Indiana Academy of Science

141st Annual Meeting

March 21, 2026

JW Marriott Downtown Indianapolis

2025-2026 Academy Council

The Academy Council consists of the current elected Academy officers, Chairs of the Foundation and Senior Research Grants Committee, two at-large members, and the Director. The Council is responsible for all business of the Academy. Any individuals interested in serving in a position on the Academy Council should contact the Academy for more information.










Top Row (L-R): Luis Palacio, Academy President; Jennifer Kowalski, President-Elect, Samina Akbar, Past President

Second Row (L-R): Christopher Schmidt, Member-at-Large; Michelle Marincel-Payne, Secretary; Luke Jacobus, Parliamentarian; Moses Prabu, Treasurer; Michelle Marincel-Payne, Secretary

Third Row (L-R): Phillip Villani, Senior Research Grants Chair; Tom Dolan, Foundation Commitee Chair; Erin Gerecke, Member-at-Large;

A list of Academy Elected and Appointed Committees can be found on the Indiana Academy of Science Website.

2025-2026 Staff

- Liz Subrin
- Executive Director
- Second Year of IAS Membership

- Dr.Wes Tobin
- Webmaster
- 2024-2027 Term
- 17 Years of IAS Membership

- Colin Topping
- Social Media Coordinator
- 2025-2026 Term
- Second Year of IAS Membership

- Paul Doss
- INSPECT Fellowship Coordinator
- 2025-2026 Term
- 41 Years of IAS Membership

- Dr. Horia I. Petrache
- Proceedings Editor
- 2025-2026 Term
- 19 Years of IAS Membership

2025-2026 Section Leadership

Section Chairs preside at meetings, contribute to the planning and execution of the annual academy meeting, and contact section members when necessary. Section vice chairs are elected in the section business meeting at each annual meeting to serve one year as vice chair (chair-elect) and then one year as chair.

Section	Section Chair and Vice Chair
Agriculture	Chris Sedlacek
Anthropology	Amandine Eriksen and Lilly Bucher
Biochemistry & Physiology	Michelle Malott and Hisako Masudah
Botany	Darrin Rubino and Phillip Villani
Cell Biology	Takuya Akiyama and Kris Schwab
Chemistry	Kamila Deavers and Meden Isaac-Lam
Computer Science	Debanjali Banerjee and William D. Moscoso Barrera
Conservation, Sustainability and Land Management	Jordan Marshall and Andrea Echeverry-Alcendra
Earth Science	Ben Dattilo
Ecology	Matt Harmon
Engineering	Abi Nazari and Yunting Yin
Environmental Science	Jia Xue
Health Science	Armando Peña and Neetu Mahendraker
History of Science	Rex Bickers and Jesse Hannan
Mathematics	Kevin Drury
Microbiology and Molecular Biology	Elizabeth Delery and Kyu Hong Cho
Physics and Astronomy	Horia Petrache and Maarij Syed
Plant Systematics and Biodiversity	Joanna Stebing and Elizabeth Mabee
Science Education	Rona Robinson-Hall and Catherine Steding
Zoology and Entomology	Glené Mynhardt and Christopher Wirth

Complete descriptions of the content areas for each section can be found on the Indiana Academy of Science website.

Section Business Meeting
4:30-5:00pm

Section	Meeting Room
Agriculture	TBD
Anthropology	109
Biochemistry & Physiology	103
Botany	White River F-J
Cell Biology	White River A-E
Chemistry	104
Computer Science	108
Conservation, Sustainability and Land Management	207
Earth Science	203
Ecology	202
Engineering	209 (shared)
Environmental Science	208
Health Science	206
History of Science	TBD
Mathematics	209 (shared)
Microbiology and Molecular Biology	105
Physics and Astronomy	209 (shared)
Plant Systematics and Biodiversity	204
Science Education	201
Zoology and Entomology	205

President's Welcome

Welcome to the 141st Annual Indiana Academy of Science Meeting!

141st Annual Academy Meeting Agenda

7:30-8:00 AM	**Poster Set Up & Oral Presentation Download**	White River F-J
7:30 - 9:00 AM	**Registration**	In Front of Room 108
8:30 -9:00 AM	**Morning Plenary Session: President's Welcome & Address – Dr. Luis Palacio**	White River A-E
9:00 - 10:30 AM	**Oral Presentations, Hot Topics & Workshops**	103- 105, 109 201 - 209
10:00 AM - 12:15PM	**Poster Session and Emerging Scientist Research Poster Competition**	White River F-J
12:15 - 1:30 PM	**Academy Luncheon**	White River A-E
12:30 - 1:15 PM	**Keynote Address**	White River A-E
1:00 - 4:00 PM	**Professional Headshots**	108
2:30-3:30 PM	**Emerging Scientist Research Oral Competitions**	White River A-E , White River F-J
1:30 - 4:30 PM	**Oral Presentations, Hot Topics & Workshops**	103- 105, 109 201 - 209
4:30 - 5:00 PM	**Section Meeting**	103- 105, 109 201 - 209
5:00 - 6:00 PM	**Awards & Networking Reception: Awards - Emerging Scientist, DEI Advocate, Distinguished Scholar, Fellowship & Distinguished Service**	White River A-E

Keynote Address

Dr. Franklin Carrero-Martinez

About Dr. Franklin Carrero-Martinez

Franklin Carrero-Martinez joined the National Academies of Sciences, Engineering, and Medicine in 2018, where he directs the Science and Technology for Sustainability program within the Office of International Networks, Collaboration, and Security. He has led cross-sector initiatives spanning sustainability, international partnerships, and support for displaced scientists and engineers. He is a scientist–diplomat whose work connects research, innovation, and international cooperation to advance sustainability and strengthen science systems globally. Prior to joining the National Academies, Dr. Carrero-Martínez served as Acting Deputy Science and Technology Adviser to the Secretary of State. He began his career in science diplomacy and policy as the American Association for the Advancement of Science (AAAS) Roger Revelle Fellow in Global Stewardship, with a joint appointment in the U.S. Department of State's Office of the Science and Technology Adviser to the Secretary (STAS) and the National Academy of Sciences. Earlier in his career, Dr. Carrero-Martínez was an associate professor at the University of Puerto Rico (UPR), Mayagüez, and held an adjunct appointment at the UPR Medical Sciences Campus. He has also been affiliated with Duke University, the Massachusetts Institute of Technology, and Japan's Institute of Genetics. Dr. Carrero-Martínez holds a B.S. in biology (honors) from the University of Puerto Rico and a Ph.D. in cell and developmental neurobiology from the University of Illinois at Urbana-Champaign, along with a certificate in business administration.

Keynote Address

Dr. Franklin Carrero-Martinez

From First-Gen to Science Diplomacy: Science as a Passport

Description Coming

Awards

2026 Academy Fellows

A Fellow is a member of the Academy for a minimum of 5 years who has demonstrated service to the Academy and to the advancement of science in Indiana; service to education in science; and achievements in scientific research. Nature of service to the Academy includes attending Indiana Academy of Science meetings, presenting papers at meetings, publishing in the *Proceedings*; serving as an officer, section or committee chair, or committee member; and playing a role in organizing Academy activities. Fellow nominees are selected by current Academy Fellows and recommended to the Academy Council by the Awards Committee.

Dr. Erin McClelland

Dr. Erin McClelland received a Ph.D. in Biology under Dr. Wayne Potts from the University of Utah. She completed postdoctoral training under Dr. Arturo Casadevall at Albert Einstein College of Medicine. She joined the faculty at Marian University Wood College of Osteopathic Medicine in 2021 to teach Immunology to first- and second-year medical students.

Dr. McClelland's research interests encompass understanding host-pathogen interactions of the pathogenic yeast, Cryptococcus neoformans, including at the level of macrophage polarization and the sex of the host, to try to understand why 70 percent of patients with cryptococcosis are male.

Dr. McClelland has served as a previous Vice Chair and Chair of the IAS Microbiology and Molecular Biology section and is the current chair of the Science and Society Committee where she has run the Science with a Twist event for the last 3 years. Dr. McClelland is also currently serving on the Emerging Scientist Research Competition committee.

Awards

2026 Academy Fellows

(continued)

Nate Engbrecht

Nate Engbrecht serves as the State Herpetologist for the Indiana Department of Natural Resources, Division of Fish, Wildlife & Nature Preserves. He received his Bachelor's Degree from Bethel University and his Master's of Science from Indiana State University where he conducted his thesis work on state endangered Crawfish Frogs (Lithobates areolatus). In his role as the Agency's Herpetologist, Nate assumes statewide responsibility of overseeing the research and management of Indiana's amphibians and reptiles. Current projects include a study of how state endangered Kirtland's Snakes (Clonophis kirtlandii) are using restored post-agricultural landscapes, range expansions of the Green Treefrog (Hyla cinerea) along Indiana's southern margin, and the conservation and recovery of Crawfish Frogs.

Nate has been a member of the Academy since 2008 and currently serves on the Biodiversity and Natural Areas Committee. He has led the herpetology team during the organization's annual bioblitz, presented his research during annual IAS meetings, and has published several papers in the Proceedings. In his spare time, Nate enjoys beekeeping, nature photography, blacksmithing, growing carnivorous plants, and gardening with his wife Jamie at their home in Monroe County.

Awards

2026 Academy Fellows

(continued)

Dr. Bikram Sharma

Dr. Bikram Sharma is an Associate Professor of Biology at Ball State University, where he leads a laboratory focused on cardiovascular development and function. He earned a B.A. in Biology from Hanover College (2007), an M.S. in Biology and Biotechnology from Ball State University (2009), and Ph.D. in Physiology from Indiana State University (2012) followed by postdoctoral training at Stanford University (2013–2018) specializing in developmental cardiovascular biology and angiogenesis. Since establishing his independent laboratory at Ball State University, Dr. Sharma has secured external funding, including an NIH R15 award (2021–2024), to support research on coronary vessel development. He has published approximately 20 peer-reviewed journal articles in the field of cardiovascular development and function, contributing significantly to understanding endothelial signaling, angiogenesis, and heart morphogenesis. His laboratory integrates genetic models, cellular and molecular analysis, and in vitro and in vivo approaches to study mechanisms underlying coronary vascular growth and regeneration.

Dr. Sharma has been an active member of the Indiana Academy of Science since 2008, serving as Co-Chair and Chair of the Cell Biology Section and on multiple committees, including the Senior Research Grant and Emerging Scientist Competition Committees. In addition, he has mentored and sponsored numerous student poster and oral presentations at IAS annual meetings (12 total since 2018) and delivered a Hot Topics lecture on coronary vessel development (2025). In addition, Dr. Sharma is also a three times recipient of Indiana Academy of Science Senior Research Grant funding. His long-standing involvement with the Academy, combined with a strong research record and commitment to student training, positions him well for this recognition.

Awards

2026 Academy Fellows

(continued)

Dr. F. Collin Hobbs

Dr. F. Collin Hobbs has been a member of the Academy since 2008. His contributions to the Academy include authoring or coauthoring 17 IAS Annual Meeting oral and poster presentations, advising two undergraduate research teams who earned IAS Emerging Scientist Research Awards in 2023 and 2024, twice serving as the Vice-Chair and Chair of the Plant Systematics and Biodiversity Section (2016-2018, 2021-2023), participating in 10 IAS Bioblitz events (2011-2025), including serving as the 2019 vascular plant Team Lead, serving on the Senior Research Grants Committee (2019-2022), and serving as a reviewer and editorial board member for the PIAS.

During his early years as graduate student at Indiana University he received an IAS Senior Research Grant (2009) which helped kickstart his PhD research and for which remains grateful to this day.

Since joining the faculty at Huntington University in 2013 he has mentored over 38 undergraduate students who conducted research in the fields of ecology and botany. His roles at Huntington University include serving as the Manager of Thornhill Nature Preserve, Curator of the Fred Loew Herbarium, and the Coordinator of the university campus vegetable gardens, beehives, and orchard. He has served twice as the President of the Indiana College Biology Teachers Association and in 2025 received his institution's annual Faculty Excellence in Teaching Award and an honorary life membership by the Alpha Chi National College Honor Society for distinguished service and undergraduate mentorship.

Awards

2026 Academy Fellows

(continued)

Dr. Wes Tobin

Wes Tobin is Associate Professor of Physics and Department Chair of Natural Sciences at Indiana University East. He has been a member of the Indiana Academy of Science since 2009 and has regularly participated in its annual meetings through research presentations and professional engagement. Since 2018, he has assumed sustained leadership within the Academy, serving multiple terms as Vice-Chair and Chair of the Physics and Astronomy Section, Chair of the Mathematics Section, as a member of the Proceedings of the Indiana Academy of Science Editorial Board, and currently as Academy Webmaster. He also served as a Scientist Mentor in the Academy's STEM Scientist Mentorship initiative developed in partnership with the Indiana Department of Education, supporting professional development for high school STEM educators. Through long-standing participation and extended section leadership, he has contributed to strengthening disciplinary exchange and advancing the Academy's mission across Indiana.

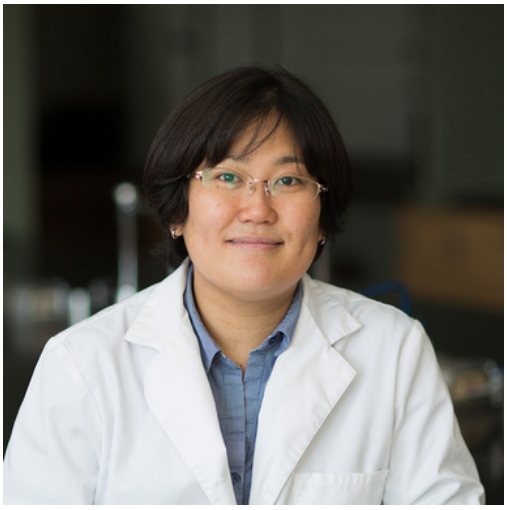
Dr. Tobin's primary research focuses on observational astrophysics, particularly close eclipsing binary systems and stellar astrophysics. He has authored 12 refereed publications with more than 200 citations collectively, including articles in Monthly Notices of the Royal Astronomical Society and New Astronomy, and has presented his work at national meetings of the American Astronomical Society. In addition, he conducts scholarship in science pedagogy, including research on technology-enhanced instruction and online learning in the physical sciences.

In his academic role, Dr. Tobin teaches courses in physics, astronomy, chemistry, and mathematics, reflecting a broad commitment to foundational STEM education. He has contributed to national astronomy education initiatives through collaboration with Pearson's Cosmic Perspective team and as a contributing author to OpenStax Astronomy. He is also an active Quality Matters reviewer, underscoring his commitment to high standards in course design and instructional quality. Together, his teaching, scholarly, and service work reflect sustained dedication to strengthening science education and the scientific community in Indiana.

Awards

2026 Distinguished Scholar

The Distinguished Scholar Award of the Indiana Academy of Science is bestowed upon individuals who have been recognized by the Academy as having an exceptional record of scholarship. Award recipients are selected from nominations submitted to the Awards Committee and recommended to the Academy Council for final approval.



Dr. Hisako Masuda

Dr. Hisako Masuda is a Professor of Biochemistry in the School of Sciences at Indiana University Kokomo. She received her Ph.D. in Microbiology and Molecular Genetics from Rutgers University. She studies bacterial metabolism, genomics, and their phenotypic plasticity. Her current research primarily focuses on biodegradation and chemical repurposing of nylon. Using soil bacterial, her lab studies bacterial biodegradation of nylon and other environmental pollutants. She applies principles of Green Chemistry while developing a method of converting nylon waste into other non-toxic polymers. In collaborative work with health scientists, her lab investigates gut microbiomes of Indiana native birds as well as human subjects in a clinical study. Dr. Masuda has involved over fifty undergraduate students in her research at IU Kokomo and published 23 articles with many student co-authors. She was the recipient of the Distinguished Research Award and the Trustee's Teaching Award at IU Kokomo. She has been a member of the Indiana Academy of Science since 2013. She has served on multiple committees and as a section chair. Currently she is a co-chair of the Emerging Scientist Poster Competition committee and vice chair of the Biochemistry section. She was elected as a fellow of IAS in 2025.

Awards

2026 Distinguished Service

The Distinguished Service Award of the Indiana Academy of Science is bestowed upon individuals who have been recognized as having supported the Academy through service exceeding any normal expectation. Award recipients are selected from nominations submitted to the Awards Committee and recommended to the Academy Council for final approval.

Dr. Marc Milne

Dr. Marc Milne is a Professor of Biology at the University of Indianapolis, a taxonomist and ecologist, and one of the few experts on North American sheet-web spiders. Dr. Milne regularly teaches General Biology, Evolutionary Biology, Conservation, and Entomology and acts as a research advisor for several students within the Biology Department. He has helped students publish as co-authors on manuscripts detailing taxonomic revisions of spider genera, ecological effects of fire on spider communities, and updates to spider distribution records in the state. He has been an author on more than 45 scientific publications in journals such as Ecosphere, ZooKeys, and Zootaxa and has presented research at international and national scientific conferences, including the International Congress of Arachnology and the Ecological Society of America. Dr. Milne and a cohort of his research students have attended every IAS meeting since arriving in the state in late 2014. Dr. Milne's service to the Indiana Academy of Science began in that same year, when he became a member of the Academy and joined the Biodiversity and Natural Areas Committee. In 2017 was elected as the Vice Chair for the Zoology and Entomology section and then Chair of that section the following year. Dr. Milne joined the Senior Research Grant Committee in 2019 and was elevated to the Chair of the Biodiversity and Natural Areas Committee in the same year but had to step down from both soon after because he was elected as the President-elect of the Indiana Academy of Science in 2021. Dr. Milne began his Presidency of IAS in 2022, during which he worked with Sarah Mordan-McCombs to overhaul of the IAS website, with Delores Brown to manage the 2023 IAS conference and to implement Conservation Management as a new meeting section, with Sergio Henriques to represent the Society at the Indiana Conservation Partners meeting, and with Andrew Huntington to form a strong partnership between IAS and the Indiana Land Protection Alliance to found the Indiana Biodiversity Grant. Since its founding, this grant has grown to gain a partnership in the Indiana Native Plant Society and currently gives thousands of dollars to local taxonomists to document biodiversity on natural sites around the state. Dr. Milne served as the Immediate Past-President of IAS until 2024 and since then has continued to attend meetings with his students to highlight spider discoveries they have made from around the nation.

Awards

2026 Dr. Delores G. Brown Advocate Award

The Dr. Delores G. Brown Advocate Award is bestowed upon individuals who have promoted diversity, equity, inclusion, belonging, and/or justice within the Academy and/or their scientific communities through actions sustained over time of that have made a recent critical impact. Nominations are submitted to the DEI Committee and recommended to the Academy Council.

Dr. Maram Said

Dr. Maram Said is an obstetrician and gynecologist (OB-GYN) with Ascension St. Vincent in Carmel, Indiana. She received her medical degree from Des Moines University College of Osteopathic Medicine and Health Sciences and subsequently trained at St. Vincent Indianapolis Hospital. She specializes in minimally invasive and complex gynecologic surgery, routine and high risk obstetrical care, and all aspects of female reproductive health including menopause and fertility. Dr. Said is a member of the Society of Laparoendoscopic Surgeons, has served as Chair of her hospital's OB GYN Department, and has presented at the ACOG Annual Clinical Meeting and at the American Association of Gynecologic Laparoscopists (AAGL). She currently serves as a clinical assistant Professor for Marian University in addition to the Ascension St. Vincent OB-GYN Residency program. Importantly, Dr. Said has lectured by webinar to the Palestinian Society of Obstetricians and Gynecologists, as well as to residency programs throughout the United States. Dr Said aligns with the mission of PAMA to mentor and train both American and Palestinian physicians and medical students, and she is very passionate about improving outcomes, access, innovation, and medical education in women's health.

Special Guest Speaker

Dr. Brandy Mmbaga

Founder | CEO
Command The Room Coaching

About Brandy Mmbaga, Ph.D.

Dr. Brandy Mmbaga is a leadership development and culture strategist, communication expert, and Founder of Command The Room Coaching. She partners with organizations to strengthen culture, develop leaders, and improve performance through intentional communication and people-centered strategies.

With a Ph.D. in Organizational Studies and Communication and a background in higher education leadership, Brandy has designed and led initiatives focused on onboarding, leadership development, and organizational effectiveness. Some of her work has been featured in journals such as the Journal of Management and presented at widely respected conferences such as the Oxford Reputation Conference at Oxford University and the Academy of Management Annual Conference. Her work centers on helping leaders create environments where people can perform, grow, and contribute meaningfully.

Special Guest Speaker

Dr. Brandy Mmbaga

Founder | CEO
Command The Room Coaching

Session #1: Culture by Design: Building Environments Where People Authentically Perform and Belong

This session explores how leaders intentionally shape workplace culture to drive engagement, performance, and retention. Participants will learn how inclusive environments fuel innovation, strengthen collaboration, and allow individuals to contribute at their highest level.

Session #2: Leading What You've Built: Developing People for Performance and Growth

This session focuses on how leaders effectively develop individuals within strong cultures. Participants will learn how to coach, influence, and elevate performance while aligning individual growth with organizational goals.

Special Guest Speaker

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Schedule of Oral Presentations

Professional Development & Program Highlights

Time	Presentation Title & Presenters	Section of Interest	Room
9:15 AM	**More Than Meets the Assay: Reinterpreting Proteasome Activity in C. elegans** Erika B. Sorensen	Grant Reporting, Cell Biology	103
9:30 AM	**Successful Culture Development for Teams** Dr. Mmbaga	DEI, Leadership	103
9:45 AM	**IAS Proceedings: Information for Current and Prospective Authors** Horia Petrache	Publishing	White River A-E
10:45 AM	**Machine Learning-Based Detection of Mouse Hippocampal Sharp-Wave Ripples (SWRs) Using a Channel-Specific Training Approach to Advance Understanding of Memory Disorders** Lauren Kleinert	Grant Reporting. Biochemistry & Physiology	103
11:45 AM	**Reactive Oxygen and Nitrogen Species (RONS) as a Potential Modulator of Metal Dependent Protein Function in Neutrophils** Michael W. Thompson	Grant Reporting. Biochemistry & Physiology	103
12:15 - 1:30 PM	**Academy Lunch**		**White River A-E**
1:30 PM	**Inspect Fellowship** Paul Doss, Jesse Hannan, Alexandra Hicks, Lean Hong Tan,	INSPECT Fellowship	103
1:45 PM	**Successful Culture Development for Teams** Dr. Mmbaga	DEI, Leadership	103
3:30 PM	**Leadership in the Indiana Academy of Science** Kristen Schunk Moreland and Jo Nahod-Carlin	IAS Leadership	103
4:30 PM	**Section Meeting**		**103**

Schedule of Oral Presentations

Hot Topics

Sponsored By: Taft Law

Time	Presentation Title & Presenters	Section of Interest	Room
9:15 AM	**Harnessing Artificial Intelligence to Address Engagement, Technical Writing, and Content Mastery in Collegiate Science Instruction** Ashlee Tietje	Science Education, Computer Science	209
9:45 AM	**Alternative Grading STEM Courses** Dr. Sarah Justice, Dr. Sarah Klanderman	Science Education, Mathematics	209
12:15 - 1:30 PM	**Academy Lunch**		**White River A-E**
2:15 PM	**From Inquiry to Innovation: Preparing Elementary Science Teachers with AI and 3D Printing** Dr. Brittany Garvin	Science Education	209
2:45 PM	**AI for Health: Discovering Digital Biomarkers Across Speech, Text, and Echocardiography** Dr. Yunting Yin	Engineering, Health Sciences	209
3:15 PM	**The New Order: How AI Rewrites the Narrative of Science** Dr. Chris Edwards	History of Science, Physics & Astronomy	209
3:45 PM	**The Bee Campus Effect: Integrating Applied Research, Service Learning, and Teaching at the University of Southern Indiana** Dr. Edith Hardcastle	Conservation, Sustainability and Land Management, Plant Systematics & Biodiversity	209
4:30 PM	**Section Meeting**		**209**

Schedule of Oral Presentations

Workshops

Sponsored By: Taft Law

Taft/

Time	Presentation Title & Presenters	Section of Interest	Room
9:15 AM	**The State of Indiana and Highlights from the History of Genetics A sampling of legendary Hoosiers and their noteworthy contributions to this modern science.** Jesse Hannan, Seth Hamby, Yagmur Metin, Dr. Rex Bickers	History of Science, Health Sciences	208
12:15 - 1:30 PM	**Academy Lunch**		**White River A-E**
1:45 PM	**Integrating Entrepreneurial Mindset into Undergraduate STEM Research** Dr. Michelle Marincel Payne, Dr. Irene Reizman	Science Education, Engineering	208
2:45 PM	**Non-AI and AI-Powered Tools for Species Conservation Planning and Monitoring: Different tools, Same Purpose!** Andrea Echeverry-Alcendra, William Moscoso Barrera	Conservation, Sustainability and Land Management, Computer Science	208
4:30 PM	**Section Meeting**		**208**

Schedule of Oral Presentations

Agriculture

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
3:30 PM	**Microbial nitrifier denitrification: Linking genetic makeup to physiological traits and real time nitrous oxide emission potentials** Chris Sedlacek	105
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Anthropology

Time	Presentation Title & Presenter	Room
9:30 AM	**Anthropology and Anthropophagy: Reevaluating Herxheim, Germany** Belle Custodio	109
9:45 AM	**Childhood in Early Indianapolis: Growth and Health Disparities among the Juveniles from the Greenlawn Cemetery** Jessica Giles	109
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Applied Osteology in Active Medicolegal Investigations: Field Recovery Challenges and Adaptations** Ella Uren	109
2:00 PM	**Unmingling an Unprovenienced and Under-Documented Skeletal Collection with Commingled Forensic, Anatomical and Historical Remains** Krista Latham	109
2:15 PM	**Mounted Search and Recovery: The Benefits of Utilizing a Scent Horse in Interdisciplinary Search and Recovery Operations** Lillian Bucher	109
2:30 PM	**Review of the Flora Mastodon Site Cultural Materials** Daniel Lebakos	109
2:45 PM	**Topotooth: A novel online software program to measure dental occlusal characteristics.** Christopher Schmidt	109
4:30 PM	**Section Meeting**	**109**

Schedule of Oral Presentations

Biochemistry & Physiology

Time	Presentation Title & Presenter	Room
9:15 AM	**Investigation of the potential ligand-binding partners of the G protein-coupled receptor FSHR-1 under oxidative stress in C. elegans** Milica Nenadovich	104
9:30 AM	**Lipidomic Analysis of SCS-Deficent Muscles in Mouse Models of Mitochondrial Myopathy** Jada Radford	104
9:45 AM	**Robustness of Carbonic Anhydrase for Application in Nanoscale CO2 Capture Technologies** Arjun Sharma	104
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Botany

Time	Presentation Title & Presenter	Room
9:30 AM	**Noteworthy Natives - An Intersection of Botany, Art, and Music** Marcia E. Moore	202
9:45 AM	**Using tree-ring analysis to explore the history of three nineteenth-century buildings in Hanover, Indiana (Jefferson County)** Darrin Rubino	202
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Mnium cuspidatum meristem growth and caulid branching control** Sophia Dobosiewicz	202
2:00 PM	**Minium cuspidatum: New Model Organism for Plant Pathogen Interactions** Clayton Reames	202
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Cell Biology

