affiliations: Louisiana State University. COBRE, Short Research Presentation

513. Umesh D. Wankhade, Arkansas Children Nutrition Center, UAMS. **From Conception to Adipose Tissue: Investigating the Role of Housing Temperature on Offspring Response to Dietary Challenge.** Co-Authors: Henry A. Paz, Ying Zhong, James D. Sikes, Reid D. Landes, Roy Morello, Samrat Roy Choudhury. Co-Authors Institutional Affiliations: Arkansas Children's Nutrition Center, University of Arkansas for Medical Sciences, Arkansas Children's Research Institute. COBRE, Short Research Presentation

514. Xhoela Bame, Dartmouth College. **Mitochondrial network reorganization and transient expansion during oligodendrocyte generation.** Co-Authors: Robert A. Hill. Co-Authors Institutional Affiliations: Dartmouth College. COBRE, Short Research Presentation

515. Yun-Seok Choi, Black Hills State University. **A general method for the development of quantitative biosensors enables the measurement of free Nedd8.** Co-Authors: Zachary Wyatt Davis. Co-Authors Institutional Affiliations: Black Hills State University. INBRE, Short Research Presentation

516. Zim Warda Hasan, Western Kentucky University. **Effect of Glucocorticoid Blockade on Inflammatory**

Responses to Acute Sleep Fragmentation in Mice. Co-Authors: Van Thuan Nguyen, Noah T. Ashley. Co-Authors Institutional Affiliations: Western Kentucky University. INBRE, Flash Talk

517. Zugui Zhang, Christiana Care Health System. **The Effectiveness of the Community Health Workers Program in Primary Care in Delaware: Impact on Health Utilities and Outcomes.** Co-Authors: Alexandra Maree Mapp, James T Laughery. Co-Authors Institutional Affiliations: Christiana Care Health System. CTR, Short Research