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**PHYSIOLOGICAL RESPONSES OF SEA CUCUMBERS TO THERMAL STRESS: CHANGES IN COELOMOCYTE NUMBERS** Fateha Arefin	105
2:00 PM	**The characterization of a Drosophila continuous mesodermal/muscle cell line to study trithorax and Polycomb regulation of Hox expression in embryonic heart development** Grace Martin	105
2:15 PM	**Defining the Treatment Period for Drug Screening in Zebrafish Models of Retinitis Pigmentosa** Mia K. Tsou	105
2:30 PM	**The Role of 5-HT1A Autoreceptors in Drosophila Activity Levels and Circadian Rhythm and its Relationship to Sex** Emma A Walker	105
2:45 PM	**PHYSIOLOGICAL RESPONSES OF SEA URCHINS EXPOSED TO GRADUALLY INCREASED TEMPERATURE AS A STRESSOR: CHANGES IN COELOMOCYTE NUMBERS** Sayed Mamun	105
3:00 PM	**trithorax (trx) regulation of Drosophila cardiac Hox gene activity and anterior-posterior patterning** Sumaiya Islam	105
3:15 PM	**Evaluating the Role of BIRC6 in Driving Chemotherapy Resistance in T-cell Acute Lymphoblastic Leukemia** Samson B. Miller	105
4:30 PM	**Section Meeting**	**White River A-E**

Schedule of Oral Presentations

Chemistry

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Investigation of Generalizable Engineering Strategies Through Rieske Dioxygenase Engineering** Froese, J. T.	104
2:00 PM	**Magnetic Resonance Imaging and Spectroscopy (MRI/MRS) in Post-Traumatic Stress Disorder (PTSD)** Meden F. Isaac-Lam	104
2:15 PM	**Interfacial Structure Matters: Adsorption of Organic Pollutants on Microplastics** Amrit Ojha	104
2:30 PM	**Structural and Catalytic Investigations into a Novel Tetrazolone-based Coordination Polymer** Kyle Petersen	104
2:45 PM	**Solid State Approaches for Synthesizing Biocompatible Composites for Osseointegration** Dr. Alexandra Tamerius	104
3:00 PM	**Exploring Synthetic Approaches of Metallation of Protoporphryn IX** Dylan S. Troglen	104
3:15 PM	**Development of fluorescent and colorimetric ionic nanosensors for forensic detection of controlled substances** Joel Moss	104
3:30 PM	**Paper-Based Microfluidic Devices for Multiplexed Colorimetric Detection of Disease Biomarkers** Doondeeshwar Patnala,	104
3:45 PM	**Liposome nanoparticles for the delivery of combinatorial therapeutic agents with doxorubicin and a near-infrared ionic dye against cancer** Mackenzie Gordon	104
4:00 PM		104
4:30 PM	**Section Meeting**	104

Schedule of Oral Presentations

Conservation, Sustainability, and Land Management

Sponsored By: Indianapolis Zoo

Time	Presentation Title & Presenter	Room
9:15 AM	**Road to Recovery: Using Headstarting and Egg Mass Translocations to Recover State Endangered Crawfish Frogs (Lithobates areolatus)** Nate Engbrecht	207
9:30 AM	**Shell yeah - getting active for freshwater mussels via AZA SAFE North American Freshwater Mussel** Monika Böhm	207
9:45 AM	**Project RESTORE: Research, education, and outreach to help private landowners steward their woodlands in the face of invasive species and deer.** Heather Reynolds	207
10:00 AM	**Investigating How Migration and Weather Affect Bird-Building Collisions and Bird Populations on The University of Indianapolis' Campus** Cassara Randall	207
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
4:30 PM	**Section Meeting**	**207**

Schedule of Oral Presentations

Earth Science

Time	Presentation Title & Presenter	Room
9:15 AM	**Indiana's Earthquakes: Updating the Record to Improve Hazard Assessment** Victoria Leffel	203
9:30 AM	**Updated Subsurface Temperature Gradients to Inform Emerging Energy Opportunities in Indiana** Rachel Culver	203
9:45 AM	**Upscaling Upper Ordovician Mapping Units in SE Indiana** Ben Dattilo	203
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Hinge and Muscle Morphology of Strophomena and Strophodonta from the Ordovician of Southeastern Indiana** Jacqueline Miller	203
2:00 PM	**Geological Legacy of New Harmony, Posey County, Indiana: Emphasis on Historic Studies of Caverns, Karst, and Sinkholes** William Elliott	203
2:15 PM	**Early Hoosier Footprints: The Warren County Trackway Site** Peggy Fisherkeller	203
2:30 PM	**Dinosaurs vs. Crustaceans: Preservation of Fossil Footprints from Joanna's Tracksite (Lower Cretaceous Glen Rose Formation, Texas)** James O. Farlow	203
2:45 PM	**Last glacial maximum and late-glacial eolian sand activity, south-central Indiana** Henry Loope	203
3:00 PM	**Assessing antler weathering rates across a latitudinal gradient** Rachel Laker	203
3:15 PM	**Variation in proboscidean isotope ecology across deglaciation** Catalina Tomé	203
4:30 PM	**Section Meeting**	**203**

Schedule of Oral Presentations

Ecology

Sponsored By: SALIX Ecological Consulting & Restoration, LLC

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
2:15 PM	**Variation in proboscidean isotope ecology across deglaciation** Catalina P. Tomé	202
2:30 PM	**Population Monitoring Methods of Blanding's Turtles (Emydoidea blandingii) Through Live Capture and Permanent Marking Techniques** Matt Harmon	202
2:45 PM	**Effect of Prescribed Burn Treatment of Creeping Juniper on Spiders in Little Missouri National Grasslands** Elijiah Birtchman	202
4:30 PM	**Section Meeting**	**202**

Schedule of Oral Presentations

Environmental Science

Time	Presentation Title & Presenter	Room
9:30 AM	**Determining X-Ray Fluorescence accuracy against Microwave Plasma Atomic Emission Spectroscopy for Lead Quantification** Ava Cothern	206
9:45 AM	**Comparison of Macroinvertebrate Populations and Their Connection to Water Quality in Two Indiana Watersheds: Big Walnut Creek (Putnam County) & Elkhart River (Elkhart County)** Kelsey Moore	206
10:00 AM	**Microbial Source Tracking of Water Pollutants Reveals Why Animals Aren't to Blame** Hunter J. Jaykoski	206
10:15 AM	**The who is who of Hoosier anglers – Segmenting the unique** Josef Hrabowski	206
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
3:00 PM	**Utilization of Rhizofiltration for Removal of Ibuprofen from Natural Waters** Ryley Kidd	206
3:15 PM	**Combined Effects of Heat Stress and Microplastics Exposure to Algal-Cnidarian Symbiosis in Aiptasia** Gillian Thompson	206
3:30 PM	**The Impacts of Different Colored Microplastics on Aiptasia** Elizabeth Weitzel	206
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Health Sciences

Sponsored By: Indiana University Indianapolis School of Health & Human Sciences

INDIANAPOLIS
SCHOOL OF HEALTH & HUMAN SCIENCES

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Vaccination Rate Changes Among Hoosier Youth: County-level Trends and Predictors Before and After the COVID-19 Pandemic** Isaac Masquelier	206
2:00 PM	**Refractory Cytomegalovirus Reactivation Following Haploidentical Peripheral Blood Stem Cell Transplantation for Diffuse Large B-Cell Lymphoma With Treatment Failure of Maribavir: A Case Report** Risha Mehta	206
2:15 PM	**Reducing Loneliness in Older Adults Through Virtual Reality Travel: Examining Emotional and Meaning-Based Mechanisms** Ruiping Ren	206
2:30 PM	**Fostering Peer Belonging Through Medical Student Wellness Conference** Melissa Ullmer	206
4:30 PM	**Section Meeting**	206

Schedule of Oral Presentations

History of Science

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
2:00 PM	**A History of Mathematics at Indiana University, 1890-1990** Samantha Duckworth	201
2:15 PM	**Evolutionary Cooperation and Transitions in Science** Zachary Hamby	201
2:30 PM	**Conservation and Change: A History of Science in North American Wildlife Management** Jesse Hannan	201
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Mathematics

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Hidden Geometry Beneath Simple Outcomes in Nonlinear Dynamical Systems** Dr. Kevin L. S. Drury	201
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Microbiology and Molecular Biology

Sponsored By: Indiana Biosciences Research Institute

INDIANA BIOSCIENCES RESEARCH INSTITUTE

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
3:45 PM	**Comparative analysis of gut microbiome in wildtype and cancer inducible alleles (RasG12V and RasQ61H) of Drosophila melanogaster** Shishir Sarker	105
4:00 PM	**Widespread Multi-Drug-Resistant Bacteria and Resistance Genes in Indiana's Reservoirs** Eshaan Patel	105
4:15 PM	**Extracellular Vesicles Secreted by Babesia-Infected Erythrocytes Modulate Host Neutrophil Response** Jose Thekkiniath	105
4:30 PM	**Section Meeting**	**105**

Schedule of Oral Presentations

Physics and Astronomy

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
3:00 PM	**Dopamine and its Precursor L-DOPA Interaction with Lipid Membrane** Osei Emmanuel	207
3:15 PM	**Confinement Potentials in Lipid Membranes** Abhinav Ramkumar	207
3:30 PM	**Interaction of Perfluoroalkyl Substances with Lipid Membranes** Sekou Koisiah	207
3:45 PM	**Time of First Return in Boolean Networks** Hope D. Gerst	207
4:00 PM	**Examining the Stability of the Van der Pol Oscillator using Gauge Functions** Nathaniel Viewegh	207
4:15 PM	**Search for Photon–Magnetic Field Coupling Effects in 241-Am Decay** Gunjan Akbari	207
4:30 PM	**Section Meeting**	

Schedule of Oral Presentations

Plant Systematics & Biodiversity

Sponsored By: Central Indiana Land Trust

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Gleanings from Deam's Flora of Indiana: The Good, The Bad, and The Priceless** Michael Homoya	204
2:00 PM	**Revision of Panicum L. (Poaceae) sensu stricta in Indiana** Nathanael J. Pilla	204
2:15 PM	**Graminoid Inventory of the Sandin Property in La Porte County, Indiana: Evaluating Taxonomic Subsets using the Floristic Quality Assessment** Derek Nimetz	204
2:30 PM	**Larimer Fen Mitchell's Satyr Butterfly Surveys and Other Findings: June 2025** Max Gerke	204
2:45 PM	**Non-native Brambles (Rubus spp.) that are Spreading within Indiana** Scott Namestnik	204
3:00 PM	**The Vascular Plants of Atherton Island Natural Area, Parke County, Indiana** Richard Hull	204
3:15 PM	**Analysis of the Floristic Quality of the Upland Woodland at White River Woods, Delaware County, Indiana** John Taylor	204
3:30 PM	**Estimating the Age and Phylogenetic Placement of Rare and Extinct Oceanic Island Endemics** Katie Greene	204
3:45 PM	**Distribution and Characteristics of the Newly Invasive Yellow-Flowered Teasel** Natalie Zagorski,	204
4:00 PM	**Floristic Inventory on Four Northern Indiana Sites** Nathanael J. Pilla	204
4:30 PM	**Section Meeting**	204

Schedule of Oral Presentations

Science Education

Sponsored By: Science Education Foundation of Indiana

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
3:00 PM	**Development of Lead Poisoning by Educational Classes** Khaled Masharqa	201
3:15 PM	**Geoscience Identity and Belonging in Science: Student and Graduate Perspectives on Undergraduate Geoscience Education** Carrie Wright	201
3:30 PM	**Disaster! - A Serious Game about Atmospheric Hazards** Dr. Nathan Hitchens	201
3:45 PM	**From Molecules to Medicine: Teaching the Drug Discovery Pipeline in a Research-Centered STEM Camp** Erika B. Sorensen	201
4:30 PM	**Section Meeting**	201

Schedule of Oral Presentations

Zoology and Entomology

Sponsored By: Indiana Herpotological Society

Time	Presentation Title & Presenter	Room
12:15 - 1:30 PM	**Academy Lunch**	**White River A-E**
1:45 PM	**Distribution and abundance of reptiles and amphibians at Chelsea Flatwoods Nature Preserve (Chelsea, Indiana)** Flick, Shane	205
2:00 PM	**A minute resurrection: Rejected synonymy and male description of Ceratinopsis tybeensis (Araneae: Linyphiidae)** Stahl, Taylor	205
2:15 PM	**Exploration of the antimicrobial potential of honey bee (Apis mellifera) propolis** Ammons, Andrew	205
2:30 PM	**Sensitivity of echinoderm immunological systems to temperature fluctuations: Changes in anticoagulant and antioxidant properties** Rahman, Noshin Atiya	205
2:45 PM	**A new species of sheet weaving spider, Pelecopsidis ozark (Araneae: Linyphiidae)** LaFlair, Holly	205
3:00 PM	**Why Indiana mayflies are being lost (Insecta: Ephemeroptera)** Jacobus, Luke M.	205
3:15 PM	**The use of nutraceuticals in growth enhancement and inflammatory gene modulation in largemouth bass and predictive modeling for long-term efficiency determination** Khaled, Shah Sumaiya	205
3:30 PM	**Indiana insect diversity: What do we know and where do we go from here** Johnston, M. Andrew	205
3:45 PM	**Effects of five nutraceuticals on growth performance and health status of hybrid catfish** Deng, Elena	205
4:30 PM	**Section Meeting**	205

Schedule of Oral Competition

Undergraduate Investigators

Inclusive of undergraduate students, undergraduate interns, individuals in post-bac academic programs that are preparing for application to professional or graduate school, and high school students involved in supervised research in industry or college/university laboratories at the time research was performed

Time	Presentation Title & Presenter	Room
2:30 PM	**Analysis of intra-annual radial growth patterns in southeastern Indiana forests** Chet Paulsen	White River A-E
2:45 PM	**Associations of metabolic and inflammatory mediators in human milk with infant growth and body composition in the first 6 months of life** Chandhini Suresh	White River A-E
3:00 PM	**Native Tree Canopy and the Effects on Soil Invertebrate Diversity, Microbes, and Ecological Function in Urban Sites** Milo Moss	White River A-E
3:15 PM	**Serial Sampling and Stable Isotope Analysis of Tusk Enamel belonging to Flat-Headed Peccary** Isaac Morris	White River A-E

Schedule of Oral Competition

Post-baccalaureate Investigators

Inclusive of industry and academic interns, graduate students, medical/health professional students, medical or postdoctoral fellows, and/or interns

Time	Presentation Title & Presenter	Room
2:30 PM	**The role of DFM1, HRD1, and STE24 in translocon quality control in Saccharomyces cerevisiae** James A Avaala	White River F-J
2:45 PM	**Morphological Variation of the Crista Galli Utilizing Postmortem Computer Tomography (PMCT)** Chastity Gilbert	White River F-J
3:00 PM	**Long NonCoding RNAs in Paclitaxel Chemoresistance** Kenneth Pin Cheng Pan	White River F-J
3:15 PM	**Phylogenomics Reveals Congruence, Conflict, and Reticulate Evolution in Spermacoceae (Rubiaceae)** Nusrat Huda	White River F-J

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
1	Optimization of GAN Architectures for Synthetic Image Generation **Dr. Debanjali Banerjee**
2	Comparative Analysis of a Two-Stage Deep Learning Framework for ACL Tear Detection in Knee MRI **Dr. Debanjali Banerjee**
3*	Development of a Live Scoring App for Track Cycling **Stephanie Lawrence**
4	Integrating HYSPLIT Trajectory Modeling and Stable Isotopes to Characterize Moisture Sources in the Northern Tropical Andes **Alejandra Rodriguez-Abaunza**
5*	Chasing the Sun: Comparing Geospatial Models with IUN Solar Data **Mykhaylo Severinov**
6*	Implementing Green Infrastructure in Terre Haute: Low-Impact Strategies for Urban Stormwater Management **Sierra Snowden**
7*	MAGNETIC FIELD GEOMETRY AND ITS INFLUENCE ON FERROFLUID DROPLET MOTION **Oluwatomilola Femi-Adejuwon**
8*	Integrating Computational Modeling and Experimental Analysis to Characterize Autophagosome Size and Number **Rakan Alnsour**
9*	Predicting Vacuole Autophagy in 3-Dimensions with Generative Neural Networks **Evan Snowgold**
10*	INTERACTION OF ACETAMINOPHEN WITH MODEL LIPID MEMBRANES **Rahber B. Syedae**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
11	Analysis of New and Archival Data on Eclipsing Binary Star TIC 262032874 **Sara Chaudhry**
12	Modeling and O-C Analysis of NSVS 5196635 and ASAS J081500-5743.4 **Wyatt Baxter**
13	An O-C Analysis of the W UMA Type Star ASAS J000425-5346.4 **Gavin Kling**
14	Numerical Modelling of a Third Light in NSVS 6103255 **Ashlee Martin**
15	Analysis of Short-Term Eclipsing Binary NSVS 1088506 **Caleb Whitcomb**
16	Megacrysts and Xenoliths from the Grants Intrusive Breccia: Insights into Mantle Metasomatism **William Myers**
17*	Phosphorus Diagenesis in Lake Tanganyika Core TANG16-5B-1G **Jaylen Price**
18	Phytolith-based reconstruction of vegetation variability over the Zambezi River basin using marine sediment core U1477, Expedition 361 **Madiha Hassan**
19*	Uneven sediment filling inside the Ordovician Rafinesquina from near Manchester, western Dearborn County, Indiana: post-mortem scavenging or soft part molding? **Bethany Cisz**
20	Heavy Metal Analysis of Markle Mill Dam Sediments, Terre Haute, Indiana **Hallie Townsend**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
21*	Mineralogical Controls on Lead Bioavailability and Geochemical Partitioning in Amended Garden Soils **Jeffrey Buell**
22	Comparison of historic stratigraphic nomenclature of part of the Indiana Upper Ordovician– an example from a composite section in Madison, Ind., and Milton, Ky **Mason Frauhiger**
23*	Spatiotemporal Dynamics of Freshwater Algal Assemblages **Fatma Badie**
24	Exploration of Microplastic Contamination in Water Sources of Terre Haute, IN **Clara Westcott**
25*	Investigating How Migration and Weather Affect Bird-Building Collisions and Bird Populations on The University of Indianapolis' Campus **Cassara Randall**
26	What should we do about cultivated mushroom invasions? **Jeffery Stallman**
27*	Interacting Impacts of Climate and Pasture Management on Grassland Birds and Plants **Jaime J. Coon**
28*	Using Citizen Science & Machine Learning to Track Individual Sea Turtles in the Florida Keys **Mary-Katheryn Dunderman**
29*	Dimensional Stability and Creep Performance of Glass Fiber Reinforced Thermoplastic Polyurethane as a Recyclable Alternative to Fiberglass Epoxy Composites for Wind Turbine Blade Applications **Olivia Snell**
30	**HEAVY METAL CONCENTRATIONS IN SEDIMENTS OF THE WHITE RIVER WATERSHED IN ANDERSON, INDIANA: A PRELIMINARY STUDY** **Paa Kwesi Mbroh**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
31*	Ibuprofen Behavior in Natural Waters **Hayden Netral**
32	Assessing Potential Coal-Ash Contamination in the White River Noblesville: Case Study **Dorothy Gidisu**
33	Tracking Sources of Fecal Pollution in the White River at Muncie: A Case Study **Mabel Kumi**
34	A Comprehensive Survey of the Unionid Mussel Community of the Upper West Fork White River in Delaware County, Indiana (Map Display) **Sam Gradle**
35*	Determination of the Roles of Keratin 18 and 19 in Early Xenopus laevis Development **Elisabeth Pennington**
36	Activity timing in an open-cup nesting bird: individual repeatability and environmental effects **Andrea S. Grunst**
37*	Tree and Bird diversity in three urban greenspaces in South Bend, Indiana **Kitty Koontz**
38*	Plant-insect-fungal interactions in White False Indigo (Baptisia alba) on Indiana tallgrass prairies **Lilith Rengstorf**
39*	Using Chromosome Numbers to Understand Evolution of Genomic Size of the Spermacoceae Tribe (Rubiaceae) **Peyton Rodgers**
40*	First Draft Genome of North American Bluets Using ONT Sequencing **Ainsley Tierney**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
41*	Investigating methods of chemical control for novel invasive yellow-flowered teasel **Molly Hobson**
42	Integrating GIS Technology for Enhanced Urban Forestry Education: A Redesign of the Butler University Tree Walk **Alexa Simpson**
43	Exploration of Temperature on the Growth Stages of Tomatoes, Solanum lycopersicum **Savanna Amschl**
44	Dendroarchaeological and Timber Analysis of Four Log Structures of Brown County State Park **Erin Terry**
45*	Fifty-Year Study of Post-Tornado Forest Succession in Happy Valley, Jefferson County, IN **Victoria Zwilling**
46	Fireflies of Indiana (Coleoptera: Lampyridae) **Amelia R. Meyer**
47*	Bridging Fragmented Habitat: Modeled Connectivity Zones Predict Zebra Swallowtail Occurrence **Caden Zuehsow**
48*	Insect Fragment Analysis of Big Brown Bat (Eptesicus fuscus) Guano During Brood X 2021 Emergence **Surraya Wagner**
49*	Comparing Family-level Insect Diversity Between Habitats at the DePauw Nature Park **Sahit Liyanage**
50*	A comparison of field and experimental observations of arboreal behavior in multiple species of fossorial salamanders **Marieke Young**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
51	An Archaeological Survey of Salamonie River State Forest, Wabash County, Indiana **Nolan Sterns**
52	An Accessory Head of the Biceps Brachii: Clinical Implications from a Gross Anatomy Case Study **Layken McGuire**
53*	A Human Case Study of a Rare Morphological Variation of the Liver **Natalie Reynolds**
54	An Anatomical Dissection Case Study of a Rare Left Pleuro-Pericardial Cyst in a 90+ Year Old Donor **Peytin Penny**
55*	A Case Study of a Rare Accessory Muscle in the Human Leg **Amanda Walker**
56	Assessing patient knowledge and perceptions of physicians, physician assistants, and nurse practitioners in a primary care clinic in Indiana **Yasmin A. Ali**
57*	HIPAA Noncompliance of Radiologic Images Shared on Social Media **Shreyas Bulusu**
58*	Food Is Medicine: Medically and Culturally Tailored Food Preferences **Alyssa Reinoso**
59	A Recruitment Process for the Perinatal Lifestyle Drivers Study that Leverages the Indiana Community Learning Health System **Armando Peña**
60*	Characterizing the Literature of Associations Between Appetite-Related Hormones, Appetite, and Adiposity in Infancy: An Ongoing Scoping Review **Annelise Stolarz**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
61	Characterizing Total, Regional, and Ectopic Adipose Tissue Fat Content and Diabetes Risk Factors among Youth Using Lancet Commission Obesity Definitions **Macy Lei Shepard**
62*	Examining Inflammatory Markers as Mediators of Obesity-Induced Reductions in Insulin Sensitivity among Latino Youth **Zoe Barnsfather**
63*	Evaluating Pragmatic Estimates of Insulin Sensitivity Against the Hyperinsulinemic Euglycemic Clamp in Early and Late Pregnancy **Shiv Patel**
64*	Co-designing a Community-Based, Multi-Systems Lifestyle Intervention for Preventing Gestational Diabetes **Saida Nassour**
65*	Weight Stigma as an Overlooked Driver of Inflammation and Cardiovascular Disease Risk **Kaitlyn Mathews**
66	Assessment of Sex Differences in Urethane-Induced Lung Tumorigenesis in the Four Core Genotype Mouse Model **Maksat Babayev**
67*	Bioinformatics Analysis of Gene Expression in Lynch Syndrome Progression **Drithi Raipet**
68*	Investigating the Expression of Cyclin E1 (CCNE1) in Mantle Cell Lymphoma **Faith Sponseller**
69*	In Vivo Modulation: The Real Time Monitoring of Vascular Implants by Utilizing Optic Fiber-Based Cardiovascular Stents **Palak Jha**
70*	RADical Imaging: Stratifying Lung-RADS 0 with Inflammatory Markers **Vedika Vyas**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
71	A Rapid, Reproducible AI-Assisted Tool for Generating Course-Aligned Anki Decks in an Accelerated Biomedical Sciences Master's Program **Martin Matov**
72	From Indianapolis to Nairobi: How the NeoInnovate Collaborative Consortium at Indiana University Indianapolis Creates Award-Winning Global Research Opportunities for Students **Sherri Bucher**
73	A STEM Collaboration with Two African American Sistas in the Academy: "More than Me: Exploring the Environments Around Us" **Dr. Rona M. Robinson-Hill**
74*	Empowering The Community With Environmental Chemistry In The Classroom **Eshaan Patel**
75	Needs Assessment of 3D-Printed Anatomical Models for Indianapolis Secondary School Life and Health Sciences Education **Dakota R. Merkel**
76*	From Brain to Build Plate: 3D Printing the Cerebral White Matter for Neuroanatomy Education **Salma Kherallah**
77	From Implementation to Impact: Multi-Year Outcomes of Anatomage Table Integration in Anatomy Education **Elizabeth McEntee**
78	Charles Bonsett, M.D., 1921-2020, medical historian extraordinaire. **Dr. Richard Feldman**
79	Do Spiders Share More Genes With Humans or Flies? Orthologs Reveal the Answer **Katherine Bowman**
80	America steps to the world stage with Philadelphia's 1876 International Medical Congress Rubbing elbows with the world's greatest surgeon and some notable Hoosiers **Olivia DeHaven**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
81	
82	IAS leaders frequently showed an interest in History of Science over the Academy's140 year history and many of them made presentations at the annual meeting. **Dr. Rex Bickers**
83	Light Scattering Technique for the Study of Molecular Adsorption onto Heterogeneous Colloidal Microplastics **Clayton Snider**
84*	Paper-Based Microfluidic Devices from Hydrophobic Ionic Liquid for Colorimetric Detection of Disease Biomarkers **Auden DeCaprio**
85*	Enantiomeric recognition of flavor compounds using amino acid-based chiral ionic liquids **Lily Haley**
86	Synthesis and Evaluation of Biological Activity of Novel Highly Substituted Pyrroles and Pyrrolidones **Kaitlyn Rochester**
87	Synthesis and Evaluation of Penta-substituted Pyrrolidones with Ester Group in the Third Position **Jakob Morton**
88*	A fluorescent ionic liquid nanosensor for forensic detection of gamma-hydroxybutyrate drug **Will Mawhorr**
89*	An ionic liquid nanosensor for dual colorimetric and fluorescent detection of gamma-hydroxybutyrate drug **Donita Wright**
90	Reaction of Spirooxindoles in the Presence of Trifluoroacetic Acid as a Catalyst **Sam Stucko**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
91	Natural Product-Based Dye Sensitized Solar Cells in Series **Arianna Cooley**
92	In Vitro Photodynamic Assessment of Photosensitizer-Antibiotic Conjugates Against Lung Cancer Cell Line **Kailey M. Callander**
93*	Using UV and Diffuse reflectance spectroscopy to analyze photodegradation of silver doped nickel tungsten as nanostructures **Jordan Smith**
94	Investigation of Substrate Tunnel Remodeling as a Generalizable Strategy through Biphenyl Dioxygenase Engineering" **Madilyn Shepherd**
95*	Liposome nanoparticles for the delivery of combinatorial therapeutic agents with doxorubicin and IR820 near-infrared ionic dye against cancer **Eric Fettinger**
96*	Metabolomic and Functional Differences Between EDL and SOL Muscles in SUCLA2-Deficient Mice **Clark Chustz**
97	Computational Modeling and Analysis of Improved Rieske Dioxygenase Variants **Corbin Prince**
98*	Investigating exercise to mitigate muscle dysfunction in SUCLA2 KO models within EDL vs SOL **Luna Holley**
99*	Tyrosine Nitration of Apolactoferrin by Peroxynitrite Alters Metal Affinity **Jetta Harmon**
100	"Application of Rational Enzyme Engineering in the Development of Improved Naphthalene Dioxygenase Variants" **Reece Dale**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
101*	Absence of Brain Glycogen Decreases Incidence of Loss of Righting Reflex during Insulin-induced Hypoglycemia **Alyssa McDonald**
102*	Muscle Glycogen Concentration Predicts Strength and Endurance in Transgenic Mouse Models **Raina L. Wolf**
103	Development of Improved Cumene Dioxygenase Variants through Substrate Tunnel Remodeling **Madison Kasten**
104*	Physiologic responses of Hypoxia **Avery Renshaw**
105	Analysis of Phytocannabinoid Effects on Macrophages **Radmila S. Stanic**
106*	Brain glycogen does not reduce severity of pilocarpine-induced seizure in mice **Mathilda A. Geyer**
107	Evaluating Antioxidant Status of a Ginger- and Curcumin-Supplemented Pesco-Vegetarian Diet Intervention **Annastasia Hutchings**
108*	Requirement of Microtubule Stability in Degradation of Aberrant Proteins **Kaikeyi M. Paxton**
109*	DHX36/G4R1 Knockdown Rescues Stress Granule Density in C9orf72 ALS Neural Progenitor Cells **Chance S. Creviston**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
110*	Polycomb (Pc) and Polycomb group genes (PcG) regulate cardiac patterning by repressing trithorax (trx)-mediated Hox expression in the embryonic heart tube. **Md. Sayeed Abu Rayhan**
111*	Reconstructing the Fox transcription factor-regulated modular subnetworks mediating distinct cardiac progenitor cell divisions **M. Rezaul Hasan**
112	Investigating the Role of TRAF2 in Chemotherapy Resistance in T-Cell Acute Lymphoblastic Leukemia **Isabella Torres**
113*	Establishing a Genetic Tool to Induce Multinucleated Polyploidy in Drosophila Tissues **Krista Cottom**
114*	Elucidating the Effect of Diet on Intestinal Stem Cell Division in the Drosophila midgut **Devyani Purohit**
115*	Drosophila Spalt genes in heart development and their relevance to human congenital heart defects **Mofazzal K. Sabbir**
116*	Roles for jumeau and Checkpoint suppressor 1-like in alary muscle morphogenesis: expanding the cardiogenic functions of Fox genes **Kuncha Shashidhar**
117*	Unraveling the mechanism of Fox transcription factor-driven Polo kinase activation during cardiac progenitor cell division **Rajnandani Katariya**
118	p53 inhibits 2-chloroethyl ethylsulfide (2-CEES)-induced centrosome amplification in human osteosarcoma cells (Saos2) **Richard A. Bennett**
119*	Assessing the impact of Nicotine during coronary artery vessel development in mice **Kenneth Reed**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

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Poster Number	Poster Title & Presenter
120*	Differential Signaling and Functional Outcomes of APELIN and ELABELA in Venous and Arterial Endothelial Cells **Rupak Parajuli**
121*	Oxidative Stress Reveals Distinct Roles of FSHR-1 and its Ligands in C. elegans **Joshua R. Gerber**
122*	Intestinal regulation of neuromuscular function by the glycoprotein hormone receptor, FSHR-1 **Lillian Groves**
123	Targeted Silencing of DHX36/G4R1 in C9orf72 ALS/FTD and Impacts on Stress Granule Abundance. **Nana Akua O. Koranteng**
124*	Oncogenic Ras Induces Biomechanical Stress-Mediated EMT in the Drosophila Wing Disc **Kaleigh Kelley**
125*	Elucidating the Molecular and Cellular Mechanisms of Ras-Induced Cyst Formation in the Drosophila Wing Disc **Jaxon Howell**
126*	Pathways of Protein Degradation and Stress Tolerance During Translocon Clogging **Hailey J Barton**
127*	Beyond the Proteasome: Hidden Sources of Peptide Degradation **Cole J. Shifferly**
128*	Who's Cleaving What? Defining the Enzymes Behind CT-L Activity in C. elegans **Hugh T. Ford**
129*	Determining whether hypoxia stimulates DHX36 and SOX17 expression in coronary endothelial cells **Kendra Eller**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
130	The pseudo-kinase EphB6 receptor can act as a "loser" gene in human cancer cell competition **Masaru Nakamoto**
131*	Investigating the Molecular Mechanisms of Ras Tumor Cell Regression in the Drosophila midgut **Dreama Cronin**
132*	Establishing a Genetic Tool to Induce Multinucleated Polyploidy in Drosophila Tissues **Haley Lorey**
133*	Cellular Characterization of Mesenchymal-like Cells Derived from Ras-induced Biomechanical Stress-mediated EMT in the Drosophila Wing Disc **Phillip Bilby**
134*	Regulation of SYD-2/Liprin Alpha in GABA motor neurons **Sarah Daly**
135*	The Role of Dfm1 in the Hrd1 Translocon Quality Control Pathway **Sudhee Bommineni**
136	Elucidating the Molecular Mechanisms Underlying Tumor Cell Expansion in Drosophila Myoblasts **Woasifur Rahman Chowdhury**
137*	Retinal Vasculature Changes in a Model of Papilledema **Maggie Evans**
138*	Putting the Puzzle Together: Hyperadhesive Desmosome Protein Complexes in Early Vertebrate Embryonic Ectoderm **Rochelle M. Maxson**
139*	Effect of Lipid Chain Length on Structural Dynamics of ABC Transporter Sav1866 **Divya Rajendran**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
140*	Targeting CPSF73 to Inhibit Adenovirus Replication **Cal Swartzendruber**
141*	Effect of simulated microgravity on Candida albicans resistance to caspofungin and fluconazole **Kendall Carter**
142*	Effect of estrogen on Candida albicans filament growth in the presence and absence of an epithelial layer **Matthew Gaetano**
143	Translocation of Pus7 within C. albicans **Taylor Smith**
144*	Identification of Candida albicans Mutants that can Filament in the Presence of Hygromycin B **Vivana Bhagat**
145*	Comparative Analysis of Gene LDH, and MDH in the Puerto Rican Parrot, and Chicken **Mariana Berdugo**
146*	Developing DNA Barcodes for Species Identification of North American Azaleas **Alexis Cantrell**
147*	The effects of abnormal temperature patterns on Batrachochytrium dendrobatidis density and size in vitro **Megan Lawson**
148	Agricultural Microbes as a Source of Antimicrobials **Mana Shahrokhi**
149*	Widespread Multi-drug-Resistant Bacteria and Resistance Genes in Indiana's Reservoirs **Ashley Durnil**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
150*	Evaluation of Antibiotic Resistance and Species Identification of Gram-Negative Bacteria from the Geist Reservoir **Kiley Wardwell**
151	Characterizing PUG1 mutants in the opportunistic fungal pathogen Candida auris **Summer Davis**
152*	Efficacy of MCP-1 in C. neoformans killing by CITED1 Knockout Macrophages **Garrett Roberts**
153*	CITED1 Effect on Macrophage Apoptosis when Exposed to Cryptococcus neoformans **Claire Kinder**
154	A Potential Role for DHX36/G4R1, a G4 helicase, in Genomic Maintenance in C9orf72 ALS/FTD **Kelsey Slattery**
155*	Using LUHMES cells to measure MST-312's impact on Herpes Simplex Virus Latency **Kayli Liles**
156*	The Effect of Fetal Alcohol Spectrum Disorders on Development of the Hippocampus in Relation to ADHD-Like Behaviors **Ash Bishop**
157	Dose-Dependent Inhibition of hRSV and Clinically Relevant Pathogens by Mānuka Honey Without Cytotoxic Effects **Grant Ipsen**
158*	Analysis of Previously Reported SARS-CoV-2 3CLpro Inhibitors for Broad Neutralizing Activity Against the 3CLpro of Human Common Cold Coronavirus Strain HKU1 **Sahar Atmar**
159*	SARS-CoV-2 3CLpro Inhibitors Exhibit Neutralizing Activity Against the 3CLpro of Human Common Cold Coronavirus Strain OC43 **Aarish Sakib**

***Emerging Scientist Research Poster Competition**

Poster Presentations by Number

Odd-numbered posters will present from 10:00-10:45; Even-numbered posters will present from 11:00-11:45

Poster Number	Poster Title & Presenter
160	The Role of RIPI in T-Cell Acute Lymphoblastic Leukemia Chemoresistance **Katelyn Ellison**
161*	Defining supporting structures: the Back seat driver kinase orchestrates the development of heart-anchoring alary muscles. **Brady Matthew Verdon**
162	Physics begets biophysics, from the early 1900s to the 1950s. Its role in the birth of twentieth century molecular biology, with a focus on Nobel laureates and legendary Hoosiers who made crucially important contributions **Dr. Paul Todd**
163	
164	An Indiana History of Solar Eclipses: Connecting Science to Community **Sarah J. Reynolds**
165	
166	
167	

***Emerging Scientist Research Poster Competition**

Poster Abstracts

Poster Number	Poster Title, Author(s), & Abstracts
1	**Optimization of GAN Architectures for Synthetic Image Generation** **Dr. Debanjali Banerjee, Sora Owada, Samadhi Chandrasena, Musa Tora, Parsa Mallik, Jackson Swopes** Generative Adversarial Networks (GANs) have demonstrated substantial potential in synthetic image generation and downstream classification tasks, particularly within computer vision domains. This research study presents a comparative performance evaluation of three GAN architectures - Deep Convolutional Generative Adversarial Network (DCGAN), Conditional Generative Adversarial Network (cGAN) and Auxiliary Classifier Generative Adversarial Network (ACGAN) on the "Cats and Dogs" dataset a subset derived from ImageNet Dataset. The primary objective of this research was to evaluate model performance using the Fréchet Inception Distance (FID) score. Fréchet Inception Distance is a widely used metric to evaluate the quality and diversity of images generated by AI models, such as GANs or diffusion models. It measures the statistical similarity between features of real and generated images, with a lower score indicating better quality and higher similarity to real-world data. All three models were trained under comparable conditions, and systematic adjustments were made to learning rate, batch size, and network depth to improve performance. Initial baseline experiments resulted in FID scores above 150 across all architectures. After targeted parameter tuning and architectural refinements, model performance improved significantly, with some configurations achieving FID scores closer to 100. Based on the results, cGAN achieved the best overall performance, producing the lowest FID score among the three models. This suggests that incorporating class labels during training improved the realism and class consistency of generated images. DCGAN performed moderately well but had a slightly higher FID score, likely due to the absence of label conditioning. ACGAN produced the highest FID score, indicating that the additional classification objective may have increased training complexity in our experimental setup. These findings provide insights into effective strategies for optimizing GAN performance in image classification contexts.
2	**Comparative Analysis of a Two-Stage Deep Learning Framework for ACL Tear Detection in Knee MRI** **Dr. Debanjali Banerjee, Sora Owada, Bách Phạm** Accurate detection of Anterior Cruciate Ligament (ACL) tears in knee MRI scans is a challenging task requiring the identification of subtle fiber discontinuities rather than simple intensity changes. Standard Convolutional Neural Networks (CNNs) often struggle to distinguish between healthy fibrous tissue and torn structures using raw pixel data alone. This study presents a comparative deep learning framework integrating region localization and tear classification to improve diagnostic performance. The dataset consisted of 200 patients and was nearly balanced, including 98 confirmed ACL tears and 102 normal cases. In the first stage, an object detection model was trained to localize ACL relevant regions of interest (ROI) from full MRI slices. By isolating anatomically meaningful regions, the system standardizes inputs for downstream analysis and reduces background noise that may interfere with classification. In the second stage, two classification models were explored. A baseline ResNet50 model was trained on ROI-cropped slices with patient-level aggregation. To further improve structural sensitivity, a novel 2.5D architecture was developed that incorporates multi-channel inputs highlighting anatomical continuity, fiber structure, and tissue variability. A custom slice attention mechanism was introduced to dynamically emphasize diagnostically relevant slices across the MRI volume. Comparative evaluation demonstrated that incorporating structured inputs and slice-level attention improved sensitivity to ACL tears, though specificity remains an area for further refinement. During training and validation, the proposed 2.5D architecture achieved strong performance, demonstrating high sensitivity and balanced accuracy on the augmented validation set. However, evaluation on an independent test cohort revealed more modest patient-level accuracy, comparable to the baseline model. This work highlights the challenges of generalization in small

	medical imaging datasets and the importance of combining localization, domain-informed feature engineering, and architectural design to build clinically meaningful AI systems for medical image analysis.
3*	Development of a Live Scoring App for Track Cycling **Stephanie Lawrence** This work investigates how rule-driven algorithms and structured race-state models can enable accurate, real-time scoring of track cycling events without specialized hardware. Accurate scoring and tracking of points in track cycling is critical and complicated due to dynamically changing point values, multiple concurrent scoring events, and strict race-specific rule constraints in points and madison races. Despite this many existing scoring systems rely on expensive and specialized hardware that is not available to most venues. Most organizations rely on officials using handwritten notes for scoring these events, even when there are national championship titles and cash purses being decided. To solve this, we are developing web-based live scoring application that allows officials to input race specifications, then quickly and accurately score the event using this application. The system will follow regulations set forth by the Union Cycliste Internationale (UCI), which governs cycling at the international level. The application will be able to handle multiple race formats, including stand-alone points races, omnium points races, and madison races, each of which has unique scoring constraints and initialization requirements. A rule-driven scoring algorithm and structured race-state model were designed to encode UCI regulations while maintaining computational accuracy and traceability. System accuracy will be evaluated by comparing application-generated results with official hand-scored race outcomes, while performance will be measured through updated latency and error rates. The goal of the application is to improve scoring efficiency, reduce manual calculation errors, and enhance clarity for officials and racers. The project contributes to the broader field of sports technology and applied software by demonstrating how structured rule modeling and real-time data processing can improve competitive accuracy and operational transparency. Compared to existing transponder-based systems, the proposed solution emphasizes accessibility, reduced cost, and adaptability across race formats without specialized hardware.
4	Integrating HYSPLIT Trajectory Modeling and Stable Isotopes to Characterize Moisture Sources in the Northern Tropical Andes **Alejandra Rodriguez-Abaunza, Broxton Bird, Jaime Escobar, Byron A. Steinman, Bronwen Konecky, Felipe Velasco, Daniel Plazas Jimenez** The 'Andes-Amazon-Atlantic' pathway is the main hydroclimatic system in northern South America, linking the regional water cycle and transporting moisture between the Amazon and the Andes. In Colombia, multiple moisture sources combined with the complex topography of the northern Andes modulate the annual rainfall cycle, complicating the interpretation of water isotope signals in paleoclimate archives from the northern Andes. The Tota Basin (5.54°N, 72.92°W), located in the Eastern Colombian Andes, lies at the transition between the bimodal Andean and unimodal Orinoco rainfall regimes and exhibits pronounced spatial and seasonal heterogeneity in precipitation. To establish a modern interpretative framework for paleo-isotopic records, we combine daily precipitation isotope measurements ($\delta^{18}O$, $\delta^{2}H$) collected between March 2023 and June 2025 with backward air-parcel trajectory modeling using the Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT) model. HYSPLIT, an open-access atmospheric transport model developed by NOAA's Air Resources Laboratory, computes three-dimensional air-parcel trajectories using gridded meteorological fields and enables quantitative source–receptor attribution from regional to continental scales. For each precipitation event, seven days backward trajectories were calculated to identify dominant moisture pathways and quantify relative source contributions. Rainfall isotopes showed marked seasonal variability, with depleted values during the rainy seasons and enriched values during the dry season. Back-trajectory analysis indicates that 45% of precipitation originates from the Tropical North Atlantic, 36% from regional recycling, and 18% from the northern Amazon Basin. Seasonal shifts in d-excess correspond to changes in transport pathways and secondary evaporation processes, highlighting the combined influence of large-scale circulation and local moisture recycling. This approach establishes a modern calibration dataset that improves interpretation of hydrogen and oxygen isotope signals preserved in plant waxes and other sedimentary archives, advancing paleoclimate reconstructions in the Northern Tropical Andes.

5*

Chasing the Sun: Comparing Geospatial Models with IUN Solar Data

Mykhaylo Severinov, Dr. Jessica Warren

To understand the potential for energy resilience at IUN, we have expanded on previous work done collecting on-the-ground measurements. Combining state LiDAR data with geospatial methods for analysis we were able to generate a model predicting the total solar energy impact for the total surface of IUN's campus with a 3ft-by-3ft resolution. Current work focuses on comparing the accuracy of the prediction generated with 3000 hand collected measurements taken over the course of the past nine months. The goal of this is to create a fine grained, hyper localized model of solar energy impact on campus. This would significantly increase the accuracy of predictions for optimal placement of solar panels on campus.

6*

Implementing Green Infrastructure in Terre Haute: Low-Impact Strategies for Urban Stormwater Management

Sierra Snowden, Dr. Namita Shrestha

Stormwater management is the ability to direct and control rainwater to prevent damage to local infrastructure and the natural environment. There are two main infrastructure types: green and grey. Green infrastructure is implementing the natural environment into human designs. Grey infrastructure relies heavily on materials like concrete and steel and is not concerned with integrating into the natural world. Green infrastructure has many benefits including improving stormwater runoff water quality.

In this study we are exploring ways to implement green infrastructure into urban areas (Terre Haute, Indiana) with minimal construction and disturbances to existing infrastructure. We started by conducting interviews with City of Terre Haute engineers and staff at Rose-Hulman Institute of Technology. We sampled and tested stormwater comparing results between green and grey infrastructure. Preliminary results prove that green infrastructure has better water quality than grey infrastructure. Next, we toured public parks in Terre Haute, Indiana. Parks are green infrastructure that already exists in most urban areas and have significant potential for enhancement to a city's stormwater management. Based on our preliminary results we found stormwater-based improvements that can be easily implemented into urban settings without requiring major construction or disrupting existing infrastructure.

The stormwater samples will be analyzed for several constituents, including any potential pollutants associated with the facility, pH (field measurement), oil and grease, carbonaceous biochemical oxygen demand (CBOD), chemical oxygen demand (COD), total suspended solids (TSS), total Kjeldahl nitrogen (TKN), total phosphorus, and nitrate plus nitrite nitrogen. Additionally, stormwater and surface water quality will be evaluated before and after storm events to better assess the impacts of green and grey infrastructure.

7*

MAGNETIC FIELD GEOMETRY AND ITS INFLUENCE ON FERROFLUID DROPLET MOTION

Oluwatomilola Femi-Adejuwon

Magnetic control of liquid droplets offers a way to move and mix fluids without pumps or tubes, which is useful for micro-scale chemical and biological systems. This study examined how different magnet arrangements affect the motion of ferrofluid droplets on a smooth acrylic surface. Six field geometries Under, Beside, Opposite, Diagonal, Triangular, and Offset were compared through an experiment conducted that tested each configuration's influence on droplet speed, direction, and merging rate. The Under and Diagonal setups produced the fastest average droplet speeds (1.78 mm s^{-1} and 1.61 mm s^{-1}) and the highest merging rates, while the Beside and Offset geometries caused slower movement and incomplete coalescence. Statistical analysis (one-way ANOVA, $p < 0.05$) confirmed that field shape had a significant effect. The results matched trends reported in published ferrofluid experiments: stronger vertical magnetic gradients lead to faster and more directed motion. These findings point toward

	inexpensive, passive ways to route or merge droplets using only permanent magnets. The approach also provides a model for
8*	Integrating Computational Modeling and Experimental Analysis to Characterize Autophagosome Size and Number **Rakan Alnsour, Katherine Sowell, Dr. Steven K Backues** Autophagy is a key cellular recycling process that helps cells maintain homeostasis and survive stress by breaking down damaged organelles and misfolded proteins. When autophagy is disrupted, it contributes to diseases such as cancer, Parkinson's disease, and Alzheimer's disease, so getting accurate measurements of autophagosome size and number is important for understanding how this pathway works. In this project, I am working on improving a computational model in CompuCell3D that simulates how autophagic bodies clump inside the yeast vacuole, which we later compare to real Transmission Electron Microscopy images. I generate PIFF files with defined body numbers and sizes, simulate how they squash together, and analyze the output using Python code that measures data such as aspect ratio, circularity, coziness, and compactness. To improve the speed and accuracy of the simulations, I have been testing different Neighbor Order values and implementing a new "Global Forces" approach that uses distance-dependent force vectors to pull bodies together faster. While this has improved convergence, some parameter settings caused unwanted "squaring" of the bodies, testing different variables ranges currently to maintain realistic shapes is a work in progress. Alongside the modeling, I have collected and analyzed about 600 Transmission Electron Microscopy images of yeast vacuoles, using an AI-based segmentation tool to gather actual size and number distributions of autophagic bodies. These combined computational and experimental results are helping us refine the simulation so it better matches the real biological data, which will ultimately make it easier to estimate autophagosome size and number more accurately.
9*	Predicting Vacuole Autophagy in 3-Dimensions with Generative Neural Networks **Evan Snowgold, Dr. Ourania Spantidi** Autophagy is the process by which a cell breaks down and recycles old or damaged components, playing a critical role in cellular health and disease. CompuCell3D can simulate autophagy, however it lacks the speed needed to be used effectively in an automated pipeline. The purpose of this research is to investigate different artificial intelligence models on the prediction accuracy of autophagic body movement, effectively replacing the computationally expensive CompuCell3D software. This accelerates future disease research, supports drug discovery, and creates a reusable platform for future 3-dimensional biological modeling and simulation.
10*	INTERACTION OF ACETAMINOPHEN WITH MODEL LIPID MEMBRANES **Rahber B. Syeda, Gabrielle Tomich, Mallory Saldana, Emmanuel O. Osei, Horia I. Petrache** Understanding acetaminophen lipid membrane interactions is essential for elucidating drug efficacy and potential side effects. However, its influence on membrane structure and dynamics, particularly in the presence of cholesterol, remains unclear. In this study, we investigated the interactions of acetaminophen with lipid bilayers both in the absence and presence of cholesterol using nuclear magnetic resonance (NMR) spectroscopy and molecular dynamics (MD) simulations. Our results indicate that acetaminophen preferentially localizes within the polar headgroup region of the membrane, leading to a reduction in lipid rigidity. However, the presence of cholesterol had only a minor effect on the positioning of acetaminophen within the bilayer. These findings reconcile previous experimental observations and provide new molecular-level insight into acetaminophen-lipid membrane interactions.

Poster Number	Poster Title, Author(s), & Abstracts
11	Analysis of New and Archival Data on Eclipsing Binary Star TIC 262032874 **Sara Chaudhry, Jadin Payton, Dr. Todd Vaccaro** TIC 262032874 is an eclipsing binary star that has been observed by TESS (Transiting Exoplanet Survey Satellite) and by Ball State University faculty using the remote, ground-based SARA (Southeastern Association for Research in Astronomy) observatories. Light curves produced from these observations have been analyzed to reveal a steady orbital period of 0.613432+- 0.000086 days. The light curve shape is consistent with a W UMa class of binary system. Light curve models fit to the data indicate that the binary is two F spectral type stars of the same mass and size in a contact configuration at high orbital inclination.
12	Modeling and O-C Analysis of NSVS 5196635 and ASAS J081500-5743.4 **Wyatt Baxter, Robert Berrington** We present a study of the eclipsing variable stars, NSVS 5196635 and ASAS J081500-5743.4. The AstroImageJ software suite was used for all differential ensemble photometric measurements taken in the Johnson-Cousins B, V, and R for SARA-CT and in the TESS band for the Transiting Exoplanet Survey Satellite (TESS) data. The research is a work in progress and all results at the current moment are preliminary. We present an observed minus calculated (O-C) study of NSVS 5196635 found within seven TESS sectors producing a total of 503 times of minimum light. For the system ASAS J081500-5743.4, we have a total of 20 SARA-CT nights from which we have determined a total of 18 times of minimum light. PHysics Of Eclipsing BinariEs (PHOEBE) was utilized to fit SARA-CT and TESS data for each passband. We present preliminary models of NSVS 5196635 TESS data and ASAS J081500-5743.4 SARA-CT data.
13	An O-C Analysis of the W UMA Type Star ASAS J000425-5346.4 **Gavin Kling, Robert Berrington** We present a preliminary study of the eclipsing variable star ASAS J000425-5346.4. All photometric measurements were made using the AstroImageJ (AIJ) software suite and are differential ensemble photometric measurements taken in the Johnson-Cousins B, V, and R bands. Times of minimum light are measured using the SARA-CT observatory data and the Transiting Exoplanet Survey Satellite (TESS) data. With TESS data, eight sectors were analyzed for a total of 1,051 times of minimum. We present a folded light curve and perform a preliminary observed minus calculated (O-C) study of ASAS J000425-5346.4.
14	Numerical Modelling of a Third Light in NSVS 6103255 **Ashlee Martin, Robert Berrington** We present new modeling of the eclipsing variable star NSVS 6103255. Models are compared with photometric measurements made using the AstroImageJ (AIJ) software suite. All differential ensemble photometric measurements were taken in the Johnson-Cousins B, V, and R bands for the Ball State University Observatory (BSUO) data, and in the TESS band for the Transiting Exoplanet Survey Satellite (TESS) data. Times of minimum light,

	measured using the BSUO and TESS data, are presented. The orbital period and stellar ephemeris are determined. PHysics Of Eclipsing BinariEs (PHOEBE) was used to fit the BSUO data and TESS data for each passband. Due to the lower resolution of TESS data compared to the BSUO data, we know there is a third light in the TESS light curves. We investigate modeling this third light in comparison between the BSUO and TESS data. We present a folded light curve, perform an observed-minus-calculated (O-C) study, present orbital parameters, and multiple fits in various bands, along with a spot model of NSVS 6103255.
15	Analysis of Short-Term Eclipsing Binary NSVS 1088506 **Caleb Whitcomb, Dr. Robert Berrington** We present a photometric study of the eclipsing binary system NSVS 1088506. Observations were made via a 20-inch telescope at the Ball State University Observatory from June to July 2019. Observations were made using three passband filters, Johnson B, Johnson V, and Cousins R. Multi-aperture photometry was performed via the AstroImageJ (AIJ) image software and observed light curves were used to determine initial parameters including the orbital period, Times of Minimum light and Effective Temperature of the system. The Physics of Eclipsing Binaries software (PHOEBE2) was used to refine the system parameters as well as narrow down other parameters such as the mass ratio. Light curve data from the Transiting Exoplanet Survey Satellite (TESS) was also used to help constrain the period of the system. We analyzed the observed light curves and created an Observed minus Calculated (O-C) times of minimum light to constrain the period of the system. Lastly, we determine any evidence of the O'Connell effect and analyze its influence on the model of the system.
16	Megacrysts and Xenoliths from the Grants Intrusive Breccia: Insights into Mantle Metasomatism **William Myers, Dr. Anton Maria** Thin sections from the Grants Intrusive breccia on Hicks Dome in southern Illinois indicate a variably carbonatized, diatreme-facies ultramafic lamprophyre breccia consistent with the Midwest Permian Ultramafic District. Previous work characterizes the MPUD lamprophyres as silica-poor igneous rocks enriched in Mg, K, Ni, Sr, Ba, Cr, and volatile components, derived by small degrees of partial melting of a metasomatized lithospheric mantle source. The Grant Intrusive is distinguished by its exceptionally high abundance of xenoliths, macrocrysts, and megacrysts transported to the surface during explosive magma ascent. These xenoliths and crystal fragments commonly form the cores or kernels of pelletal lapilli, a distinctive form of magma clast consisting of a central crystal or xenolith surrounded by concentric rims of quenched magma. Pelletal lapilli are associated with volatile-rich, explosive diatreme-forming intrusions. The pelletal lapilli within the Grant Intrusive are up to 12 mm in diameter and contain kernels of pargasitic amphibole (Ti- and Mg-rich), clinopyroxene, phlogopite, apatite, and spinel-group opaques. The kernels exhibit abraded margins and typically lack reaction rims that might represent disequilibrium during ascent. A few kernels consist of heterogranular xenoliths composed of clinopyroxene extensively replaced by amphibole, with interstitial anhedral apatite and Fe-Ti oxides, which are interpreted as lithospheric mantle fragments and likely sources of the macrocryst population. Phlogopite occurs as laths and melt-like lenses consistent with modal metasomatism. Collectively, these features suggest metasomatism of off-craton mantle at depths of ~30–65 km, compatible with models of lithospheric thinning and underplating beneath the Reelfoot Rift and New Madrid Seismic Zone. The xenoliths resemble metasomatized pyroxenite and may represent intruded magmas within an underplate zone that were subsequently overprinted. Additional xenoliths of sedimentary and felsic igneous rock likely represent crustal incorporation at shallower levels during volatile-rich diatreme emplacement.
	Phosphorus Diagenesis in Lake Tanganyika Core TANG16-5B-1G **Jaylen Price, Laura Shreib, Michael McGlue, Jennifer Latimer**

17*	Lake Tanganyika is the second deepest lake in the world and the second largest freshwater lake by volume, holding an estimated 18,880 km3 of freshwater. As one of the largest freshwater reservoirs supporting an estimated 12 million people, it is an important site for studying biogeochemical cycling. Because the lake is meromictic and strongly thermally stratified, it is particularly sensitive to changes in nutrient and redox conditions. For this study, we are looking at phosphorus (P) diagenesis in sediment core TANGI6-5B-1G from Lake Tanganyika to better understand P burial, remobilization, and long-term cycling. We are using a modified SEDEX method developed by (Anderson & Delaney, 2000) which separates sedimentary phosphorus into four main pools. Fe-bound phosphorus which consist of P adsorbed into or associated with iron oxides, is sensitive to redox conditions, and can be released under reducing environments. Authigenic P is a stable long-term sink for P that forms in the sediments as a result of organic matter degradation and release of P to pore waters. Detrital P is composed of mainly resistant apatite minerals from terrigenous sources. Finally organic P includes P that was once contained within organic matter. By quantifying these P fractions, we aim to reconstruct changes in P cycling and evaluate how diagenetic processes and redox conditions influence P preservation in this deep lake system. Understanding the distribution of P pools in sediments provides insight into nutrient limitations, internal recycling, and the lake's response to environmental and climatic changes in the past.
18	Phytolith-based reconstruction of vegetation variability over the Zambezi River basin using marine sediment core U1477, Expedition 361 **Madiha Hassan, Dr. Chad Yost, Dr. Jennifer Latimer** Understanding the response of vegetation to glacial and interglacial climate change in the past can inform future vegetation change in response to current and projected atmospheric warming. Understanding past vegetation change in southeastern Africa can also provide an environmental context for studying human evolution. The goal of this study is to reconstruct relative changes in tree cover, dominant vegetation structure, and fire activity in the Zambezi River basin using phytoliths and charcoal deposited in marine sediments captured by IODP Expedition core U1477. Phytoliths are silica remains of plants (microfossils) that can be recovered from soils and sediments for vegetation reconstructions. Phytoliths are particularly useful in southeastern Africa to reconstruct vegetation structure in savanna-woodland systems. The objective of this study is to reconstruct changes in vegetation, hydroclimate, and fire activity during glacial (dry and cool) and interglacial (warm and humid) periods over the past ~220,000 years. To reconstruct dominant vegetation structure, we used the phytolith-based Iph (aridity) and D/P (tree cover) indices. The D/P index can estimate the percent canopy cover using the relationship between spherical ornate and saddle phytoliths, whereas the Iph index uses the ratio of xeric C4 grass phytoliths to mesic C4 grass phytoliths to reconstruct relative changes in hydroclimate. Preliminary findings indicate variability in hydroclimate, vegetation, and fire activity in the Zambezi River basin is correlated with Northern Hemisphere glacial and interglacial periods. The Iph and D/P indicies mostly show contrasting trends that peaks at glacial-interglacial boundaries. Tree cover is higher, and the aridity index has lower values during glacial periods, and vice versa. Whereas microcharcoal peaks were observed during interglacial periods when C4 xeric grasses were abundant. Thus, there appears to be glacial/interglacial scale variability in the savanna-forest systems of southeastern Africa.
	Uneven sediment filling inside the Ordovician Rafinesquina from near Manchester, western Dearborn County, Indiana: post-mortem scavenging or soft part molding? **Bethany Cisz, Katlynn Lamble, Rebecca Freeman, Dr. Benjamin Dattilo** While some fossil brachiopods, including Devonian spiriferids, have preserved lophophore (feeding structure) supports, others lack them, requiring lophophore geometry to be inferred from comparison with modern descendants and physiological shell constraints.

19*	Strophomenids dominated Paleozoic muddy seafloors, lacking distinct mineralized lophophore supports, and featuring instead enigmatic dorsal valve calcifications unrelated to muscle attachment. While the relationship of Strophomenidae to modern Thecidellinidae is unclear, they are hypothesized descendants of either Strophomenates or Spiriferida. Later Strophomenates show clearer lophophore shapes, with physiological and phylogenetic evidence suggesting Rafinesquina possessed a schyzolophe or ptycolophe lophophore. An unweathered clay-rich shale block was collected in the early 2000s from a stream cutbank near Manchester, Indiana, within the Corryville Member of the Grant Lake Formation. The stratum at the site was chosen for its well-preserved specimens of the Edrioasteroid Streptaster attached to articulated Rafinesquina. The articulated and conserved multielement echinoderm skeletons and the articulated partly spar-filled brachiopods suggest rapid burial of both epibiont and host. Polished slices reveal a 10 cm thick, single-event obrution deposit burying articulated Rafinesquina brachiopods, with scattered Chondrites-like burrows. Serial slices reveal that complex, pyritized, and undercut internal sediment interfaces in brachiopods deviate from the flat, passive infilling expected from purely physical processes. The complex interface suggests either burrow-feeding on soft parts disturbing the sediments post burial-death, molding of soft part anatomy by smothering mud during the burial and death process, or a combination of both. Spar-filled, mud-free zones where muscles should be strongly suggesting soft-part molding. We are reconstructing 3D sliced infills to investigate these hypotheses. To reconstruct infills, we aligned brachiopod serial slices using SPIERS align software. We traced valves and pyrite using SPIERSedit. We will generate 3D reconstructions using SPIERSview. These reconstructions will help determine whether the irregular fills are shaped as expected for molds of soft parts.
20	Heavy Metal Analysis of Markle Mill Dam Sediments, Terre Haute, Indiana **Hallie Townsend, Dr. Jennifer Latimer, Dr. Jim Speer** At the height of the Industrial Revolution, Markle Mill, located in Terre Haute, Indiana, was a booming gristmill, operating for over 100 years. By some accounts, the mill, built in 1817, was the longest-running gristmill east of the Mississippi River. The mill ceased operations in 1938 following a fire, but the dam remained in place until 2024. Prior to the removal of the low head dam, a stratigraphic sequence of bank sediments was collected, potentially representing deposition since the early 1800's. Using this historical record of deposition at the dam site, we investigated the concentration of heavy metals present in the sediments located behind the dam. Samples were collected every 2cm for optimal resolution and analyzed using an X-ray Fluorescence (XRF) analyzer. Although the data showed decreased elemental variability with the older sediments, several anthropogenic metals were found in concentrations above background levels, with some reaching values of concern. Lead (Pb), zinc (Zn), copper (Cu), Nickle (Ni), chromium (Cr), and vanadium (V) all have concentrations above typical background levels, while elements such as mercury (Hg) and arsenic (As) have many concentrations below the level of detection for the XRF. Correlations between these metals and variations with depth will be further explored.

Poster Number	Poster Title, Author(s), & Abstracts
21*	Mineralogical Controls on Lead Bioavailability and Geochemical Partitioning in Amended Garden Soils **Jeffrey Buell, Dr. Jennifer Latimer, Ravin Gaines** Lead (Pb) contamination in soils remains a persistent environmental and public health concern. The geochemical behavior of Pb in soils is influenced by mineralogy and environmental variables such as pH. The purpose of this study was to investigate how four common lead minerals—cerussite ($PbCO_3$), litharge (PbO), anglesite ($PbSO_4$), and galena (PbS)—contribute to lead bioavailability and geochemical partitioning in soils. To accomplish this, garden soils were amended with lead mineral powders and tomatoes, cucumbers, and grass were grown under controlled greenhouse conditions. Total Pb concentrations in soils and plant tissues were quantified using X-ray fluorescence (XRF), while bioaccessible Pb was estimated using a simulated gastric fluid extraction followed by ICP-OES analysis. To determine how lead is bound in these soils, a subset of samples were subjected to the sequential extraction (Tessier, 1979). The extraction isolates metals that are exchangeable, carbonate-bound, Fe and Mn oxide-bound, and associated with organic fractions. Preliminary results from total Pb and simulated gastric bioaccessibility analyses indicate that $PbCO_3$ and PbO amendments exhibit higher relative bioavailable fractions compared to $PbSO_4$ and PbS treatments. These findings are consistent with expected differences in mineral solubility and suggest that mineral form exerts strong control over potential exposure risk. Sequential extraction analyses are currently underway to determine how these differences in bioavailability correspond to operationally defined geochemical fractions and to evaluate how plant presence influences Pb redistribution within soil systems. By integrating mineralogy, simulated bioaccessibility, and sequential extraction analysis, this study provides a mechanistic understanding of how lead speciation governs environmental risk in amended agricultural soils.
22	Comparison of historic stratigraphic nomenclature of part of the Indiana Upper Ordovician– an example from a composite section in Madison, Ind., and Milton, Ky **Mason Frauhiger, Ben Dattilo, Victoria Leffel, Carl Brett** Exposures of the uppermost Ordovician in and around Madison, Ind., have served as Cincinnatian Ordovician reference sections for more than 100 years. Natural exposures are abundant and resulted from rapid downcutting of tributaries after the establishment of the current course of the Ohio River. Navigating in and around the steep-sided Ohio River canyon has also required extensive roadcuts that have provided focal points for geologic study. Famous cuts discussed by geologists include Railroad Incline Cut (1841); cuts along Cragmont Street (Hanging Rock) Hill (1900–1910); U.S. 421; the Milton, Ky., Hill Cut (1929); Ind. 56-Hanover Hill (1930); and the long series of cuts along U.S. 421 north of Madison (1970). We examine correlated sections and different stratigraphic unit schemes made over time including: 1) Hattin's (1961) Hanover Hill Section (traditional units: Arnheim, Waynesville, Liberty, Saluda, and Whitewater Formations, 210 ft); 2) Swadley's mapping through Milton Hill in USGS Geologic Quadrangle 1469, Madison West, applying Kentucky Ordovician units (Grant Lake Limestone, Bull Fork Formation, and the Saluda Member of the Drakes Formation); and 3)

	Oldroyd's (1978) U.S. 421 north Madison roadcuts, applying Indiana units (Dillsboro and Saluda Formations, 250 ft). We include our measured sections of parts of the Milton Hill, Ky., and the Madison, Ind., cuts, both on U.S. 421—including lithologic descriptions, thin-section work, faunal counts, and gamma logs—and apply revised traditional unit names (Grant Lake, Arnheim, Waynesville, Liberty, and the Saluda/Whitewater Formations). New data points calibrate measured sections to LIDAR-based digital elevation models. These elevation models are a powerful tool that reveals the physiographic expression of formation contacts that can be related directly back to measured
23*	Spatiotemporal Dynamics of Freshwater Algal Assemblages **Fatma Badie, Noah Dilley, Greg Monzel** Tracking changes in algal biodiversity is a key indicator of freshwater ecosystem health, as it responds to biotic, environmental, anthropogenic, and geographic drivers. In this project, we analyzed the Interagency Ecological Program (IEP) dataset package edi.1320.9, following the public access instructions provided through the Electronic Data Interchange (EDI) Portal. We applied a hierarchical analytical framework to 26 river stations over 15 years, examining algal abundance, richness, community composition, and functional group resilience. Our goal is to uncover long-term spatiotemporal patterns in freshwater algal communities in the Sacramento-San Joaquin Bay-Delta region in San Francisco–California, providing insight to inform targeted land and water management strategies.
24	Exploration of Microplastic Contamination in Water Sources of Terre Haute, IN **Clara Westcott, Hannah Harvey, Jeanna E. Brown, Dr. Keeley Cleghorn** Plastic production and use have increased exponentially in the last few decades due to its convenience and cheap prices. Once plastic is thrown away, it slowly begins to physically and chemically break down into microplastics. Microplastics are particles of less than 5 mm and have been found in air, water, soil and even in our icecaps. Not only have they been found in the natural environment, but they have been found in vegetation, animals, and humans. Most of these particles are difficult or impossible to see with the human eye. Because of their small size, they are easily ingestible. Once ingested, the microplastics can't be digested and can start to accumulate. This leads to a myriad of health issues, such as DNA damage, alterations to the gut microbiome, neurological damage, and more. Public knowledge of microplastics is low due to news outlets not reporting on the issue or oversimplifying the information. This project tries to calculate the average microplastic concentration in Terre Haute, Indiana's various water sources. The purpose of this study is to be able to enlighten the members of the community to make them aware of what they could possibly be ingesting daily and what that can mean for their health. We took ten water samples from a variety of sources including: each aquifer system located in Terre Haute, well water, bottled water, the Wabash River, and a reverse osmosis filtration system of the city's water. These samples were filtered to isolate the microplastics to be counted and categorized.
	Investigating How Migration and Weather Affect Bird-Building Collisions and Bird Populations on The University of Indianapolis' Campus **Cassara Randall, Dr. P. Roger Sweets**

25*

In the United States, 365-988 million birds are estimated to die from collisions with buildings, specifically windows, each year (Riding et al., 2021; Van Doren et al., 2021). College campuses have been examined in the past as a source of research, but prior to the completion of this project, the University of Indianapolis had not yet been surveyed to determine its campus' impact on local and migratory bird populations. Anecdotal evidence from professors and peers suggests that bird-building collisions on campus are a significant problem that needs to be addressed. In order to address this knowledge gap, this project aims to identify the deadliest regions on campus for birds. Data on the bird species that live on or visit campus and weather data was tracked to address additional goals of determining what birds use the University of Indianapolis' campus as a residential habitat, breeding habitat, or migratory stopover site and if weather (wind speed, wind direction, and precipitation presence or absence) plays a role in bird building collisions. The overall purpose of this project is to provide data that can be used to apply interventions with the goal of conserving the bird populations that utilize the University of Indianapolis throughout

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What should we do about cultivated mushroom invasions?

Jeffery Stallman, Jessica Allen

Invasive fungal pathogens have caused populations declines and extinctions of native species, but less is known about what effects non-pathogenic fungi may have when they establish outside their native ranges. The Golden Oyster Mushroom, Pleurotus citrinopileatus, established a population outside its native range in eastern and midwestern North America, and a recent study shows that it displaces native fungal species in Elm trees. The Golden Oyster Mushroom is a popular edible species commonly cultivated, and it was likely introduced after escaping from cultivation. As increased interest in commercial and at-home cultivation of fungi for food and medicine increases, we argue that more research, action, and policy changes are needed to avoid future fungal invasions from these species. We suggest awareness campaigns aimed at both consumers and producers to limit the cultivation and transportation of known invasive fungi, and to properly dispose of them after use. We also suggest research to predict the invasion potential of cultivated species and develop sporeless strains that are less likely to establish populations in the wild. Finally, policy changes limiting the trade of high-risk species to certain areas may help prevent future invasions.

27*

Interacting Impacts of Climate and Pasture Management on Grassland Birds and Plants

Jaime J. Coon, Lena Bill, Sarah Osburn, Moises Zacatelco, Emerson Tallitsch, Aija Bowman, Wendy P. Tori

Grassland bird populations are decreasing due to increased habitat loss and climate variability. Our research in the Grand River Grasslands examines how drought and land management affect (i) the abundance of obligate grassland birds, (ii) the success of their nests, and (iii) vegetation composition. In summer 2025, 13 Iowa DNR-managed sites with varying management regimes were censused, seven of which were nest searched. We monitored 78 obligate grassland bird nests and sampled their surrounding vegetation. We also developed new protocols for measuring microclimates using iButton sensors. iButtons were placed adjacent to 30 Dickcissel nests to measure nest microclimate. Site-wide vegetation composition was assessed using the Daubenmire method, measuring 90 quadrats per site (1170 total). We next analyzed our data with existing long-term data (15 years) to evaluate the impacts of drought on grassland birds and plants. We found strong interacting effects between grazing management and drought on both native and non-native grasses. Native grasses decreased in drier years on ungrazed sites, and increased on grazed sites, with the opposite result present for the invasive grass tall fescue (Schedonorus arundinaceous). This result has implications for land management for grassland birds, which rely on diverse native-grass dominated grasslands for both foraging and nest sites during the breeding season.

Using Citizen Science & Machine Learning to Track Individual Sea Turtles in the Florida Keys

Mary-Katheryn Dunderman, Phil Allman

28*	Understanding the movement and site fidelity of sea turtles is critical for effective conservation, particularly in heavily visited reef ecosystems like those of the Florida Keys. Traditional methods for monitoring individual turtles, such as tagging or telemetry, can be invasive, costly, and logistically complex. To address these challenges, we launched a novel photo-identification (photo-ID) project that combines citizen science and machine learning to monitor individual sea turtles in a non-invasive, cost-effective manner. Divers and snorkelers are invited to submit photographs of sea turtles encountered during their time on the reef. Submitted images are processed using software that employs machine learning algorithms to identify individuals based on the unique scale patterns on the sides of their heads—akin to a fingerprint. This approach allows us to build a growing catalog of identified turtles and track their presence, re-sightings, and movement patterns over time. While data collection is ongoing, the project has already garnered strong interest from the diving community and has established a workflow for photo submission, quality control, and image processing. This framework creates the foundation for a scalable, community-powered monitoring program with the potential to improve our understanding of turtle residency, movement, and site fidelity across the Keys. Our poster will outline the project design, software tools, citizen engagement strategies, and future
29*	Dimensional Stability and Creep Performance of Glass Fiber Reinforced Thermoplastic Polyurethane as a Recyclable Alternative to Fiberglass Epoxy Composites for Wind Turbine Blade Applications **Olivia Snell** If glass fiber-reinforced thermoplastic polyurethane (GFRTPU) matches or exceeds the creep resistance and thermal stability of fiberglass epoxy resin, then GFRTPU should be considered an alternative material for wind turbine blades. Wind turbine blades are typically manufactured with fiberglass epoxy resin, which presents significant recycling challenges. This research investigated Elastollan® R3000, a recyclable GFRTPU, as a potential alternative material. GFRTPU samples were tested under three thermal conditions (68°F, 120-140°F, 160-200°F) with a ~5.5 oz load to measure creep behavior, and three samples were tested on an electronic tensile testing machine at ~65% ultimate tensile strength (UTS). Comparative analysis with wind turbine blade specifications revealed that Elastollan® R3000 maintains predictable dimensional stability with minimal creep throughout testing. Unlike traditional fiberglass epoxy composites that require complex modeling to predict progressive deformation over 20–25-year service lives, GFRTPU ensures the 23× safety factor remains constant throughout the blade's operational lifetime while enabling full material recyclability at end-of-life. The research supports the hypothesis that GFRTPU has the potential to replace fiberglass epoxy resin in wind turbine blade applications.
30	**HEAVY METAL CONCENTRATIONS IN SEDIMENTS OF THE WHITE RIVER WATERSHED IN ANDERSON, INDIANA: A PRELIMINARY STUDY** **Paa Kwesi Mbroh, Klaus Neumann** The industrial legacy of the American Rust Belt has resulted in persistent heavy metal contamination in river sediments, posing risks to aquatic ecosystems and human health. Much of this pollution predates the Clean Water Act (CWA) of 1972. Anderson, Indiana, a former automotive manufacturing center, exemplifies this legacy, yet sediment contamination in its White River segment, acting as a contaminant sink, remains poorly documented. This preliminary study quantifies concentrations of priority heavy metals (Pb, Cd, Cr, Cu, Ni, As) in surface sediments along the White River in Anderson. Objectives include assessing spatial distribution, inferring anthropogenic sources, and evaluating risks from legacy pollution. Sampling sites were chosen to capture high- and low-energy depositional environments for representative coverage. Sediments were collected via USEPA wading protocols, microwave-digested, and analyzed by Inductively Coupled

	Plasma Mass Spectrometry (ICP-MS) per USEPA Methods 3050B and 6020B. Contamination severity will be assessed using sediment quality indices: Pollution Load Index (PLI), Contamination Factor (CF), Enrichment Factor (EF), and Geoaccumulation Index (Igeo). Results will be benchmarked against EPA sediment criteria and compared with data from nearby Muncie to identify industrial sources. Spatial patterns and hotspots will be mapped via statistical analyses and GIS visualization. Additionally, machine learning models will predict contamination zones, simulate trends, and forecast scenarios under varying watershed conditions. This integrated approach, combining environmental geochemistry, geospatial analysis, and predictive modeling, addresses a critical data gap in Anderson's watershed. Findings will inform remediation strategies, land-use planning, and public health measures, while contributing to discussions on river resilience in post-industrial landscapes and supporting policies for environmental restoration.

Poster Number	Poster Title
31*	**Ibuprofen Behavior in Natural Waters** **Hayden Netral, Ryley Kidd, Dr. Kamila Deavers** Ibuprofen is a widely used nonsteroidal anti-inflammatory drug (NSAID) frequently detected in surface waters due to incomplete removal during conventional wastewater treatment. Chronic exposure to ibuprofen causes harmful effects in aquatic ecosystems, including endocrine disruption, oxidative stress, and impaired reproduction. These concerns have led the U.S. Environmental Protection Agency (EPA) to classify ibuprofen as an emerging contaminant, since municipal wastewater treatment systems are not designed to effectively remove pharmaceuticals. As a result, the investigation of a sustainable, natural-based method is suggested using the Poplar trees' root system for ibuprofen removal. Ibuprofen (IBU) tends to persist in treated runoff because of its low solubility, eventually accumulating in natural water bodies and posing a long-term ecological risk. To better understand ibuprofen's persistence and mobility in aquatic systems, its physicochemical properties were studied under various temperature and pH, and concentration conditions. Poplar hybrid trees (Populus spp.) were chosen because of their native adaptation to Indiana as well as their extensive root systems and fast growth. The absorption and retention of ibuprofen in poplar roots were tested in hydroponic solutions with different ibuprofen concentrations. UV-visible spectroscopy was utilized to measure changes in concentration, along with the phytotoxicity of plants. In addition, IBU removal was performed in a controlled environment without trees to observe the differences between phytodegradation and tree-mediated removal. The poplar trees were adaptable at an IBU concentration of 10 mg/L and removed IBU without phytodegradation effect.
32	**Assessing Potential Coal-Ash Contamination in the White River Noblesville: Case Study** **Dorothy Gidisu,Dr. Bowen Zhang, Dr. Rick Whitman, Dr. Bangshuai Han, Dr. Joshua Gruver, Dr. Tykhon Zubkov , Dr. Carson Wright** Coal ash disposal remains a long-term environmental concern because it can release toxic heavy metals into nearby waterways. This study investigated coal ash–related contamination in the White River Noblesville, where legacy, unregulated coal ash landfill is located adjacent to the river despite the 2015 Coal Combustion Residuals Rule. The objective was to assess potential coal ash contamination in the White River by analyzing heavy metal concentrations in water and sediment samples. Water and sediment samples were collected from five sites, two upstream reference locations and three downstream sites near landfill. Water samples were acid-preserved (HNO_3, pH < 2) and analyzed using ICP-MS (EPA 6020B; Hg via 7470A). Sediments were oven-dried (40 °C), homogenized, sieved (<63 µm), microwave-digested (EPA 3050A) and analyzed by ICP-MS. Dissolved arsenic ranged from 1.95 to 3.75 µg L^{-1} and was slightly elevated downstream. Boron consistently detected, showing trends increasing from 71.1 µg L^{-1} upstream to 104 µg L^{-1} in downstream waters. Cadmium was below detection but appeared at one downstream site (0.331 µg L^{-1}). Lead was mostly below detection, with downstream detections up to 7.69 µg L^{-1}. Selenium and mercury were not detected. Mean downstream sediment concentrations of As (2.21 mg kg^{-1}), Pb (11.0 mg kg^{-1}), B (5.30 mg kg^{-1}), Cd (0.29 mg kg^{-1}), and Se (0.24 mg kg^{-1}) exceeded upstream values, indicating observed patterns of heavy metal accumulation near landfill. Overall, sediments act as long-term reservoir for coal ash–associated metals, with consistent downstream enrichment suggesting ongoing influence from legacy landfill sites. While dissolved metal mobility appeared limited under hydrologic conditions observed during study period, changes in flow regime or sediment disturbance could enhance remobilization. These findings provide a geochemical baseline to support monitoring and management efforts by Indiana Department of Environmental Management and local policymakers to protect ecological integrity of White River system.

33	Tracking Sources of Fecal Pollution in the White River at Muncie: A Case Study **Mabel Kumi, Bowen Zhang, Jia Xue, Sean Behling** Fecal contamination of surface waters remains a significant environmental and public health concern, particularly in areas with multipurpose land use and dynamic hydrological conditions. This study applied quantitative Polymerase Chain Reaction (qPCR)-based Microbial Source Tracking (MST) to identify the dominant sources of fecal pollution in the White River in Muncie, Indiana. Nine sampling events were conducted across seven sites and analyzed for three host-specific genetic markers: human- (HF183), Canada goose- (GFD) and cattle-associated marker (CowM3). The results identified site 6 (Grace Baptist Church) and Site 7 (Morrow's Meadow Park) as primary "hotspots", with HF183 geometric mean of 1,660 and 1,333 gene copies per liter (GC/L), respectively. In contrast, Site 1(Prairie Creek Reservoir) was the only location where GFD dominated, accounting for 85% of the site's total detected pollution, although this site exhibited the lowest overall marker load. CowM3 concentrations were below the detection limit in all samples, indicating no significant cow-derived fecal inputs. Site 5 (Westside Park) showed the strongest response to rainfall events. HF183 concentration surged from 733 to 16,454 GC/L in periods associated with runoffs events, where HF183 accounted for 93.3% of the total marker load at this location. Similarly, elevated HF183 concentrations were observed at site 6 and 7 (downstream sites), with peak values of 15,941 and 12,994 GC/L, respectively. The findings highlight the critical need for targeted infrastructure improvement to reduce human-associated waste inputs and protect local water quality. Continued sampling will enable more comprehensive spatial analysis and further characterize the environmental factors that influencing fecal pollution sources.
34	A Comprehensive Survey of the Unionid Mussel Community of the Upper West Fork White River in Delaware County, Indiana (Map Display) **Sam Gradle, Laura Bowley** Since the 1970s, the Muncie Bureau of Water quality has monitored local freshwater mussel populations in the West Fork White River (WFWR) in and around Muncie Indiana. Until recently there has never been a comprehensive survey of the WFWR unionid population in Delaware County Indiana. Starting in 2018 a county-wide unionid mussel survey was conducted in the WFWR within Delaware County. The goals of this survey were to document local mussel populations for biomonitoring purposes in relation to water quality, examine the full extent of unionid communities of the upper WFWR, and to potentially reveal species previously not found in the WFWR. This project was conducted using timed search surveys. This undertaking took six years to complete and covered approximately thirty river miles. 53,765 live individuals were surveyed throughout this effort, representing nineteen different species. During this endeavor two live Ptychobranchus fasciolaris were found upstream of Muncie. These were the first live individuals of this species ever to be recorded by BWQ staff in this drainage system. This survey also confirmed that population abundances are substantially highest upstream of Muncie with over ninety percent of the total mussels surveyed being in this section. This may be because mussel populations have not yet fully recolonized the farther downstream sections of the WFWR in Delaware County. The data collected from this project could provide useful information for conservation and restoration efforts of local unionid mussel populations.
	Determination of the Roles of Keratin 18 and 19 in Early Xenopus laevis Development **Elisabeth Pennington, Koby Goodwin, Madison Townsend, Lina Rifai** Grasslands, wetlands, and forests in Indiana are essential habitats for thousands of pollinating insects, including the declining Monarch Butterfly (Danaus plexippus). Habitat loss and pesticide use have severely impacted Indiana populations of these long-distance migrants. In this pilot study, we used CTT's lightweight, solar-powered BlūMorpho tags to track Monarch movements on and beyond IU Kokomo's campus. Butterflies were captured and tagged in fall of 2025. Data was collected via CTT's IoT-

35*	based detection service, which uses cellular-connected devices to provide real-time location information of tagged butterflies. Data from tagged butterflies provided movement patterns between native plant restoration patches on campus. One butterfly was successfully tracked beyond campus, providing data on its travel speed, direction, and behavior at stopover sites en route to Mexico. Despite the small sample size, this study demonstrated the effectiveness of this technology. To help reverse population declines of Indiana Monarchs, future, larger-scale studies will improve our understanding of habitat connectivity and migration ecology and provide information for targeted conservation strategies.
36	Activity timing in an open-cup nesting bird: individual repeatability and environmental effects **Andrea S. Grunst, Melissa L. Grunst, Jackson Kinder** Repeatable among-individual differences in daily activity timing, or chronotypes, can affect ecological interactions, social networks, and fitness in humans and wildlife alike. For example, recent research in the great tit (Parus major), a model, cavity-nesting, passerine, suggests that early rising females fledge more young than late rising females, perhaps reflecting higher efficiency of early morning foraging bouts. However, to date, few studies have demonstrated individually-repeatable chronotypes in free-living birds, with these data being notably absent for open cup nesting passerines. Furthermore, few studies investigate how individual repeatability and environmental variables interact to determine the distribution of activity timing and fitness within populations. We deployed thermochron iButtons in song sparrow (Melospiza melodia) nests to track female chronotype, as defined by activity onset in the morning and activity offset at night. Only female song sparrows incubate and females display continuous, overnight incubation. Thus, thermochron-derived records of nest temperature (3 min intervals, precision of ± 0.2°C) allowed us to accurately determine the timing of female activity onset and offset. We document the repeatability of female chronotype across the up to 7-day duration of thermochron recordings, and discuss environmental effects on activity timing, including effects of temperature and urbanization level. We highlight implications for understanding the evolution of chronotypes across environmental disturbance gradients.
37*	Tree and Bird diversity in three urban greenspaces in South Bend, Indiana **Kitty Koontz, Dr. Andrew Schnabel, Dr. Deborah Marr** Abstract: The city of South Bend has started an urban tree canopy project with a goal of increasing canopy cover to 40% by 2050. We collected data on tree and bird diversity in three city parks to provide baseline data on current biodiversity and provide data that can be used to inform decisions that better support biodiversity. We found that City Cemetery, Southeast Park, and Veterans' Memorial Park, respectively, had on average 10, 23, and 107 native trees per acre. Tree species richness was also lower in Southeast Park (34 species) and City Cemetery (39 species) compared Veterans Memorial Park (43 species). Bird species diversity followed a similar pattern: 26 species at Southeast Park, 28 species at City Cemetery, and 37 species at Veterans' Memorial Park. Additionally, we found that City Cemetery and Southeast Park had an uneven distribution of bird species. At City Cemetery, 7 species accounted for 70% of the birds observed and at Southeast Park, 6 species accounted for 74% of the birds observed. Veterans' Memorial Park had a more even distribution in which 10 species accounted for 71% of the birds observed, and it was the only site in which yellow warbler, wood thrush, red eye vireo, and purple martin were observed. These results suggest that increasing native tree diversity and density in urban spaces can better support bird species.
	Plant-insect-fungal interactions in White False Indigo (Baptisia alba) on Indiana tallgrass prairies

38*	**Lilith Rengstorf, Emma Smith, Emma Williams, Ava Like, Gabby Roper, Kyryll Savchenko, Andrew Stoehr** The highly diverse North American tallgrass prairie occupies less than 5% of its historical range; in Indiana tallgrass prairie loss is 99.9%. The ecological value, and precarity, of prairie has inspired the recent protection of remnant prairie patches, reconstruction of destroyed prairies, and construction of novel prairies on historically forested lands. Restorations typically focus most on the iconic prairie plants but to restore any ecosystem to full ecological functioning requires that important but neglected organisms be studied and restored. We investigated the interactions among the iconic tallgrass prairie plant white false indigo (Baptisia alba), a weevil that feeds on its seeds (Trichapion rostrum), and the fungi that grow in the seed pods across 35 sites in Indiana. Sites included preserved remnant prairies, reconstructed prairies within the historical range of tallgrass prairie in Indiana, and prairie constructions in areas not historically covered in prairie. Weevils were present on, on average, 82% of plants sampled and in on average 64% of seed pods sampled but there was considerable variation in weevil prevalence and abundance among plants and across sites. As a result, seed production varied considerably and was generally highest in Baptisia populations with fewer weevils. Weevil exclusion experiments demonstrated that weevils reduce seed production from about 18 seeds per pod, in the absence of weevils, to less than three seeds per pod when weevils are present. Fungal growth was common but only weakly associated with weevil presence, and weevil exclusion experiments demonstrated that weevils are not required for fungi to thrive. DNA sequence analysis of fungal cultures isolated from seed pods reveals that several species of fungi are present on seed pods. This work provides insight into basic plant-insect-fungal interactions and could be valuable for future prairie restorationists.
39*	Using Chromosome Numbers to Understand Evolution of Genomic Size of the Spermacoceae Tribe (Rubiaceae) **Peyton Rodgers, Eden Elpers, and Suman Neupane Ph.D.** The angiosperm family, Rubiaceae, comprises about 14,000 species, with the tribe Spermacoceae containing approximately 1,300 herbaceous taxa found throughout subtropical and tropical regions. Despite indepth taxonomic revision, chromosome evolution in this tribe is still poorly understood due to incomplete cytogenetic sampling from uncharacterized species. Previous studies share that Spermacoceae commonly had a base number of x=14 chromosomes with diploid and tetraploid sets, but in recent work there is evidence to support paleotetraploid and descending aneuploidy events happening within the Houstonia genera leading to new potential lineages. Chromosome variation is linked to genome size changing which can be triggered by events of polyploidy doubling. Unresolved cytogenetic data limit our understanding of the diversification and speciation within the lineage. This study aims to count chromosomes and determine ploidy levels from previously uncharacterized Spermacoceae species to infer ancestral chromosome events. Using a herbarium as a seed bank, uncounted for species will be germinated and chromosome counts will be conducted on seedlings. Newly developed cytogenetics along with past works would be integrated into a software “Chromevol” to calculate and infer ancestral chromosomal evolution and identify polyploidization events. Understanding the chromosome evolution allows a deeper understanding on developing new emerging lineages within the Spermacoceae tribe.
	First Draft Genome of North American Bluets Using ONT Sequencing **Ainsley Tierney, Madeline Grove, Peter Schafran, Suman Neupane** Houstonia longifolia var. glabra Terrell, the Granite Dome long-leaf bluet, is an annual flowering plant endemic to the Smoky Mountains of the Blue Ridge region. It belongs to the tribe Spermacoceae within the coffee family (Rubiaceae),

40*	the fourth largest angiosperm families. Despite the ecological and evolutionary importance of Rubiaceae, very few species have chromosome-scale genome assemblies available. Currently, only one genome is available from Spermacoceae, a clade of approximately 1,500 species that includes the bluets, diamond flowers, and star-violets of North America. We have generated a partial nuclear genome assembly of Houstonia longifolia var. glabra completed using the Oxford Nanopore MinION (ONT), a third-generation platform. The portable ONT technology pulls native DNA molecules through nanopore sensors producing long continuous reads that improve assembly across repetitive and complex genomic regions compared to short-read approaches. This initial assembly also provided practical insight into the high molecular weight DNA extraction and library prep processes that provided the longest DNA strands for ONT sequencing and what needed to be adjusted for longer DNA strands to be extracted moving forward. This project aims to generate the first whole-genome sequences for any species within the bluets group of the Spermacoceae—providing a foundation for future genomic studies within this group and the broader coffee family. After completing the whole genome of Houstonia longifolia var. glabra, we hope to also construct genomes for two other North American species: Houstonia purpurea L. and Stenaria nigricans (Lam.) Terrell. Despite being closely related, these three species have differing ecological niches impacting their geographic ranges. With the constructed genomes, we will apply comparative genomic analyses to investigate potential genetic differences associated with habitat specialization, range variation, and hybridization reported in bluets.

Poster Number	Poster Title, Author(s), & Abstracts
41*	Investigating methods of chemical control for novel invasive yellow-flowered teasel **Molly Hobson, Marcia Moore, Dr. Hilary Madinger** Yellow-flowered teasel (Dipsacus strigosus) is an invasive plant species that was first observed in 2020 in Indianapolis, IN. In recent years, the observed spread of D. strigosus has made clear the need for an effective and environmentally friendly method of chemical control. D. strigosus plants were separated into four treatment groups: a negative control group, Garlon 3A at a 3% rate, a salt-based natural herbicide, and an herbicidal soap solution. We observed and rated plant health approximately once per week for six weeks following treatment. Plant health was monitored according to leaf color, degree of leaf shriveling/wilting, number of healthy leaves, and overall plant size. Our results indicate that herbicidal soap is the most effective of the herbicides tested. Plants treated with herbicidal soap showed the most drastic health decline in the shortest amount of time, while plants treated with Garlon 3A showed the smallest change in health following treatment. Here we demonstrate that herbicidal soap is an environmentally safe and highly effective alternative treatment to Garlon 3A for the chemical control of D. strigosus. These results have promising environmental implications as well as providing guidelines for future efforts to eradicate the invasive D. strigosus population.
42	Integrating GIS Technology for Enhanced Urban Forestry Education: A Redesign of the Butler University Tree Walk **Alexa Simpson, Marcia E. Moore, Dr. Hilary Madinger** Butler University, founded in 1855 and located in a residential part of Indianapolis near the Broad Ripple neighborhood features a rich diversity of flora and fauna and particularly, majestic trees located across campus. In the late 1990s and early 2000s, a project titled the Tree Walk was created to connect campus communities to urban forestry, in aim to educate the public about the ecological and historical significance of the university's most notable trees. However, as campus landscapes evolve, maintaining accurate spatial data becomes a significant challenge, especially since many of the trees once on the Tree Walk no longer exist today. This project aimed to modernize the long-standing Tree Walk through a comprehensive redesign utilizing Geographical Information System (GIS) software. This process involved gathering of spatial data and navigating the complex interface of GIS in order to create an interactive walk through that ensured geographical accuracy. The resulting redesign provides a more precise and interactive experience for users, demonstrating how geospatial tools can bridge the gap between communities and traditional botanical studies and learning. In doing so, we have made a fun, practical experience to educate people at all levels of understanding, including college students as well as local elementary and middle schools when touring the campus. The updated Tree Walk brings a modern approach to forestry education and highlights why connecting with nature remains more important than ever.
43	Exploration of Temperature on the Growth Stages of Tomatoes, Solanum lycopersicum **Savanna Amschl, Clara Westcott, Dr. Keeley Cleghorn, Dr. Robert Vandermolen** Tomatoes, Solanum lycopersicum, are one of the most important and popular crops grown at the White Violet Center for Eco-Justice in Saint Mary-of-the-Woods, Indiana. However, rising temperatures during Indiana's growing season may be reducing tomato yields. This project investigates how temperature affects tomato harvest amounts by identifying which stage of tomato growth is most sensitive to high temperatures. Tomato harvest data from 2021 to 2024 (measured in pounds) was collected from the White Violet Center, and daily high temperature data was

collected from the National Weather Service. A multi-linear lag model was created in R-Studio using temperatures from ten to twenty-five days before harvest as predictive variables. Results showed statistically significant temperature effects on days sixteen through eighteen before harvest. Day sixteen had a positive effect while day seventeen had a strong negative effect, however on day eighteen a strong positive effect was observed. The model explained approximately 83% of the variation in harvest yield. These findings suggest that a short two-to-three-day period during tomato development that may be especially sensitive to temperature changes.

44

Dendroarchaeological and Timber Analysis of Four Log Structures of Brown County State Park

Erin Terry, Darrin L. Rubino, Christopher Baas, Liz Marthaler

When Brown County State Park was established, several log structures emulating Indiana's pioneer period were constructed. The goals of this study were to analyze four of these structures to a.) document their form; b.) determine their likely construction date or identify the age of the timbers that were recycled and used in their construction; and c.) to ascertain the types of timber used in construction. Using standard dendroarchaeological techniques, cores were obtained from the buildings and dated; wood identifications were made for all accessible timbers. Forty-six samples were successfully dated from 36 timbers. Composite chronologies were created for white oak (34 samples, 1661–1868) and tulip poplar (10 samples, 1728–1860). The buildings were constructed with eight different timber types. Red (49) and white (46) oak and tulip poplar (10), were, as is the case in many 19th century buildings, the most commonly used taxa. Intact half-dovetail corner notching, building form, and similarity in timber harvest dates suggest that the Original Custodians House was constructed in 1861 and was likely moved and rebuilt in the park. The three other structures appear to be 20th century recreations built with recycled 19th century timbers. The Hoosier's Nest was built from timber harvested in 1860, 1861, and 1868; the form of this building is not characteristic of 19th century architecture, but it does have period corner notching. The Research Shed and Cabin lack period corner notching; log ends were cut off, and corners were encased in sawn timber. The Research Cabin was built from a structure that was built in 1870 and the Shed from logs harvested in 1861. This study expands our understanding of Indiana's historic architecture and early builders' material choices. Each newly dated sample strengthens existing tree-ring chronologies and provides insights into past climate, land management, and local human activity.

45*

Fifty-Year Study of Post-Tornado Forest Succession in Happy Valley, Jefferson County, IN

Victoria Zwilling, Dr. Darrin Rubino

A tornado struck Jefferson County in April 1974, causing significant damage to a forested area of Hanover College's campus. The goals of this study were to describe the forest dynamics since the tornado and to compare the damaged and undamaged forest area. Three permanent transects with varying damage were sampled repeatedly over 50 years using the point-center-quarter method. The data were used to calculate importance values (IV) for each species based on relative density (number of trees), basal area (size of the tree), and frequency (number of points at which the species was present). The highest number of species (26) was recorded in 1981 and the lowest (19) in 2025. Acer saccharum had the highest IV in all transects. Ulmus rubra was second in importance on the damaged transects over time due to high density and frequency while Acer negundo was second on the undamaged transect because of high density. Ulmus rubra rose in importance after the tornado due to an increase in frequency before decreasing beginning in 1989, especially on the damaged transects. Tilia americana's IV has steadily increased on the damaged transects because of increasing basal area. Aesculus spp. spiked in importance on the damaged transects in 1989 due to increasing basal area but has increased since then due to increasing frequency. Shannon-Wiener Index values indicated diversity was highest in 1981. The undamaged transect had the highest diversity during every sampling except 2011. Fraxinus americana and F. pennsylvanica were not sampled in 2025, despite consistent presence in previous years. In addition to showing how secondary succession has affected community composition, the study provides insights into how other factors such as invasive species and pathogens affect successional trajectories.

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Fireflies of Indiana (Coleoptera: Lampyridae)

Amelia R. Meyer, Christopher C. Wirth

With their flashy displays during summer evenings, fireflies are highly visible, charismatic insects that are widely popular, featured in dedicated field guides and as state insects of three U.S. states. There are 179 described species and subspecies in North America, with 30 species reported from Indiana and nine likely from adjacent states. Since the last review of Indiana's fireflies was published 30 years ago there have been major taxonomic changes and new species described, limiting the utility of this resource. With growing concerns of declining firefly populations, there is a clear need for an updated review of and identification tools for Indiana's fireflies. We examined and verified identifications for over 3,300 museum records and human observations. From these we extracted county, collection date, and taxon name to determine distribution, seasonality, and diversity of fireflies in Indiana. The dataset includes records from 92% of Indiana counties across 104 unique years. We identified ten putative new state species records for a total of 40 species in nine genera and present updates to previous generic identification resources.

47*

Bridging Fragmented Habitat: Modeled Connectivity Zones Predict Zebra Swallowtail Occurrence

Caden Zuehsow

Habitat fragmentation presents a challenge for specialist species dependent on host plants whose habitats are sparsely distributed. The zebra swallowtail (Protographium marcellus) formerly Eurytides marcellus relies exclusively on pawpaws (Asimina triloba) as a larval host species. This makes pawpaw distribution a large part of zebra swallowtail distribution. I was able to model a connectivity framework using Python, and it was evaluated using occurrence data from Brown County, Indiana as a case study.

A connectivity surface was created to show potential habitat linkage across a region, using river systems and known pawpaw (Asimina triloba) locations as structure. Areas of high connectivity were identified using a percentile threshold. Distances from zebra swallowtail observation records from iNaturalist were compared to randomly generated points across the county. Statistical differences between observed and random distances were evaluated using a Mann–Whitney U test.

Results indicate that zebra swallowtail observations occur significantly closer to these modeled connectivity zones than the random points, supporting the ecological relevance of the connectivity framework. This method provides a scalable and transferable framework for assessing habitat connectivity in host specific butterflies.

48*

Insect Fragment Analysis of Big Brown Bat (Eptesicus fuscus) Guano During Brood X 2021 Emergence

Surraya Wagner, Aria Baker, Dr. Scott Bergeson, Dr. Benjamin Dattilo

Periodic cicada emergences lead to large but temporary increases in prey availability that may influence the foraging behavior of insectivorous predators. During the 2021 Brood X cicada emergence, we investigated how this prey pulse event affected the dietary composition of the Big Brown Bat (Eptesicus fuscus). We hypothesized that the increase in cicada availability would result in increased cicada fragment frequency in guano samples. To conduct this study, we collected guano samples from a barn in northern Indiana between May 28th to August 21st, 2021. We dried the samples for storage and later soaked them in 70% EtOH, in preparation for analysis. We used vacuum filtration to isolate insect fragments, then manually separated the resulting residue, and mounted the fragments on permanent slides. We used epoxy to position and secure fragments onto each slide, allowing for long-term preservation of the samples. Using reference collections, we identified the fragments to the lowest possible taxonomic level. So far, we have analyzed slides from the May 28, 2021 collection date and found no cicada fragments. This project establishes a

	replicable method for processing and permanently mounting insect fragments from bat guano for identification, enabling dietary analysis and contributing to our understanding of how temporary ecological events influence foraging behavior in insectivorous bats.
49*	Comparing Family-level Insect Diversity Between Habitats at the DePauw Nature Park **Sahit Liyanage, Samantha Floyd, Thomas Manning, Madison Stillabower, Dr. Olivia Gearner** The Depauw Nature Park hosts a broad diversity of life and insects represent a significant portion of that diversity. However, the insect diversity in the park has never been formally studied. We sought to document species composition across two habitat-types at the DePauw Nature Park. We sampled and identified insects in two woodland and two prairie habitats in the park using both active sampling (e.g., insect nets) and passive sampling (e.g., insect traps) methods. All specimens were mounted, labeled, and databased. Preliminary data suggests that the woodland habitat has higher family-level diversity than the prairie habitat. About half of the families were found in only one habitat-type, suggesting that the habitat diversity found in the park supports higher overall insect diversity. Future work includes assessing species level diversity in the two habitats and creating a checklist of species found in the nature park.
50*	A comparison of field and experimental observations of arboreal behavior in multiple species of fossorial salamanders **Marieke Young, Dr. Brian Gall** Salamanders provide a critical link in food webs between leaf-litter invertebrates and higher vertebrates such as small mammals and birds. While their perception as secretive and fossorial is well deserved, observations from night-time field excursions suggest that many species frequently exhibit arboreal behavior. Arboreal activity in multiple species of salamanders was evaluated in a laboratory study and compared to field observations. All species climbed vertical structures in the lab, but the propensity to climb differed between species and genera. During nocturnal surveys, multiple genera, including Desmognathus, Eurycea, and Plethodon were observed climbing vertical structures. Four of these species were consistently observed on vertical tree trunks and rocky structures, with some species climbing up to a meter above the substrate. Both experimental and field observations suggest that many species of salamander are likely to exhibit arboreal behavior during nocturnal activity, despite being primarily considered terrestrial or fossorial. While observational in nature, these results suggest that arboreal behavior is common among terrestrial salamanders with climbing behavior likely corresponding to the ecology and natural history of each clade.

Poster Number	Poster Title, Author(s), & Abstracts
51	An Archaeological Survey of Salamonie River State Forest, Wabash County, Indiana **Nolan Sterns, Sophie Hill, Graham Kennedy, Dr. Carson Wright, Hannah Ryker, and Dr. Kevin C. Nolan** The Applied Anthropology Laboratories (AAL) conducted an archaeological investigation of a 40-acre Survey Area (SA) on a bluff overlooking the Salamonie River (SR) within Salamonie River State Forest during the summer of 2025. This project was funded by an Indiana Historic Preservation Fund Grant. The SA was chosen for its proximity to the SR and its adjacency to a known historic foundation that extends partially into the river channel. Additionally, the SA is situated near Treaty reserve lands retained by Myaamiaki (Miami) people prior to their forced removal from the region in 1846. Due to the location and known history, we expected recovery of substantial quantities of pre-contact and post-contact Native artifacts and post-contact Euroamerican artifacts. We defined six new archaeological sites which yielded 305 artifacts representing multiple occupation and use periods. However, the number of artifacts recovered was considerably fewer than initially anticipated. A historic well was documented and extant timbers from the previously recorded foundation were sampled for dendrochronological analysis, contributing to the understanding of historic land use and settlement patterns within the forest. Precontact artifacts recovered during the survey include lithic shatter and cores, indicating on-site tool production or maintenance activities, as well as several ground stone tools and fire-cracked rock suggesting a broad range of behaviors. The distribution of different activity indicators appears to be structured independent of each other. The pattern of land use is consistent with ephemeral and opportunistic use of primarily landform edges. Each portion was visited repeatedly and activities were not specific to location, with the possible exception of use of fire. Historic artifacts included glass, ceramic, and metal materials, reflecting domestic and possibly agricultural use of the landscape during the historic period. Collectively, the results demonstrate that the SA contains a limited but complex, multi-component archaeological record of the SR landscape.
52	An Accessory Head of the Biceps Brachii: Clinical Implications from a Gross Anatomy Case Study **Layken McGuire, Anizha Young, Makenzi Patterson, Dr. Amandine Eriksen** Typically, the biceps brachii muscle, located in the anterior compartment of the human arm, is composed of two muscle bellies with associated tendons: the short head and the long head. The long head is expected to originate from the supraglenoid tubercle of the scapula, while the short head originates from the coracoid process of the scapula. The two muscle bellies converge and share a common point of insertion at the radial tuberosity of the radius and via the bicipital aponeurosis. The muscle is innervated by the musculocutaneous nerve and receives its blood supply from the brachial artery. This case study reports on a variation discovered in a male donor in the Gross Anatomy lab at the University of Indianapolis. Routine dissection identified an accessory head of biceps brachii on the donor's right arm. While the presence of a third head is the most common anatomical variation of this muscle (reportedly found in 4.2% to 19.8% across populations), we have identified a less commonly reported subtype. The accessory head is significantly smaller in size than the short and long heads, and is located medially. It attaches to the short head of biceps brachii tendon and inserts on soft tissues on the medial elbow, near the origin of the forearm flexor muscles. Additionally, it receives direct blood supply from a branch of the brachial artery and is in close proximity to the nerve that controls the biceps brachii muscle. This accessory head of biceps brachii directly overlies the median nerve, which during contraction could impinge the nerve and nearby blood vessels, potentially causing reduced innervation and blood flow in the forearm. It is important to be aware of human anatomical variations of this accessory muscle for a range of clinical applications.
	A Human Case Study of a Rare Morphological Variation of the Liver

53*	**Natalie Reynolds, Makenna Mizell, Dr. Amandine Eriksen** The liver is consistently found in the upper right quadrant of the abdomen. It is typically composed of four lobes; however, morphological variations are very common. Some of the more frequent variants have been studied more thoroughly; however, many of the rarer variants have been documented in only one or two living individuals per variant. As a result, the full spectrum of hepatic morphology is likely broader than the literature suggests. Due to natural human anatomical variation, and because phenotypic expression differs across individuals, no two variants appear exactly the same. The rarity of documented cases for individual variants, combined with the limited research on the physical liver (as opposed to image-based studies), constrains comprehensive and comparative investigations. However, these variations are important to understand and visualize, especially for clinicians performing imaging studies and hepatobiliary surgeries. Here, we present a case study of a liver found in a dissected human donor from the University of Indianapolis Gross Anatomy lab that veers from typical liver morphology in multiple ways. These differences include deviations in hepatic surface anatomy and blood supply. Recognizing the range of liver variations, and the possibility that multiple congenital anomalies may coexist in one individual, broadens our understanding of anatomical diversity. Because liver variations are normally only seen via MRI and CT scans on living individuals, finding an example on a human decedent indicates that different variations in living individuals may occur at higher frequencies than previously thought. In summary, this finding provides researchers and clinicians an additional means to visualize liver variation, as it would appear in the human body.
54	An Anatomical Dissection Case Study of a Rare Left Pleuro-Pericardial Cyst in a 90+ Year Old Donor **Peytin Penny, Kendall Thor, Mattie Gragert, Dr. Amandine Eriksen** Known by several names, pleuro-pericardial cysts affect approximately 1 in 100,000 individuals. Defined as an abnormal growth of the mediastinum, or middle thoracic cavity, a pleuro-pericardial cyst is a rare congenital defect that occurs when the pleural (lung) and pericardial (heart) cavities improperly fuse during development. However, research also cites external thoracic trauma, cardiothoracic surgery, and infection as contributing to the emergence of such cysts. Despite the first reported case appearing in 1854, there is minimal knowledge regarding pleuro-pericardial cysts, their clinical manifestations, and methods of treatment. Likely due to incidental findings in asymptomatic patients—around 50-75% of all cases—this has led to discrepancies in statistics and demographic data regarding the phenomenon. However, it is generally accepted that pleuro-pericardial cysts range from 3 to 8 cm in diameter, present more commonly on the right side of the mediastinum (51-70%), and are often diagnosed between the third and fifth decades of life. While these structures are often asymptomatic, symptoms can emerge due to the compression of nearby structures such as the heart and lungs. Common symptoms include persistent cough, shortness of breath, and chest pain/pressure. However, rarer symptoms such as cardiac tamponade, pericardial effusion, respiratory infection, pneumonia, and chronic heart failure can occur, often due to the rapid growth or rupture of the cyst. In the case of a 90+ year old anatomical female in the University of Indianapolis Gross Anatomy Laboratory, a left sided pleuro-pericardial cyst with an approximate circumference of 9.8 cm and a length of 10.2 cm emerged during an anatomy course dissection. Comparing these measurements to those of prior case studies, we predict that this individual likely experienced mild to moderate symptoms due to the size and location of the pleuro-pericardial cyst within the mediastinum.
	A Case Study of a Rare Accessory Muscle in the Human Leg **Amanda Walker, Belle Custodio, Katie Dolen, Dr. Amandine Eriksen** Six muscles are commonly found in the anterior and lateral compartments of the human leg. In the anterior compartment, muscles include tibialis anterior (TA), extensor digitorum longus (EDL), extensor digitorum brevis (EDB), and fibularis tertius (FT). The lateral compartment consists of fibularis brevis (FB) and fibularis longus (FL). The anterior compartment muscles function to dorsiflex the foot and extend the toes, while the lateral compartment everts and weakly plantarflexes the foot.

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The following case study of a routinely dissected human donor from the University of Indianapolis Gross Anatomy Lab presents bilateral accessory muscles in the leg, including a rarely observed muscle inserting on the calcaneus, and the presence of the fibularis digiti quinti (FDQ). We hypothesize that the rare accessory muscle may represent the anterior fibulocalcaneus, an extra muscle observed in a handful of individuals via medical imaging. Based on its location, this muscle would assist in dorsiflexion and eversion of the foot. In contrast, the FDQ appears in 70% of individuals. When present, the FDQ is often observed as a tendon attaching to the FB and may aid in stabilization of the fifth metatarsophalangeal joint, extension, and abduction of the fifth toe. Although some clinical studies suggest that the FDQ may contribute to crowding of structures in the foot and increased susceptibility to tendon pathology, it also offers advantages, particularly in graft harvesting procedures. Awareness of these muscles is important for clinicians performing surgical interventions in the anterolateral leg and dorsal foot, as the ability to recognize accessory muscles may help prevent injury and ensure surgical precision. Although these muscles have been studied, many authors note limited knowledge among clinicians and students regarding their location and function. These

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Assessing patient knowledge and perceptions of physicians, physician assistants, and nurse practitioners in a primary care clinic in Indiana

Yasmin A. Ali, Andrew S. Cale

Introduction

Advanced care providers (ACPs; e.g., nurse practitioners and physician assistants) emerged to address a nationwide physician shortage, especially in rural Midwestern communities. While several studies have analyzed the usefulness of ACPs compared to physicians, little research has assessed the patient perspective and knowledge of their primary care provider options. This study seeks to analyze (1) the public understanding of the scope of practice of various primary care providers and (2) the public perception of the various primary care providers.

Methods

Patients visiting a primary care clinic in Terre Haute, IN were invited to complete a two-part survey assessing their knowledge and perceptions of physicians (MD/DO), physician assistants (PA), and nurse practitioners (NP). This survey included a 10-item multiple choice quiz and 18 perception items.

Results

A total of 45 patients completed the survey. Results of the knowledge survey revealed that participants scored an average of 6.5 ± 0.11 out of 10 possible points. No statistically significant differences in scores were identified based on educational level ($p=0.152$) or healthcare affiliation ($p=0.548$). Overall preference for primary care provider was largely split between physicians (40.0%) and no preference (42.2%). Perceptions data demonstrated willingness to schedule a future appointment with physicians and NPs, with 93.3% of respondents stating they would schedule an appointment again with a physician and 60.0% with an NP.

Conclusion

Overall, most participants demonstrated a reasonable understanding of the differences between primary care providers and had varying perceptions on each, which can be used to guide areas for improvement in patient care for each profession.

HIPAA Noncompliance of Radiologic Images Shared on Social Media

Shreyas Bulusu, Dr. Andrew Cale

57*

Social media platforms allow medical professionals to discuss medical cases or topics relevant to their specialty with a worldwide community of medical experts. However, these platforms are often user-moderated, meaning disclosure of protected health information (PHI) and compliance to the Health Insurance Portability and Accountability Act (HIPAA) may not be strictly regulated. This study evaluated the prevalence of HIPAA-noncompliance radiologic images shared on radiology-related Reddit community pages. In this cross-sectional descriptive study, a web scraper was employed to extract 496 posts from 7 radiology-related Reddit pages. Extracted posts containing medical images were then evaluated for inclusion of 18 different HIPAA identifiers, intended purpose and tone, and anatomical regions. Overall, of the 496 posts extracted, a total of 173 posts (34.9%) contained radiologic images. Fourteen image-based (2.82%) contained visible HIPAA identifiers, such as geographic data or medical record numbers. Among image-based containing posts, 50.3% included the original poster's own medical images, followed by 38.7% of patient posts for discussion. The predominant tone was questioning or diagnosis (53.8%), followed by neutral or informative (42.2%). Frequently represented anatomical regions included the spinal cord, chest, pelvis, brain, foot, knee, and hand. The presence of even a small percentage of HIPAA identifiers within Reddit posts shows the privacy risk that people can experience with publicly accessible medical imaging forums. This emphasizes the need for stronger awareness and safeguards that further restrict radiologic image sharing.

58*

Food Is *Medicine*: Medically and Culturally Tailored Food Preferences

Alyssa Reinoso, Kyle Geller, Laura Szyld, Haleigh Kampman, Dr. Deanna Reinoso

Introduction: Food insecurity has been linked to poor health outcomes and multiple chronic conditions including heart disease, cancer, diabetes, and obesity, as well as premature death. To address this health-related social need, health systems are increasingly integrating food pantry and nutrition resources into clinical care. This study sought community input using self-administered surveys to understand household food preferences, addressing existing gaps in literature. Results from this study can help inform health systems' abilities to medically and culturally tailor food programming.

Methods: In this observational study, food-insecure individuals accessing co-located food pantry resources within a safety-net health system were surveyed to ascertain medical and cultural food preferences. Paper surveys were administered and collected at clinical and integrated food pantry settings from February 2022 to March 2026. Surveys included closed- and open-ended questions and were available in English, Spanish, French, Haitian Creole, and Arabic. Descriptive statistics, including counts and frequencies, were used to identify individuals' preferences within different food categories (e.g. carbohydrates, proteins, dairy, etc.). Food preferences were also stratified by key participant and household characteristics.

Results: Of 1,422 participants surveyed, most identified as Black/African American (n=663, 46.6%) and Hispanic/Latino (n=529, 37.2%). 53.4% of participants (n=760) had at least one chronic condition, and 26.2% (n=372) reported 2 or more chronic conditions. The more prevalent chronic conditions included diabetes (24.2%, n=344), hypertension (21.9%, n=312), depression/anxiety (15.8%, n=224), and obesity/overweight (12.4%, n=176). Overall, 16.9% (n=241) reported having dietary restrictions, with the top dietary restriction being pork, and top preferred foods included beans, chicken, rice, bananas, and carrots.

Conclusion: Health systems could better address food insecurity by evaluating household food preferences and health needs. This study's findings can help guide food and nutrition procurement and programming to medically and culturally tailor foods based on the community served.

A Recruitment Process for the Perinatal Lifestyle Drivers Study that Leverages the Indiana Community Learning Health System

Armando Peña, Raquel Marquez, Cicely Overton, Sirle Vasquez, Erin Phillips

59	**Introduction**: Our team is recruiting pregnant women with obesity in a longitudinal study by leveraging the Indiana Community Learning Health System (LHS). Here, we describe our recruitment process and up-to-date results for this study whose purpose is to understand the drivers of maternal lifestyle behaviors (nutrition, physical activity, infant feeding) during the perinatal period. **Methods**: Regenstrief Data Services provide research staff with a list of potentially eligible women in Eskenazi Health's EHR who meet eligibility criteria based on ICD-10 codes for: pre-pregnancy BMI⩾30kg/m^2, ⩾18 y age, expected to deliver at Eskenazi Health, and 20-32 wk gestational age at enrollment. Patients are contacted via MyChart and followed up the next day with a phone screen. A virtual pre-informed consent call is scheduled via Zoom to establish rapport and deliver the study information in a digestible manner via power point slides with photos of study personnel they will encounter, equipment used, explanation of risks and benefits, etc. A full informed consent visit is scheduled prior to the first interview in person or virtually and delivered in English or Spanish. Consent is provided through electronic signature via REDCap. Once consent is provided, we proceed with the first interview. **Results**: Our first data pull included 251 patients. Of those patients, 165 women have been contacted via MyChart messages; 95 women were excluded with top three reasons as "Not pregnant" (N=35), "No longer 20-32 wk gestation" (N=33), and "Enrolled in another study" (N=7). We have scheduled 42 phone screens and 22 pre-informed consent calls. To date, 11 women have been enrolled in the study—a 16% enrollment success rate from patients eligible after EHR screening (N=70) and 26% after phone screening (N=42). **Conclusions**: Recruiting women with pre-pregnancy obesity through the Indiana LHS is feasible. Identifying other recruitment outlets may increase phone screen and enrollment rate.
60*	Characterizing the Literature of Associations Between Appetite-Related Hormones, Appetite, and Adiposity in Infancy: An Ongoing Scoping Review **Annelise Stolarz, Drithi Raipet, Dr. Armando Peña** **Introduction**: Targeting reductions in appetite through new generation obesity pharmacologic interventions is proven to produce astounding weight loss results in children and adults. There are data to suggest that appetite-related hormones are dysregulated as early as birth. Understanding the relationships between appetite-related hormones, appetite, and adiposity in infancy is critical for developing effective childhood obesity prevention interventions. We are conducting a scoping review to map the associations between appetite-related hormones, appetite, and adiposity in infancy. **Methods**: We are guided by the PRISM-ScR framework for scoping reviews. Eligible studies are included if they explored associations between appetite-related hormones, appetite, and adiposity among infants <2 y age**.** Hormones of interest include leptin, ghrelin, amylin, cholecystokinin (CCK), neuropeptide Y (NPY), pancreatic polypeptide (PP), anandamide, 2-arachidonoylglycerol (2-AG), insulin, and glucagon-like peptide (GLP-1). PubMed and Web of Science will be used to conduct a search of relevant articles: infant, infancy, neonate, neonatal, toddler, newborn, cord blood, placental cord, baby, appetite, food intake, hunger, cues, eating, eating behavior, feed, hormone, peptide, leptin, ghrelin, amylin, CCK, NPY, PP, anandamide, 2-AG, insulin, GLP-1, adipose, adiposity, adipocyte, fat, and obesity. Two independent raters will filter out duplicate articles and select abstracts and review full texts for eligible articles. A third reviewer will break the tie on any disagreements. For each study, we will record the magnitude of association between hormones, appetite and adiposity and tally the number of significant (vs. non-significant) studies. We will also track study characteristics, including type, design, participant demographics, geographical location, and infant phenotypes. **Anticipated Outcomes:** Appetite-related hormones will be associated with adiposity in infancy and will be altered when comparing high-risk with healthy phenotypes.

Poster Number	Poster Title, Author(s), & Abstracts
61	**Characterizing Total, Regional, and Ectopic Adipose Tissue Fat Content and Diabetes Risk Factors among Youth Using Lancet Commission Obesity Definitions** **Macy Lei Shepard, Claire Cannon, Saida Nassour, Harry H. Hu, Abigail Colburn, Gabriel Q. Shaibi, Armando Peña** **Introduction & Objective:** The field has yet to characterize cardiometabolic disease risk profiles among youth using the new Lancet Commission obesity definitions. We compared total, regional, & ectopic adipose tissue fat content, diabetes risk factors, & adiponectin across obesity phenotypes in youth with BMI ⩾95th percentile. **Methods:** We used baseline data from the Preventing Diabetes in Latino Youth study, which enrolled 117 Latino youth (12–16) with obesity. Guided by the Lancet Commission definitions, Clinical Obesity (CO) was defined as excess body fat (boys >36%, girls >42%) measured by DEXA with ⩾3 metabolic risk factors; Preclinical Obesity (PO) as excess body fat with 0–2 risk factors; & No Obesity (NO) as having no excess body fat. Metabolic risk factors included glucose intolerance (fasting glucose 100–125 mg/dL, 2-hr glucose 140–200 mg/dL, or HbA1c 5.7–6.4%), triglycerides ⩾110 mg/dL, HDL <40 mg/dL, & systolic or diastolic blood pressure >90th percentile. We compared total fat mass (FM) & lean mass (LM) using DEXA; regional adipose tissue (subcutaneous abdominal [SAAT], visceral [VAT]) & ectopic fat depots (hepatic fat fraction [HFF], pancreatic fat fraction [PFF]) using MRI; insulin dynamics (HOMA-IR, insulin AUC, oral disposition index [oDI]); glucose regulation (1-hr glucose); & serum adiponectin (AD). One-way ANOVA was conducted with α=0.05. **Results:** The prevalence of CO, PO, & NO was 40% (N=47), 41% (N=48), & 19% (N=22), respectively. CO & PO had significantly higher BMI percentile, waist circumference, FM, body fat percentage, & SAAT (all $p<0.05$), but not VAT, HFF, or PFF, compared with NO. CO demonstrated higher HOMA-IR & insulin AUC compared to PO & NO & lower AD & oDI, with higher LM, 1-hr glucose, & fasting insulin compared to NO. **Conclusion:** CO is distinguished from PO & NO by greater insulin resistance, hyperinsulinemia, beta-cell dysfunction, & LM. These obesity definitions identify youth with increased cardiometabolic disease risk using subclinical markers.
62*	**Examining Inflammatory Markers as Mediators of Obesity-Induced Reductions in Insulin Sensitivity among Latino Youth** **Zoe Barnsfather, Nicolas Escobar, Houchun Harry Hu, Gabriel Q. Shaibi, Armando Peña** **I**ntroduction: Latino youth are disproportionately impacted by obesity. Pediatric obesity is characterized by excess adipose tissue fat content in regional (viscera, subcutaneous) and ectopic (liver, pancreas) depots. In obesity, adipose tissue secretes pro- and anti-inflammatory markers that mediate reductions in insulin sensitivity. We assessed whether pro- and anti-inflammatory markers mediated the relationship between regional and ectopic adipose fat tissue content and insulin sensitivity among Latino youth with obesity. Methods: Data from 40 Latino youth (12-16 y) with obesity were included in this secondary analysis. Data was collected before and after a 12-week lifestyle intervention and averaged for this analysis. Visceral adipose tissue (VAT), subcutaneous adipose tissue (SAAT), hepatic fat fraction (HFF), and pancreatic fat fraction (PFF) were measured by 3 Tesla quantitative magnetic resonance imaging. Fasting serum was assessed for interleukin-6 (IL-6), monocyte chemoattractant protein-1 (MCP-1), interleukin-10 (IL-10), interleukin-1 receptor antagonist (IL-1RA), and tumor necrosis factor-alpha (TNF-α) by a multiplex immunoassay and adiponectin (Adpn) was measured by enzyme-linked immunosorbent assay. Insulin sensitivity was measured by the Matsuda Index (MI) as estimated by insulin and glucose concentrations collected every 30' from a 2-hr oral glucose tolerance test. A mediation analysis was conducted with logged fat measures as the independent variable, inflammatory markers as mediators, and MI as the dependent variable. Results: VAT, SAAT, HFF, and PFF levels among the cohort were 1326.00±606.26 mL (M±SD), 6786.04±2374.75 mL, 9.38±8.01%, and 4.53±4.07%, respectively. IL-RA was a significant mediator between SAAT and logged MI (indirect effect = -0.357, p = 0.036). IL-6 significantly mediated the

association between PFF and logged MI (indirect effect = -0.064, p = 0.048). There were no other significant mediation effects from other inflammatory markers.

Conclusion: Some inflammatory markers mediated the relationship between adiposity and insulin sensitivity among high-risk Latino youth. Whether these relationships are causal warrant rigorous trials.

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Evaluating Pragmatic Estimates of Insulin Sensitivity Against the Hyperinsulinemic Euglycemic Clamp in Early and Late Pregnancy

Shiv Patel, Andrew Stanford, Dr. Patrick Catalano, Dr. Armando Peña

Introduction: Measuring insulin sensitivity before and during pregnancy is vital for assessment of gestational diabetes risk but is not routine due to low pragmatism of accurate methods. We evaluated clinically practical estimates of insulin sensitivity against the gold standard hyperinsulinemic euglycemic clamp before and during pregnancy.

Methods: This is a secondary analysis of 22 pregnant adult women (age 30.7 ± 3.9 y). Each participant completed both a 3-hr Oral Glucose Tolerance Test (OGTT) and the hyperinsulinemic euglycemic clamp within several days and at 3 time points: pre- (0 wk gestational age), early (12-14 wk) and late (34-36 wk) pregnancy. Insulin sensitivity was measured by the clamp technique (IS_{CLAMP}) ([glucose infusion rate+endogenous hepatic]/mean insulin at last 40'). Insulin sensitivity from the full OGTT (IS_{OGTT}) is estimated with fasting (0') and post-OGTT (30', 60', 90', 120', 180') glucose (G) and insulin (I) concentrations: $10000/\sqrt{I_0*G_0*I_{Mean}*G_{Mean}}$. Abbreviated IS_{OGTT} estimates use reduced sample timepoints to calculate IS_{60}, IS_{120}, and $IS_{60,120}$. Homeostatic model assessment-insulin resistance (HOMA-IR) was calculated as $I_0*G_0/405$. Pearson correlation analysis compared estimates with IS_{CLAMP}. Changes in estimates were assessed between NGT and GDM using covariance pattern models.

Results: Only when adjusting for maternal age, the full IS_{OGTT}, IS_{60}, and $IS_{60,120}$—but not IS_{120}— were significantly and positively associated with IS_{CLAMP} (r range=.567-.482, p range=.014-.013). Without adjustment, IS_{OGTT} and all abbreviated estimates were significantly associated with IS_{CLAMP} in early pregnancy (r=.709-.587 and p<.001-.008). In late pregnancy, all abbreviated IS_{OGTT} estimates were significantly associated with IS_{CLAMP} (r=.592-.435 and p=.006-.029) with no association using the full IS_{OGTT}. Changes in IS_{60} most closely resembled changes in IS_{CLAMP}.

Conclusion: OGTT-based estimates of insulin sensitivity before and during pregnancy are moderately to strongly correlated with IS_{CLAMP} and may be useful in certain research and clinical scenarios.

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Co-designing a Community-Based, Multi-Systems Lifestyle Intervention for Preventing Gestational Diabetes

Saida Nassour, Raquel Márquez, Chelsy Winters, Anna McIntire, Amy Carter, Alisha Jessup, Cicely Overton, Sirle D. Vasquez, Sierra Woods, Erika Henao, Kayliegh Holsapple, Naima Gardner, Tamara Hannon, Deanna Reinoso, Christina M. Scifres, Edmond Ramly, Armando Peña

Introduction: Gestational diabetes (GD) affects 9% of pregnancies in the US, increasing the risk of maternal type 2 diabetes and offspring metabolic abnormalities. Lifestyle intervention is recommended for reducing GD risk, yet the evidence is mixed with a need for innovation in intervention design. We co-designed a lifestyle intervention for GD prevention among high-risk women.

Methods: Our co-design team included key leadership personnel from multiple community health systems in Indianapolis, including a large safety net health system (Eskenazi Health), the YMCA-Greater Indianapolis, the community, and academic institutions. We adapted the core curriculum of the Diabetes Prevention Program (DPP) for adult women (⩾ 18 y) less than 16 weeks gestational age with pre-pregnancy obesity (BMI⩾30 kg/m^2). We integrated findings from our scoping review of GD prevention interventions to inform innovations. The co-design process included 13 sessions to 1-Map referral pathway from Eskenazi to the YMCA-DPP, 2-Develop innovative

implementation strategies, 3-Adapt the DPP, and 4- Finalize the curriculum. We called it the Gestational Diabetes Prevention Program (GDPP).

Results: The GDPP integrates 5 key components across all implementer agencies: a core curriculum (15 total sessions) delivered by YMCA lifestyle coaches, medical nutrition therapy (3 1-on-1 sessions) with Eskenazi registered dietitians (RD), a structured—but flexible—exercise program, a peer navigator, and a bi-monthly peer support group that reinforces curriculum topics. The peer navigator will provide community systems navigation support and lead peer support groups. The GDPP was designed to include intensive social support from multiple levels (e.g., family, community) hypothesized to increase self-efficacy for health behaviors and improve glucose dynamics. The intervention is delivered in a hybrid manner (home/telehealth/in person). We created a rolling schedule aligned with perinatal needs

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Weight Stigma as an Overlooked Driver of Inflammation and Cardiovascular Disease Risk

Kaitlyn Mathews, Madison Pierce-Holtzman, Brooklyn Cline, Lydia Wiersma, Elizabeth Combs, Alexis Quirk, Jenna Schifferer, Bryant Keirns, & Natalie Keirns

In Indiana, cardiovascular disease (CVD) mortality and obesity rates are above national averages. Weight stigma (i.e., negative attitudes about individuals with higher weight) may be an overlooked contributor to CVD in obesity via promotion of chronic stress, especially in women. The goal of this ongoing study is to examine immune and vascular parameters as potential mechanisms linking internalized (i.e., self-directed) weight stigma (IWS) to CVD risk in women with obesity.

Participants are adult women (18-55 years) with high ($\geqslant$30 kg/m^2) or low (18.5-24.9 kg/m^2) body mass index (BMI) and high ($\geqslant$4) or low (<4) self-reported IWS (Modified Weight Bias Internalization Scale, range: 1-7). Participants are grouped as: (1) low BMI/low IWS (CON), (2) high BMI/low IWS (OB-IWS$_{low}$), or (3) high BMI/high IWS (OB-IWS$_{high}$). Participants complete an in-person study visit that includes BMI measurement (InBody), blood sample collection, vascular assessment (flow mediated dilation [FMD]), and an online questionnaire (IWS, demographics). Serum and peripheral blood mononuclear cells (PBMCs) are obtained from whole blood. Total protein is extracted from PBMCs for western blot analyses. Primary outcomes include serum biomarkers of inflammation (C-reactive protein, interleukin-6, tumor necrosis factor-α; forthcoming), NF-κB p65 and phospho-NF-κB p65 PBMC protein expression (forthcoming), and FMD. Preliminary data were analyzed with one-way ANCOVAs adjusting for age and BMI.

Completed participants (N=35/45) are 30.3±10.5 years old and 71.4% White. Mean BMI and IWS scores in each group are: CON (21.7±1.5 kg/m^2, 2.0±0.7) < OB-IWS$_{low}$ (35.0±2.7 kg/m^2, 3.0±0.7) < OB-IWS$_{high}$ (39.7±5.6 kg/m^2, 5.1±0.6) (p's<.016). Between-group differences in FMD are consistent with a non-significant (p=.21) large effect size (η_p^2=.16), with OB-IWS$_{high}$ displaying the lowest FMD (3.0±1.8%). Additional data will be analyzed and presented as available. Preliminary data suggests IWS may be associated with vascular indicators of heightened CVD risk in women.

Assessment of Sex Differences in Urethane-Induced Lung Tumorigenesis in the Four Core Genotype Mouse Model

Maksat Babayev, Omar A. Borges-Sosa, C. Damilola Ekpruke, Erik Parker, Dustin Rousselle, Lydia Dinwiddie, Praveen Chirumamilla, Michelle C. Boulos, Aakash Parekh, Matthew L. Retzner, Dr. Patricia Silveyra

Lung cancer is the leading cause of cancer-related mortality worldwide and remains among the top ten causes of death in the United States. Non-small cell lung cancer (NSCLC) accounts for approximately 85% of cases, with lung adenocarcinoma (LUAD) representing the most prevalent subtype. Notably, sex differences in LUAD incidence and mortality have been observed, particularly among non-smokers, where LUAD is more common in females.

Elucidating sex-specific mechanisms driving LUAD progression is essential for developing precision therapeutic strategies.

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We employed the Four Core Genotypes (FCG) model using ArnoJ mice (C57BL/6J background), in which gonadal sex is decoupled from sex chromosome complement. Mice aged 6–8 weeks received urethane (1 g/kg body mass, weekly for 10 weeks) or PBS control injections and were evaluated after a 20-week tumorigenesis period. Bronchoalveolar lavage fluid (BALF) cytology, body weight changes, and lung histology were assessed.

All urethane-treated animals exhibited increased BALF total cell counts and weight loss relative to controls. Among genotypes, XXM mice (female chromosomes, male gonads) demonstrated the most pronounced weight reduction between urethane and control groups. When comparing urethane- versus PBS-treated mice grouped by chromosome complement, XX animals showed greater weight differences than XY animals. When grouped by gonadal sex, mice with male gonads exhibited stronger weight reduction than those with female gonads. BALF from urethane-treated mice displayed higher total cell counts than PBS controls, with genotype-specific differences. Preliminary analysis suggested that mice with female gonads experienced a greater increase in BALF cellularity than mice with male gonads, whereas no apparent differences were observed between XX and XY chromosome complements. Immunohistochemistry using anti-RAS (Q61R) antibody demonstrated a significant effect of sex hormones on mutated RAS (Q61R) levels independent of genotype ($p = 0.00178$). Ki-67 proliferation indices did not differ significantly among groups. These preliminary findings suggest contributions of both gonadal hormones and sex chromosomes to urethane-induced systemic and inflammatory responses, warranting further histological and molecular characterization of sex-specific mechanisms in lung carcinogenesis.

67*

Bioinformatics Analysis of Gene Expression in Lynch Syndrome Progression

Drithi Raipet

Lynch Syndrome is an inherited condition that primarily increases the risk of developing colorectal and endometrial cancers. It arises from germline mutations in DNA mismatch repair genes, resulting in microsatellite instability and the accumulation of genetic mutations. Individuals with Lynch Syndrome are prone to developing tumors at a young age, yet the gene expression changes that drive the progression from precancerous lesions to early-stage malignancy are not completely understood.

To investigate this, gene expression data from GEO dataset GSE224707 was analyzed using GEO2R, with samples grouped into precancerous, advanced precancerous, and early-stage cancer categories. This analysis identified 296 differentially expressed genes (DEGs) based on log2 fold change thresholds. Of these, 138 genes were upregulated and 158 were downregulated (Figure 2a).

Enrichment analysis using SRPlot identified several significant Gene Ontology terms, including collagen fibril organization, immunoglobulin complex, transaminase activity, protein binding, and growth factor binding. KEGG pathway analysis revealed enrichment in the Hedgehog signaling pathway.

Genes such as ZG16, KIF26B, CA1, CD177, and CXCL14 were commonly differentially expressed and associated with mucosal immunity, cellular migration, metabolic regulation, and immune surveillance. These reflect early structural and immunological shifts in colorectal tissue during Lynch Syndrome progression.

This study highlights molecular changes that may serve as early biomarkers or therapeutic targets for Lynch Syndrome–associated colorectal cancer. The findings support future development of gene-targeted therapies aimed at delaying or preventing malignant transformation in high-risk patients.

68*	Investigating the Expression of Cyclin E1 (CCNE1) in Mantle Cell Lymphoma **Faith Sponseller, Chioniso Patience Masamha** Mantle cell lymphoma (MCL) is a subtype of non-Hodgkin lymphoma that arises from B cells in the mantle zone of lymphatic nodules. The aggressive form of MCL is typically diagnosed at an advanced stage and has no standard treatment, with a median survival of about 3 years. The initiating lesion in MCL is translocation of CCND1, causing abnormal expression of the cell cycle oncogene cyclin D1. CCND1 pre-mRNA undergoes alternative polyadenylation (APA), producing mRNA transcripts with identical open reading frames (ORF) but different 3' UTR lengths. APA-driven shortening of the 3' UTR allows evasion of miRNA regulation, hyperproliferation, and decreased survival in MCL patients. During the G1 phase of the cell cycle, cyclin D1 binds to CDK4/6 to phosphorylate retinoblastoma protein (Rb), followed by cyclin E1 (CCNE1) binding CDK2 to hyperphosphorylate Rb, and drive cell cycle progression to the S phase. Our goal was to determine the role of APA in CCNE1 expression in MCL cells. Cyclin E1 is an oncogene whose overexpression has been previously associated with other cancers. In order to detect CCNE1 at the mRNA level, RNA was extracted from human MCL cell lines, and primers were designed to target different regions of CCNE1. After primer validation, 3' RACE was used to target the ORF and distal 3' UTR. Following TOPO cloning, cell transformation, and plasmid DNA extraction, samples were sent for Sanger sequencing. The sequencing results determined that CCNE1 uses the polyadenylation signal AATAAA in APA and identified an alternatively spliced isoform with an exon 7 deletion, eliminating the centrosomal localization signal (CLS), arising from alternative promoter usage. This isoform encodes a protein called cyclin ET that has been found in other types of cancer. Loss of the CLS causes genomic instability and dysregulation of the cell cycle, potentially contributing to MCL oncogenesis.
69*	In Vivo Modulation: The Real Time Monitoring of Vascular Implants by Utilizing Optic Fiber-Based Cardiovascular Stents **Palak Jha, Soumya Chaudhary** The purpose of this study was to evaluate the effectiveness of a prototype optic fiber–based cardiac stent. The objective was to simulate physiological conditions of the human body, specifically those within the coronary artery, in order to assess how the prototype would perform in vivo. Silicone tubes were used to replicate human arteries, and a blood pump was used to simulate blood flow heated to normal body temperature. Optical fibers were attached to 3D-printed stents and inserted into the silicone tube. Controlled amounts of force were then applied to the prototype, and changes in the wavelength and intensity of the light transmitted through the optical fiber were recorded. Measurements related to fiber bending were collected using an optical fiber power meter across all three experiments. To optimize signal transmission and durability, the fibers were coated with epoxy glue, polyethylene, or clear nail polish and submerged in distilled water for varying durations (1 hour, 24 hours, 48 hours, and 72 hours). The results suggest that this prototype may improve the clinical management of myocardial infarction by enabling better monitoring after stent implantation, potentially reducing uncertainty and complications during the post-surgical recovery process. The findings of this study suggested a positive linear relationship between optic power and signal intensity under controlled conditions. Increased external pressures reflect signal instability introduced by mechanical deformation of the fiber, supporting the conclusion that pressure negatively impacts the reliability of optical signal transmission. Overall, the results showed consistent patterns and correlations between the optical power and intensity across conditions such as the control, pressure and optimization; this helped provide insight into how external factors in the body could influence signal transmission in fiber based medical devices.
	RADical Imaging: Stratifying Lung-RADS 0 with Inflammatory Markers

70*	**Vedika Vyas** Lung cancer ranks among the leading causes of cancer-related deaths worldwide. Part of this is the limitations of early screening and delays in accurate diagnoses. To address indeterminate findings on low-dose computed tomography (LDCT), the Lung Imaging Reporting and Data System introduced the Lung-RADS 0 category in 2022. However, its ambiguity often leads to additional follow-up imaging, higher healthcare costs, and prolonged patient uncertainty. This study examines whether inflammatory biomarkers can further stratify Lung-RADS 0 cases to enhance diagnostic accuracy. A retrospective cohort study was conducted using data from 122 patients at IU Health who underwent LDCT screening and received a Lung-RADS 0 classification. Clinical markers, including white blood cell count (WBC), peripheral oxygen saturation (SpO2), and serum albumin, were analyzed using Fisher's Exact Test and multivariable logistic regression to assess associations with diagnostic outcomes. Two-tailed p values within a 95% CI were used to determine association with values of in which the values for SpO2, WBC, and Serum Albumin were 0.0443 (95% CI: 1.1757, 19.140), 0.0181 (95% CI: 1.9731, 42.1664), and 0.1788 (95% CI: 0.6920, 11.9153), respectively. A white blood cell count under 8,000 μL was also strongly linked to cancer diagnosis. Logistic regression further supported these findings, with WBC and serum albumin emerging as the most significant predictors. A decision threshold of 0.40 was applied to improve sensitivity. These results demonstrate measurable associations between inflammatory markers and diagnostic outcomes within Lung-RADS 0. Using inflammatory biomarkers alongside radiologic assessment may reduce inter-reader variability and decrease unnecessary follow-up imaging. While preliminary due to limited complete data, this study supports the potential of inflammatory markers as a tool to improve early lung cancer detection.

Poster Number	Poster Title, Author(s), & Abstracts
71	A Rapid, Reproducible AI-Assisted Tool for Generating Course-Aligned Anki Decks in an Accelerated Biomedical Sciences Master's Program **Martin Matov, Dr. Marsha Desmet** Background: The Marian University Biomedical Science (BMS) master's program is an intensive graduate-level program designed to mimic the rigor of the first year of medical school. This requires students to implement self-directed strategies to manage cognitive load and support retention, all while being time efficient. Anki is a digital flash card program that enables spaced repetition and active recall, but manual flashcard generation is time consuming for students. Here we describe a reproducible and rapid workflow using ChatGPT 5.2 to generate Anki decks that are specifically aligned to course-director objectives and lecture content. Methods: Lecture slides were downloaded as editable PowerPoint files and modified in real time during class to remove identifying information, delete clearly non-testable figures and information, expand on or clarify key points, and condense contextual extra information. After lecture, edited slides were exported as a PDF and provided to a dedicated ChatGPT 5.2 Thinking session with a lecture-specific prompt. ChatGPT then generated two import-ready CSV files per lecture (Basic and Cloze), which were imported into Anki for student use. Results: Across six completed examination blocks, 17,222 total Anki cards were generated from BMS coursework. Mean deck size was 106 cards per lecture (range 32-232). Cards comprised 56% Basic (9,644) and 44% Cloze (7,578). Deck generation required ~3-5 minutes per lecture, and >99% of cards were retained in the decks with only minor edits for clarity or focus. Conclusion: This AI-assisted workflow functions as a scalable learner-support tool to rapidly produce high-yield, objective-aligned Anki decks in an accelerated graduate curriculum, enabling immediate post-lecture studying and scalable-recall practice that is highly customizable to the course information and to individual student needs.
72	From Indianapolis to Nairobi: How the NeoInnovate Collaborative Consortium at Indiana University Indianapolis Creates Award-Winning Global Research Opportunities for Students **Sherri Bucher, Aravind V. Kuruvikkattil, Lalitha Pranathi Pulavarthy, Hrishikesh Bhagwat, Mikayla Tuano, Eddy Odari, Ruben Thuo, Martin Wafula, Celia Kariuki, Saptarshi Purkayastha** Background: Indiana University Indianapolis (IUI) provides transformative research and educational opportunities. The NeoInnovate Collaborative Consortium (NCC) is a multidisciplinary, international coalition of faculty, students, and postgraduate trainees drawn from universities across Indiana, Ohio, Kenya, and India. Co-led at IUI by Drs. Sherri Bucher and Saptarshi Purkayastha, the NCC develops digital health and biomedical device solutions that equip health care workers with evidence-based tools and training. Students at all levels engage in rigorous, internationally collaborative research addressing urgent global challenges. Case Study: NeoSmartML: Preterm birth affects approximately 13.4 million newborns annually worldwide; in low- and middle-income country health facilities, preventable neonatal deaths are frequently attributable to lack of vital signs monitoring or availability of timely, patient-specific clinical data. The NCC developed NeoSmartML, deploying camera modules and optical character recognition (OCR) technology to automate real-time neonatal vital sign extraction from neonatal intensive care unit monitor displays. In close partnership with Jomo Kenyatta University of Agriculture and Technology and clinical staff at Mama Lucy Kibaki Hospital (Nairobi), NCC conducted a 4-day feasibility study demonstrating OCR accuracy of 62.8-91.6% and nurse annotation compliance exceeding 85%, providing foundational evidence for a neonatal risk stratification machine learning model. Educational Impact: The NeoSmartML project engaged students as active and substantive contributors, spanning biomedical engineering, data science, global public health, and clinical informatics. Students obtained real-world, mentored, international research experience. The NeoSmartML poster was one of only 7 recipients of the

Distinguished Poster Award among 256 submissions at the 2026 American Medical Informatics Association annual conference.

Conclusions: NeoSmartML illustrates the depth and breadth of research opportunities available to IUI students. Through structured mentorship, interdisciplinary collaboration, and meaningful international partnerships, the NCC equips students with the skills, global perspective, and experience to make original contributions to science, technology, engineering, and medicine. At IUI, students do not simply study STEM; they practice it, at a global level.

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A STEM Collaboration with Two African American Sistas in the Academy: "More than Me: Exploring the Environments Around Us"

Dr. Rona M. Robinson-Hill, Dr. Crystal H. Morton

In Summer 2021 two African American Sisters in the Academy joined resources to create a two-week STEM experience for 19 girls and three males in grades 6-12 from historically marginalized groups from east central Indiana. The research question, How will the Scholars be impacted by exposure to these authentic experiences and culturally relevant and transformative curriculum? The primary purpose of this STEM experience was for Scholars to learn more about themselves, others, and the world around them; as well as receive college and career readiness. The methods implemented for summers 2022 and 2023 fostered the program director to supervise the implementation of holistic STEM experiences which integrated mental wellness for two-weeks on the campus of a public university in east central Indiana. The Executive and program directors hired two local licensed school teachers and two undergraduate students. The program director facilitated a two-day training program each summer to teach all four participants how to implement culturally relevant and responsive science inquiry lessons. Daily the program director supervised the two-week program that was facilitated by the two licensed teacher and assisted by the two undergraduate students. Some of the experiences the STEM Scholars were exposed to included: inquiry labs experiences; introduction to drone science; cursive hand-writing practice; hair, mind and body care; empowerment through digital media art; manuscript development; health, food and wellness and more. The preliminary results from the Scholars were results from pre/post assessments and results from KWL charts. The Scholars, teachers, and community partners completed exit surveys to determine the impact of the program. The data shows that the program positively impacted Scholars' content knowledge and interest in science and science careers. The data shows a positive impact for the teachers and community partners too.

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Empowering The Community With Environmental Chemistry In The Classroom

Eshaan Patel, Dr.Kamilla Deavers

Lead poisoning poses a significant public health risk from legacy industrial pollution. Contaminated soil, stemming from aging infrastructure and persistent environmental inequities, contributes to ongoing exposure, disproportionately affecting low-income communities, and especially children. Recognizing an urgent need for prevention strategies, a student-led research team at Marian University developed "The Lead Poisoning Prevention Program," an educational outreach initiative that addresses lead exposure risks through school-based learning. "The Lead Poisoning Prevention Program" is a four-session curriculum for students in Pre-K through 8th grade, which incorporates hands-on activities, nutrition education, and environmental science within the realm of education. Instruction focuses on building knowledge and practical prevention strategies. Other topics introduced to students included the sources of lead, the role of a healthy diet in reducing lead absorption, using phytoremediation to sustainably remediate soil lead levels. In addition to classroom instruction, broad outreach efforts were made that mostly included informational booths at community events, where families were engaged in conversations about lead exposure risks, prevention behaviors, testing resources, and information about our four-session curriculum. Across both schools in Indianapolis and community settings, the program has demonstrated student engagement and gained educator support. Soil analyses collected during implementation indicated that nearly 11% (n=101) of student-submitted samples exceed threshold levels, highlighting the presence of environmental lead contamination. Overall, this outreach initiative enhanced environmental health literacy and empowered families and students alike

with actionable, low-cost interventions, underscoring the need for lead exposure prevention effort in the greater Indianapolis area.

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Needs Assessment of 3D-Printed Anatomical Models for Indianapolis Secondary School Life and Health Sciences Education

Dakota R. Merkel, Andrew S. Cale

Introduction High-quality anatomical models are often inaccessible to secondary school teachers (grades 7–12) who teach life and health sciences due to their exorbitant cost. However, 3D-printing can address this educational need by providing a low-cost, readily available, and customizable alternative to commercial models. This needs assessment study investigated Indianapolis secondary school teachers' perceptions of 3D-printed anatomical models to determine how educators can be effectively supported in adopting and using these tools.

Methods Life and health sciences teachers (n=61) from local secondary schools who previously participated in the Indiana University School of Medicine Anatomy Lab Tours program were invited to participate in this study. Participating teachers completed an anonymous online survey consisting of demographic items (i.e., academic degree, teaching experience, current role, learner population), current teaching practices, and perceptions of 3D printed anatomical models. Quantitative data were analyzed using descriptive statistics, and open-ended responses were qualitatively analyzed using content analysis.

Results A total of 23 teachers (38%) completed the survey. All respondents believed that 3D-printed anatomical models would benefit their students, and 91% were interested in using 3D-printed models in their classrooms. Content analysis of open-ended responses revealed that teachers believed 3D-printed models could provide both educational and accessibility benefits, such as improved understanding, visualization, and engagement. Teachers also noted that commercial models were often inaccessible and less useful due to price, availability, and inaccuracy. The most requested anatomical models included the heart, brain, digestive organs, and lungs, with ideally five copies of each model.

Conclusion These findings suggest that Indianapolis secondary school teachers are both interested in and willing to incorporate 3D-printed anatomical models into their life and health science courses to enhance student learning. Future work will involve leveraging the 3D printing resources of IUSM to meet the educational needs of these educators.

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From Brain to Build Plate: 3D Printing the Cerebral White Matter for Neuroanatomy Education

Salma Kherallah, Dr. Andrew Cale

INTRODUCTION: Recent advances in three-dimensional (3D) printing technology have transformed neuroanatomy education by offering safe, low-cost, durable, and replaceable alternatives to traditional formalin-fixed human brains while maintaining anatomical accuracy. These 3D-printed models enhance visualization and learning of neuroanatomical structures that are technically challenging to dissect and maintain, such as cerebral white matter tracts. This project explored the production of anatomically accurate 3D-printed brain models of the cerebral white matter tracts for neuroanatomy education.

METHODS: To provide an anatomically accurate basis for the 3D models, four donated human brains were dissected using the Klingler method, involving repeated freezing and thawing of formalin-fixed brains. Grey matter was then systematically removed to reveal key underlying white matter structures. Following dissection, the specimens were digitized using Polycam and 3D printed with a Bambu H2D printer using polylactic acid (PLA) filament. Three printer nozzle sizes (0.2, 0.4, and 0.6 mm) were tested to determine the optimal balance between anatomical detail and printing speed. The resulting models were then post-processed with dry-erase paint, allowing learners to actively color and label anatomical structures.

RESULTS: The dissected brains featured clear representations of several key white matter structures such as the corona radiata and arcuate fasciculus, which were replicated in the low-cost 3D-printed models (~$3.21 USD). Multi-angle scanning with Polycam presented technical challenges, particularly with artifacts; however, scanning of one side was sufficient for accurate fiber visualization. Printing with the 0.2 mm nozzle produced the highest quality, though print time increased substantially (>24 hours/model).

CONCLUSIONS: Overall, the 3D models accurately reproduced the cerebral white matter and have the potential to enhance visualization and support active learning. These models offer educators a low-cost, customizable alternative to expensive commercial models. Future work will evaluate the educational efficacy of these models in improving comprehension of the cerebral white matter tracts.

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From Implementation to Impact: Multi-Year Outcomes of Anatomage Table Integration in Anatomy Education

Elizabeth McEntee, Madhumitha Rajendra, Madison Herschberger, Dr. Erica Ausel

This multi-year study explores virtual technology integration in medical education. The Anatomage Table, a stand-alone virtual cadaver device, was implemented across various educational settings at Marian University's Tom and Julie Wood College of Osteopathic Medicine (MU-WCOM) to identify best practices. Using participant action research, second-year osteopathic medical students with prior dissection experience collaborated with the PI to develop supplemental modules for cadaver labs, including MED-612 Essential Clinical Anatomy and Development (ECAD) and BMS522/521 Anatomy, Histology, and Embryology (AHE) in the Biomedical Science Master's (BMS) program. They also facilitated weekly Anatomage Table office hours. To evaluate optimal use of this technology in STEHM education, the project used a validated perspective survey on educational technology integration. Pilot results showed survey responses varied, at times significantly, between student cohorts across six educational dimensions. Preliminary findings suggest students respond more positively to interactive sessions with formative associated assessments, particularly when paired with office hour participation. New survey data from the 2025-2026 academic year continues to support these results, that student perspectives are more favorable when table modules involve active learning, and offer additional insight into perceptions and best practices behind the Anatomage table's use in anatomy education. Overall, the table was positively perceived across all learning domains, especially for Learning Outcomes and Technology statements. Notably, time appears to significantly impact student perspectives. A year after students interacted with the technology in their lab environment, perspectives were significantly more positive across many learning categories. Those who interacted with the technology during open office hours found the technology more difficult to use but that it also enhanced their motivation towards the subject matter. The implications of these results on the educational use of the Anatomage table will be discussed as well as additional survey data collected in early March 2026.

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Charles Bonsett, M.D., 1921-2020, medical historian extraordinaire.

Dr. Richard Feldman, Dr. Tom Bonsett, Dr. Rex Bickers

"History of medicine" and "history of science" enthusiasts are birds of a feather; still, they rarely flock together. The Academy's newly re-established HoS (History of Science) section enjoyed strong participation, for many decades, but it seldom embraced history of medicine. Charles Bonsett, a clinical neurologist / researcher for six decades, was often recognized more as a medical historian and preservationist, virtually unrivaled in both. Yet he never made a presentation before the IAS.

Nevertheless, one can easily imagine this: he would've felt "at home" in the Academy. This poster presentation introduces the HoS audience to Charlie Bonsett... and maybe takes a step towards dissolving unnecessary barriers, separating history of science from history of medicine.

A proud graduate of Indianapolis "Tech" (HS), Charlie viewed his education as "pre-training" to become an Army radio operator. After WWII, he earned a chemistry degree (Butler); next came IU's School of Medicine (class of 1952). He completed neurology residency, then began a blended career: IUSM faculty plus private practice, while combining staff duties and research (mostly Krebs cycle studies in muscle cell cultures) at the "old" Central State Hospital. He directed IU's multiple sclerosis and muscular dystrophy (MD) clinics, but he focused predominantly on children with MD.

When Central State's planned "teardown" was announced, Charlie went into overdrive, seeking to save the "Old Pathology Building." He envisioned its transition to become Indiana's Medical History Museum; mission

accomplished soon afterwards. Creating a Medical History section within the Indiana Historical Society, he directed the (new) publication of Indiana Medical History Quarterly for nine years, 1974-1983, just about singlehandedly. Dodging retirement, he contributed to successfully "resurrecting" and continuing his own research, suspended decades earlier... aiding a clinical trial launch (with Australian collaborators) for a rare genetic MD variant,

Dearly departed in 2020, his story hasn't ended yet.

79

Do Spiders Share More Genes With Humans or Flies? Orthologs Reveal the Answer

Katherine Bowman

Spiders are emerging as important model systems to study an array of biological processes, including developmental patterning, behavior, neurobiology, and the origin of complex traits. With the publication of several recent high-quality spider genomes, it is now possible to create accurate gene orthology maps (i.e. genes derived via speciation, rather than through duplications) between spiders and established bilaterian models. Given the shared ancestral nature of orthologs, these genes provide a powerful framework for phylogenetic reconstruction and functional inference across taxa. This study reports on the pairwise prediction of gene orthologs between the common house spider (Parasteatoda tepidariorum) and two species with rich genomics resources: humans (Homo sapiens) and fruit flies (Drosophila melanogaster). Although flies are fellow arthropods, the exceptionally high speciation rates within Drosophila raised the possibility that extensive lineage-specific divergence might limit ortholog recovery between flies and spiders. To address this, two independent orthology inference tools were applied and their outputs collated to minimize method-specific biases. This study has revealed that P. tepidariorum shares 3,655 single-copy orthologs with D. melanogaster, and 2,924 with H. sapiens. The substantial recovery of conserved genes between spider and fly genomes demonstrates that high speciation rates in Drosophila do not preclude robust ortholog detection. These results affirm D. melanogaster as a suitable comparative framework for functional and evolutionary genomics in spider systems.

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America steps to the world stage with Philadelphia's 1876 International Medical Congress Rubbing elbows with the world's greatest surgeon and some notable Hoosiers

Olivia DeHaven, Dr. Rex Bickers

It was actually the Fifth International Medical Congress, but the U.S. had never before hosted such an event. The centennial celebration required an American "showcase" to greet doctors from around the world. It would ultimately need dozens of adjectives for its many superlatives. Any tabulation would surely begin with its huge publication, Transactions of the International Medical Congress, completed by Dr. John Ashhurst, Jr. in 1877 1143 pages long! Bestowing similar recognition is best reserved for just one other person, fellow Philadelphian, Dr. Samuel Gross, presiding over the Congress. He was also the era's most noteworthy American surgeon.

To his credit, Dr. Gross invited London's Joseph Lister, the world's most noted surgeon, putting him at the top of the organizational chart: Surgery Section President. Lecturing persuasively (then touring the U.S. for weeks after), he seized the opportunity to tell why aseptic surgery was no humbug. Among the audience members was Robert Wood Johnson, representing "S&J" (Seabury and Johnson), a start-up company not yet merged with a smaller company, named Johnson & Johnson. His brothers, James Wood Johnson and Edward Mead Johnson had founded "J&J" two years earlier. Both companies were already in the business of making and selling medicated "plasters" (bandages). All three brothers identified Lister's talks as the inspiration for a total company makeover... to produce sterile supplies. Re-opening the "new" company, they retained the J&J name. In the 1890s, (E.) Mead Johnson chose to spin off, starting a new company focused on medical (mostly infant) nutritional products. He headquartered it in Evansville, Indiana.

Ten attendees at the Congress were Hoosiers. Two, while not as high ranking as Dr. Lister, were nonetheless assigned to prominent roles: Dr. John Shaw Billings, assistant Surgeon to the (U.S. Army) Surgeon General, along with Dr. Theophilus Parvin, an Indianapolis professor of obstetrics.

Poster Number	Poster Title, Author(s), & Abstracts
81	
82	IAS leaders frequently showed an interest in History of Science over the Academy's140 year history and many of them made presentations at the annual meeting. **Dr. Rex Bickers** In 2025, the IAS voted to resurrect its History of Science (HoS) section. Presenters at this 2026 meeting seek to revitalize the field. This poster presentation reviews past Academy leaders who supported HoS. The Academy first established a section on HoS in 1944, following a Council action, appointing section leaders to draft and execute a plan. John S. Wright (Forestry, Purdue) was the first section chair; Charles O. Lee (Pharmacy, Purdue) and Will Edington (Mathematics, DePauw) provided additional leadership. Yet the roots of HoS had already emerged a decade earlier with Edington's seminal presentation "There Were Giants in Those Days." Moreover, there were multiple consecutive Presidential Addresses forty years earlier, 1894-1898, by Wm A. Noyes, Sr., Amos Butler, Stanley Coulter and others; they were possibly the Academy's finest HoS presentations up to WWII. In the gap years, HoS-pertinent Presidential Addresses appeared sporadically (1905-1925). The focus shifted in the 1920s and 1930s, reflected in tributes for the dearly departed Academy members themselves, as its earliest members grew older. In 1936, personal tributes ended, replaced by an annual "Necrology" report (obituaries). Will Edington shouldered that task for over 20 years between 1936 and 1964 (his term as IAS president was 1937). As the 1950s approached, the most prolific HoS contributor ever stepped forward: Stephen Visher, geographer / biographer from Bloomington. Two dedicated husband-wife teams overlapped, carrying the HoS banner from the late 1950s into the 1990s: Fay K. Daily and husband Bill (IAS president, 1958), followed by Gerald and Barbara Seeley of Valparaiso. Primarily in its forty "strongest" years, 151 presentations appeared in the HoS Section. Adding tributes, obituaries and 39 Presidential Addresses that touched on HoS... 311 presentations total were delivered by 168 individuals, 1894-2017. Envisioning a next century of vigorous scholarly Indiana HoS presentations would be a great legacy.
83	Light Scattering Technique for the Study of Molecular Adsorption onto Heterogeneous Colloidal Microplastics **Clayton Snider, Emily Pax, and Mahamud Subir** In aquatic environment, microplastics (MPs) are heterogeneous in respect to size, shape, and composition. In the size range of nano- to micro-meters, MPs exhibit colloidal behavior, that is, they remain suspended in aquatic solution. As a result, they provide sufficient surface area for the adsorption of organic contaminants. Light scattering techniques are common to study various properties of colloids. For example, in the last few decades Second Harmonic Generation (SHG), a laser-based technique, has gained popularity as a method to study molecular adsorption onto colloidal particles. Given that SHG is a light scattering technique, it has been limited to monodisperse particles as the effects of scattering are dependent on the size of the particles. The goal of this project has been to extend the applications of SHG to systems that are heterogeneous in size. We hypothesize that the energetics of adsorption (Gads) of a polydisperse mixture of colloids should produce a matching Gads to that of their monodisperse counterparts as there should be no effect from particle size on the equilibrium of adsorption. The adsorption should be solely dependent on surface properties of the particle. Using styrene-based particles as a model for colloidal MP, we have confirmed that the Gads values of an organic dye for polystyrene MP are consistent for a range of different sized particles, confirming the lack of size dependance for Gads. This study has been done on

	particles in the range of 0.3 m to 1.4 m. In conjunction with size and zeta potential measurements, we have further validated that for four-way mixtures of equal parts by concentration, particle surface area, and particle volume the Gads matches that of the Gads for a monodisperse system. Since the method holds against a polydisperse system, it opens up the possibility to study adsorption onto real heterogeneous microplastic systems.
84*	Paper-Based Microfluidic Devices from Hydrophobic Ionic Liquid for Colorimetric Detection of Disease Biomarkers **Auden DeCaprio, Doondeeshwar Patnala, David K. Bwambok** Microfluidic devices derived from paper are useful for colorimetric detection of disease biomarkers at low-cost. This study explored the use of hydrophobic ionic liquid "inks" to create microfluidic channels and wells on paper. The paper devices obtained by stamping and drawing with hydrophobic ionic liquids demonstrated the ability to direct fluid flow. These methods provide a rapid, single-step process for creating microfluidic patterns on paper. In addition, they are inexpensive and do not require any specialized skills, power or equipment. Such low-cost diagnostic devices are useful for early treatment of diseases particularly in resource-limited regions. We demonstrate the application of these paper-based devices in diagnostics by the colorimetric detection of glucose, creatinine and uric acid in artificial urine.
85*	Enantiomeric recognition of flavor compounds using amino acid-based chiral ionic liquids **Lily Haley, David K. Bwambok** Enantiomers of chiral compounds used in food flavors have different taste properties. For example, D-tryptophan is sweet, and L-tryptophan has a bitter taste. In contrast, L-proline is a sweet food flavor but D-proline is bitter. L-proline is a sweet food flavor, but D-proline is bitter. Another example is the enantiomers of asparagine, in which D-asparagine tastes sweet and L-asparagine tastes bitter. As a result, there is interest in the determination of enantiomeric compositions of flavor compounds used in foods and beverages. Determination of enantiomeric purity is useful in evaluating food quality, determining food product adulteration and differentiating between food flavor additives. In this study, chiral ionic liquids derived from amino acids such as valine were synthesized by anion exchange of chloride ion and anions, including lithium bis (trifluoromethane) sulfonimide. As an example, results obtained from fluorescence measurements showed that the L-valine butyl bis (trifluoromethane) sulfonimide chiral ionic liquid can distinguish enantiomers of chiral fluorescent flavor analytes including tryptophan enantiomers. Enantiomeric recognition of flavor compounds is important in the food industry and pharmaceuticals.
86	Synthesis and Evaluation of Biological Activity of Novel Highly Substituted Pyrroles and Pyrrolidones **Kaitlyn Rochester, Katelynn McPhee, Dr. Liliya Frolova** Pyrrolidones are highly substituted forms of γ-lactams, and they show great promise in the anti-proliferative drug field. Pyrroles are aromatic compounds, but they are similar to pyrrolidones in that they are 5 member nitrogen-containing heterocycles. The formation of pyrrolidones is a multi step reaction. The formation of different pyrrolidone isomers is dependent upon the substituent in the third position of the pyrroline ring. When reacted in ethanol, with an aryl or alkyl sulfonyl group in the third position, the main product is a pyrrolidone with trans orientation of aryl and ketoaryl groups. With alkyl sulfonyl substituents in the third position of the ring, the sulfonyl group attached to the nitrogen is cleaved, while aryl sulfonyl substituents in that position maintain this sulfonyl group. These aryl sulfonyl substituents also show the formation of pyrroles. Possibly due to their planar structure, pyrroles demonstrate a higher activity than their pyrrolidone counterparts when tested against B16 cancer cells. Novel pyrrolidones and pyrroles are both intriguing compounds that we wish to develop and research further.

87	Synthesis and Evaluation of Penta-substituted Pyrrolidones with Ester Group in the Third Position **Jakob Morton, Katelynn McPhee, Kaitlyn Rochester, Dr. Liliya Frolova** Pyrrolidones are highly substituted γ-lactams, which are known for their diverse biological activity. They are five membered nitrogen containing heterocyclic compounds. Many of them have important biological activities and are used widely in biochemistry and pharmacy. The focus of this research is the synthesis of highly substituted γ-lactams with an ester group in the third position of the pyrrolidone ring. It was found that these compounds possess certain antiproliferative activity. The dependence of biological activity from ester alkoxy groups and the position of substituents in aromatic rings was evaluated.
88*	A fluorescent ionic liquid nanosensor for forensic detection of gamma-hydroxybutyrate drug **Will Mawhorr, David K. Bwambok** Controlled substance abuse has significantly increased worldwide, resulting in the need to develop rapid drug screening methods. Most techniques for detecting controlled substances are labor-intensive and require skilled personnel to analyze the results. Gamma-hydroxybutyrate (GHB) is a depressant of the central nervous system. At high doses or taken with alcohol, GHB can result in a variety of intoxicating effects such as unconsciousness and seizures. Since GHB is tasteless, colorless, and odorless, it has been abused by spiking in drinks, leading to memory loss for victims intoxicated with this drug. This study describes the development of a fluorescent ionic liquid nanosensor that can be used to rapidly detect GHB in the field. The ionic liquid sensor is based on a phosphonium cation and fluorescent anion. The addition of GHB to fluorescent nanoparticles resulted in enhanced fluorescence intensity. The sensor could still detect GHB in the presence of interfering species found in drinks, such as lemonade, Coca-Cola, and sweet tea. These results suggest potential applications for using these fluorescent nanoparticles for the on-site screening of GHB in suspect samples.
89*	An ionic liquid nanosensor for dual colorimetric and fluorescent detection of gamma-hydroxybutyrate drug **Donita Wright, David Bwambok** Consumption of controlled substances increased globally and there is need to develop methods for rapid drug screening. Limitations of current detection methods for controlled substances include long analysis times in a centralized laboratory. Gamma-hydroxybutyrate (GHB) is a depressant of the central nervous system at low doses. However, when taken at high doses or taken with alcohol, GHB can result in intoxication leading to unconsciousness and seizures. The abuse of GHB by spiking in drinks has increased because the drug is colorless, tasteless, and odorless. At high doses it leads to memory loss for those intoxicated with this drug. This study describes the development of an ionic liquid nanosensor that can be used for colorimetric and fluorometric detection of GHB in the field. The ionic liquid sensor is based on a methylene blue cation and fluorescent anion. Addition of GHB to the ionic liquid nanosensor resulted in a change in color and fluorescence intensity compared to control samples. The change in color and fluorescence of the nanosensor upon addition of GHB persisted for two days at room temperature. These results suggest potential applications for using these colorimetric and fluorescent ionic nanoparticles for onsite screening of samples suspected of GHB contamination.
	Reaction of Spirooxindoles in the Presence of Trifluoroacetic Acid as a Catalyst **Sam Stucko, Sabrina Stucko, Emma Charles, Dr. Daryoush Tahmassebi, Dr. Liliya Frolova** Compounds containing Isatin and coumarin suPaper bstructures are associated with a wide range of medicinal applications, where a spirocyclic system combines these to provide useful frameworks for

90	developing new molecules. In this paper, the role of trifluoroacetic acid (TFA) in the synthesis of a novel spirocyclic compound carried out in formic acid is explored, and how variations in the volume of TFA influence reaction pathways. Previous results indicate that the catalyst volume strongly affects product formation and overall reaction yield. Product identity was verified by using 13C and 1H NMR spectroscopy. Better understanding and standardization of the role of trichloroacetic acid in this system may allow for similar methods to be applied to other compounds with similar spirocyclic scaffolds.

Poster Number	Poster Title, Author(s), & Abstracts
91	**Natural Product-Based Dye Sensitized Solar Cells in Series** **Arianna Cooley, Kailey Callander, Dr. Meden Isaac-Lam** Dye-sensitized solar cell (DSSC) is a photoelectrochemical system and a low-cost thin film solar cell based on a semiconductor formed between a photosensitized anode and an electrolyte. DSSC contains three components, namely, electrolyte (iodide redox couple: I^-/I_3^-), counter electrode (cathode: carbon or Pt), and photoanode (working electrode - zinc oxide : ZnO, or titanium oxide: TiO_2). The photoanode, which contains a glass layer, a conductive oxide layer (FTO: fluorine-doped tin oxide), TiO_2 film, and dye pigment as the photosensitizer (PS), must possess panchromatic photon harvesting property to excite the electrons from the highest molecular orbitals (HOMOs) to the lowest unoccupied molecular orbitals (LUMOs) of the PS. DSSCs are cost-effective environmentally friendly alternatives to traditional photovoltaics, which require labor-intensive fabrication and harmful materials. This study details the creation and performance of "green" DSSCs using sustainable and readily available materials. The procedure involved coating an FTO plate with TiO_2 (anode) and another with carbon soot (cathode), sensitizing the anode with blackberries, and assembling the components into a sandwich solar electrochemical cell. Anthocyanins from blackberries served as PS selected for their light-harvesting capabilities facilitating charge transfer to the metal oxide electrode. An iodide-triiodide solution regenerated the dye. Performance was evaluated by measuring voltage (mV) and current (mA) under both artificial light and natural sunlight over a three-minute period. Individual plates produced initial voltages up to 459.4 mV, though all cells exhibited gradual voltage decay over time. To assess solar collective power, nine cells were connected in series, generating a voltage of 3.34 V. This output exceeded the 1.76 V threshold required to power an external light bulb, but declined to 2.88 V after 2 minutes. Other photoanodes and dye pigments are being investigated to improve DSSC performance. This research contributes to the development of biodegradable, and renewable plant-derived materials into photovoltaic technology.
92	**In Vitro Photodynamic Assessment of Photosensitizer-Antibiotic Conjugates Against Lung Cancer Cell Line** **Kailey M. Callander, Marisa M. Planera, Arianna F. Cooley, Dr. Meden F. Isaac-Lam** Photodynamic therapy (PDT) is a non-invasive, cost-effective treatment for a variety of conditions, including cancer and bacterial infections. This therapeutic approach utilizes light of specific wavelengths to activate a photosensitizer (PS), a light-sensitive agent. When administered to diseased cells and exposed to light, the PS generates reactive oxygen species and free radicals, which cause oxidative damage and subsequent cell death. Unlike chemotherapy, PDT is highly selective and has low mutagenic potential, thereby minimizing harmful systemic side effects and avoiding damage to surrounding healthy tissues. Chlorins are chlorophyll derivatives that show enhanced tumor localization than normal tissues. Synthesized photosensitizers used in this experiment involve a chlorin conjugated to an antibiotic such as ciprofloxacin. Even though ciprofloxacin is considered an antibiotic, studies indicated its use as an anticancer therapeutic agent. It can trigger apoptosis of cancer cells causing double strand breaks in the nucleic acid sequence. Experiments showed that it inhibits the division of various cancer cell lines of the breast, prostate, skin, lung, liver and pancreas. PDT causes direct cytotoxicity on tumor cells, damage to the tumor vasculature, and local inflammatory response. Preliminary results seem to show that the chlorin-ciproflixacin conjugate may improve phototoxicity of PS in lung cancer cell line A549 compared to the unconjugated chlorin which serves as control. Current studies include optimizing experimental conditions for reproducibility and using other chlorin-antibiotic conjugates prepared in our laboratory for testing the photodynamic biological activity in lung cancer A549 cell line. PDT is beneficial to cancer treatment because it involves very low risks of normal tissue toxicity, resistance mechanisms, and organ function damage. PDT offers a promising alternative approach in an era of a growing

	number of cancer patients.
93*	Using UV and Diffuse reflectance spectroscopy to analyze photodegradation of silver doped nickel tungsten as nanostructures **Jordan Smith, Emmanuel Albert Mensah, Max Thompson, Jayla Jordan, Tykhon Zubkov Zhihai Li** Organic Contaminants can be broken down into more rudimentary molecules through the absorption of light photons, termed as photodegradation. Nanoparticles can slightly accelerate the photodegradation process, however, when introducing nanoparticles that have semiconducting properties, they can act as a photocatalyst by lowering the energy that electrons need to cross the bandgap, causing faster oxidation, making the degradation process happen more rapidly. The structure of these nanoparticles were also altered to exhibit a hollowsphere shape, which increases the catalytic capacity due to its larger surface area, further improving efficiency of the photodegradation process. To improve the semiconducting abilities of a molecule, a cocatalyst is inserted on the surface of a material to improve the flow of electrons by providing them an alternative path to travel. This is similar to the term "doping", which is the process of introducing trace impurities to an otherwise pure substance to change its electrical or chemical properties. Silver was used as a cocatalyst and was doped to a nickel tungsten sample at varying percentages. Finally, to measure the success of degradation, UV-Vis spectroscopy was used to measure the change in absorbance, and Diffuse reflective spectroscopy (DRS) was used to measure the bandgap (eV), which is the energy an electron needs to move from the valence shell to the conducive shell, essential in catalytic performance. The correlation between the bandgap and catalytic efficiency in photodegradation will be explored in this study.
94	Investigation of Substrate Tunnel Remodeling as a Generalizable Strategy through Biphenyl Dioxygenase Engineering” **Madilyn Shepherd, Daniel O’Dell, Brayden Burgdoerfer, Corbin Prince, Jordan T. Froese** Rieske dioxygenases, a class of enzyme systems found in soil bacteria, play an important role in the bacterial metabolism of aromatic “pollutants” in their environment. Rieske dioxygenases have long been utilized in organic synthesis due to their ability to catalyze the asymmetric dihydroxylation of aromatics to produce chiral diene-diol metabolites. Despite their utility, the range of potential applications for these green catalysts has been limited by steric and electronic constraints on their substrate scopes and activity. Our work in the Ball State Laboratory for Biocatalysis Research is focused on developing new green-chemical tools in the form of engineered enzymes that operate in aqueous solutions to help attenuate the reliance of the chemical industry on non-renewable energy sources. Our work in engineering improved Rieske dioxygenases has recently demonstrated that remodeling of the substrate tunnel leading to the active site in these enzymes can lead to improvements in activity for valuable substrate classes and that this may be a generalizable strategy for the successful engineering of this enzyme class. Further, our research has identified specific interactions that may be introduced along the substrate tunnel which may facilitate the passage of aromatic substrates into the active site. As this may represent a valuable engineering strategy with applications for all aromatic-metabolizing enzymes, this project seeks to investigate the generality of the methodology. Several residues lining the substrate tunnel in biphenyl dioxygenase were subjected to rational mutagenesis, and the resultant variants screened for improved activity in the asymmetric dihydroxylation of a variety of aromatic substrates.
	Liposome nanoparticles for the delivery of combinatorial therapeutic agents with doxorubicin and IR820 near-infrared ionic dye against cancer

Eric Fettinger and David K. Bwambok*

95*

Combinatorial therapy has gained interest in cancer treatment due to its ability to simultaneously provide chemotherapeutic, photothermal, and contrast imaging agents. In this study, a combinatorial therapeutic agent was synthesized, consisting of IR 820, a near-infrared dye, and doxorubicin (DOX), a chemotherapeutic drug. In addition, the study evaluates the use of liposome nanoparticles as a biocompatible drug delivery agent for the combinatorial therapeutic agent. The liposome nanoparticles containing IR820-DOX have a particle size of 265 nm and a zeta potential of -39 mV as measured using dynamic light scattering. The results from this study demonstrate that these therapeutic agents can be released from liposome nanoparticles by the change in pH and temperature, which leads to tumor cell death by apoptosis and necrosis. These findings highlight the potential for using liposomes for combinatorial drug delivery, leading to improved therapeutic outcomes in cancer treatment.

96*

Metabolomic and Functional Differences Between EDL and SOL Muscles in SUCLA2-Deficient Mice

Clark Chustz, Luna Holley, Jada Radford, Dr. Makayla Lancaster, Dr. Brett Graham

Mitochondrial dysfunction disproportionately affects skeletal muscle, particularly those that require a lot of energy. SUCLA2 encodes a subunit of succinyl-CoA synthetase within the tricarboxylic acid (TCA) cycle and is essential for ATP production. Mutations in SUCLA2 are associated with mitochondrial diseases and muscle weakness. This project aims to study the differences in muscle contraction between extensor digitorum longus (EDL) and soleus (SOL) muscles in mice with SUCLA2 deficiency. It is hypothesized that the oxidative SOL muscle would exhibit greater metabolic disruption than the more glycolytic EDL muscle, potentially contributing to differential contractile impairment.

Lipidomic and metabolomic analyses were performed on EDL and SOL muscles from SUCLA2 knockout (KO) and wild-type (WT) mice. Data were filtered and normalized (low-variance filtering, sum normalization, log10 transformation, and autoscaling) prior to differential analysis (FDR < 0.05).

Results revealed large muscle-type differences. In EDL, 534 ions were significantly altered (327 upregulated, 207 downregulated), with changes driven primarily by lipids (530 lipids; only 4 metabolites significantly different). In contrast, SOL muscle showed 6,066 significantly altered ions (5,649 upregulated, 417 downregulated), including 1,013 lipids and 5,053 metabolites.

These findings demonstrate that SUCLA2 deficiency produces far more extensive metabolic remodeling in oxidative SOL muscle compared to glycolytic EDL muscle. The magnitude of metabolic disruption in SOL suggests greater vulnerability of oxidative fibers to mitochondrial impairment, which may underlie differences in muscle contraction between fiber types. Overall, this study highlights metabolic consequences of SUCLA2 deficiency and their potential functional implications for skeletal muscle performance.

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Computational Modeling and Analysis of Improved Rieske Dioxygenase Variants

Corbin Prince, Dr. Jordan Froese

In the Ball State Laboratory for Biocatalysis Research, we strive to develop new green-chemical tools through enzyme engineering that can contribute to alleviating the chemical industry's reliance on fossil fuels.

With the recent advances in synthetic biology and directed evolution, the potential for engineering enzymes as robust, selective, and environmentally benign chemical catalysts has exploded. Rieske dioxygenases, with their unique ability to perform oxidative dearomatization to produce chiral cis-diol metabolites, have long been utilized as

green-chemical catalysts in bioremediation efforts and by synthetic chemists, although their utility has been limited by their substrate scope and selectivity. In the Ball State Laboratory for Biocatalysis Research, we have applied the tools of enzyme engineering to develop new catalysts based on Rieske dioxygenase scaffolds, which have expanded the chemical utility of this class of enzymes. In order to understand the connection between the beneficial mutations introduced into these engineered enzymes and the observed improvements in activity, we perform the in silico analysis of novel variants we produce. This includes homology modeling, active site cavity analysis, substrate tunnel modeling, docking analysis, and molecular dynamics simulations. These studies have enabled the identification of key structural changes to the enzymes that are induced by beneficial mutations, which inform all future engineering

98*

Investigating exercise to mitigate muscle dysfunction in SUCLA2 KO models within EDL vs SOL

Luna Holley, Clark Chustz, Jada Radford, Dr, Makayla Lancaster, Dr. Graham

Mitochondrial diseases are a group of disorders characterized by reduced ATP production and disrupted cellular energy metabolism. Because skeletal muscles have high energetic demands, mitochondrial dysfunction commonly presents as muscle weakness and exercise intolerance. One cause of mitochondrial disease is SUCLA2 deficiency, which impairs succinyl-CoA synthetase, a key enzyme in the tricarboxylic acid (TCA) cycle that supports substrate-level phosphorylation and overall mitochondrial function. In mouse models with skeletal muscle–specific SUCLA2 deficiency, these mitochondrial defects contribute to altered metabolism and reduced muscle performance.

This project investigates whether exercise can mitigate muscle dysfunction in SUCLA2-deficient mice and whether responses differ between the oxidative soleus (SOL) and the more glycolytic extensor digitorum longus (EDL) muscles. Foundational work for this project demonstrated that while the EDL exhibited minimal phenotypes, the SOL muscle from SUCLA2-deficient mice exhibited reduced force production and slower contraction and relaxation kinetics, along with increased mitochondrial content and lipid accumulation. These findings suggest compensatory metabolic remodeling in SOL, which informed my hypothesis that exercise will improve muscle function in SUCLA2-deficient mice, with greater improvement in SOL compared to EDL due to its enhanced oxidative capacity.

As a preliminary step, computational testing was utilized to form the hypothesis by overlapping previously identified metabolites with metabolites reported in literature from patients with mitochondrial disease. This comparison will help determine whether SOL and EDL display a disease-relevant metabolic signature and whether pathways associated with energy metabolism are differentially affected. These findings will guide future in vivo experiments in collaboration with the IU School of Medicine, including voluntary wheel running, to directly test whether exercise improves muscle function and whether adaptations differ between muscle fiber types.

99*

Tyrosine Nitration of Apolactoferrin by Peroxynitrite Alters Metal Affinity

Jetta Harmon, Dana Ping, and Michael W. Thompson

Lactoferrin (LTF) is a metal-binding protein secreted by activated neutrophils that is thought to limit microbial growth by sequestering essential metals ions and mitigate inflammation by suppressing release of pro-inflammatory cytokines. Inflammation is also associated with increased reactive oxygen and nitrogen species (RONS), such as peroxynitrite ($ONOO^-$), that affect the activities of many proteins and enzymes. The effect of tyrosine nitration by $ONOO^-$ on the affinity for LTF for Fe^{2+}, Fe^{3+}, and Zn^{2+} was determined by spectroscopy and fluorescence titration techniques. Nitrated LTF is still capable of binding Fe^{2+} and Fe^{3+}, but not Zn^{2+}. Neither addition of HCO_3^-, nor elevated temperature (39°C), had any discernable effect on the affinity of LTF for these ions. Determination of secondary structure composition of the protein after

	nitration revealed a total loss of α-helical structure with a compensatory gain in β-sheet
100	"Application of Rational Enzyme Engineering in the Development of Improved Naphthalene Dioxygenase Variants" **Reece Dale, Madison Kasten, Lucy McGovern, Dr. Jordan Froese** In the Ball State Laboratory for Biocatalysis Research, we strive to develop new green-chemical tools through enzyme engineering that can contribute to alleviating the chemical industry's reliance on fossil fuels. Rieske dioxygenases, with their unique ability to perform oxidative dearomatization to produce chiral cis-diol metabolites, have long been utilized as green-chemical catalysts in bioremediation efforts and by synthetic chemists, although their utility has been limited by their substrate scope and selectivity. Our laboratory is applying the tools of enzyme engineering to develop new catalysts based on Rieske dioxygenase scaffolds, which have expanded the chemical utility of this class of enzymes. Our work in engineering improved Rieske dioxygenases has recently demonstrated that remodeling of the substrate tunnel leading to the active site in these enzymes can lead to improvements in activity for valuable substrate classes and that this may be a generalizable strategy for the successful engineering of this enzyme class. Further, our research has identified specific interactions that may be introduced along the substrate tunnel which may facilitate the passage of aromatic substrates into the active site. Using this strategy of rationally remodeling the substrate tunnel to introduce new stabilizing interactions, new variants of naphthalene dioxygenase were engineered and screened for activity for a variety of substrate classes.

Poster Number	Poster Title, Author(s), & Abstracts
101*	**Absence of Brain Glycogen Decreases Incidence of Loss of Righting Reflex during Insulin-induced Hypoglycemia** **Alyssa McDonald, Dr. Bartholomew Pederson, Clayton Harry** Hypoglycemia is a serious complication of insulin therapy and can cause oxidative stress in vulnerable regions of the brain. Previous studies show that reactive oxygen species (ROS) increase during severe hypoglycemia and escalate further after glucose is reintroduced. During hypoglycemia, the brain's primary fuel, glucose, is limiting, and glycogen in the brain has been posited to provide fuel to the brain in pathological situations, such as hypoglycemia. This study examines how insulin-induced hypoglycemia, loss of the righting reflex (LRR), and subsequent glucose rescue contribute to neuronal stress and cell death in genetically modified mouse models. We used mice which have reduced brain glycogen stores, due to disruption of endogenous GYS1, and increased muscle glycogen stores, due to overexpression of a GYS1 transgene, and compared them with wild-type controls. Mice were injected with insulin and were monitored for behavioral and physiological markers of hypoglycemia severity, including LRR, as well as blood glucose and lactate levels. We found that mice lacking brain glycogen had a lower incidence of LRR as compared to control mice with normal levels of brain glycogen. In the future, reactive oxygen species will be measured using dihydroethidium (DHE), and neuronal death will be assessed through histological analysis to determine if brain glycogen plays a role in oxidative stress, and neuronal vulnerability. A better understanding of these mechanisms may help inform clinical strategies to prevent hypoglycemia-induced unconsciousness and reduce neurological damage associated with glucose dysregulation.
102*	**Muscle Glycogen Concentration Predicts Strength and Endurance in Transgenic Mouse Models** **Raina L. Wolf, Olivia P. Glaeser, Avery W. Renshaw, Erikka Hill, Bartholomew A. Pederson** Muscle glycogen is a major energy source during physical activity and plays an important role in sustaining performance. It is a critical substrate during physical activity, supporting ATP production required for contraction. While muscle glycogen is well established as an important energy source during exercise, its specific contribution to muscular strength, coordination, balance, and endurance remains incompletely understood. This study investigated whether increased muscle glycogen levels influence motor performance and stamina using male and female transgenic mouse models (GSL25 and GSL3) that overexpress GYS1, the enzyme responsible for synthesizing glycogen. GSL25 and GSL3 mice have ~2x and 5x higher muscle glycogen concentrations, respectively Motor coordination, balance, strength, and endurance were assessed using standardized behavioral tests over two days. On day one, muscular strength and endurance were evaluated using grip strength and wire hang tests. On day two, motor coordination and balance were assessed using an accelerating rotarod. Muscle glycogen levels were quantified for GSL3 mice before and after exhaustive treadmill exercise. Muscle glycogen levels decreased with exhaustive exercise, with more glycogen used in GSL3 as compared to wild type. However, grip strength, wire hang, and rotarod performance were not enhanced by increased skeletal muscle glycogen levels. This indicates that increased glycogen levels are available for fueling muscle contraction and may reduce the use of other fuels, such as blood glucose. Future studies will examine signaling proteins to investigate mechanisms linking fuel availability to motor performance.
	Development of Improved Cumene Dioxygenase Variants through Substrate Tunnel Remodeling

103	**Madison Kasten, Lucy McGovern, Corbin Prince, Ella Lautzenheiser, Dr. Jordan Froese** Rieske dioxygenases, a class of enzyme systems found in soil bacteria, play an important role in the bacterial metabolism of aromatic "pollutants" in their environment. Rieske dioxygenases have long been utilized in organic synthesis due to their ability to catalyze the asymmetric dihydroxylation of aromatics to produce chiral diene-diol metabolites. Despite their utility, the range of potential applications for these green catalysts has been limited by steric and electronic constraints on their substrate scopes and activity. Our work in the Ball State Laboratory for Biocatalysis Research is focused on developing new green-chemical tools in the form of engineered enzymes that operate in aqueous solutions to help attenuate the reliance of the chemical industry on non-renewable energy sources. Our work in engineering improved Rieske dioxygenases has recently demonstrated that remodeling of the substrate tunnel leading to the active site in these enzymes can lead to improvements in activity for valuable substrate classes and that this may be a generalizable strategy for the successful engineering of this enzyme class. Further, our research has identified specific interactions that may be introduced along the substrate tunnel which may facilitate the passage of aromatic substrates into the active site. This strategy of rationally remodeling the substrate tunnel to introduce new stabilizing interactions with aromatic substrates was applied to cumene dioxygenase, resulting in the development of multiple new enzyme variants with improved reactivity for multiple classes of aromatic substrates.
104*	Physiologic responses of Hypoxia **Avery Renshaw, Dr. Bartholomew Pederson** Hypoxia induces rapid metabolic stress in neonatal mammals, increasing reliance on anaerobic pathways to maintain ATP production. Glycogen serves as a critical energy reserve during oxygen deprivation. We hypothesized that in the case of a hypoxic event, the lack of brain glycogen stores would provide a noticeably detrimental effect to the survivability of mice. This study directly evaluated the effects of hypoxia on brain glycogen levels in 8–10-day-old female mice using a controlled nitrogen (N_2) displacement model. Pups with normal brain or dramatically reduced glycogen levels were exposed to hypoxia while oxygen concentration and behavioral responses were recorded. Physiologic responses were studied to determine the progression of hypoxia in both the control mice and knockout mice where GYSI, the enzyme responsible for synthesizing glycogen, was disrupted specifically in the central nervous system . By comparing the mice with differing brain glycogen levels, this study directly assessed the contribution of brain glycogen availability to neonatal survival during oxygen deprivation. We found that lack of brain glycogen resulted in significantly reduced survival times under hypoxic stress. These findings provide insight into the metabolic vulnerability of the developing brain under hypoxic stress. Accelerated glycogen depletion during hypoxia can lead to energy failure, loss of ion gradient homeostasis, membrane depolarization, and impaired synaptic transmission, seen through the physiologic responses of wandering, tremor, urination, gasping, and death. If glycogen reserves are insufficient or become exhausted, as seen in conditional mice, the developing brain is particularly vulnerable to cellular dysfunction and injury. Thus, hypoxia-induced glycogen utilization represents both a critical short-term protective mechanism and a potential source of metabolic vulnerability in neonatal mice.

105

Analysis of Phytocannabinoid Effects on Macrophages

Radmila S. Stanic, Ava Ackenhusen, Ankurpreet Kaur, Kelly Koester, Michael Medrano, Asba Mehmood, Christopher Rasmussen, Iris Rojas, Alyvia Santiago, Nolan Turoci, Mikaela Williams, Michael I. Zimmer

Phytocannabinoids, including cannabidiol (CBD) and cannabigerol (CBG), influence the immune response yet their specificity and impact on immune cell function remains incompletely understood. To investigate the possible effects of phytocannabinoids on macrophage physiology, we examined cytokine secretions from the J774.1 macrophage cell line stimulated with different phytocannabinoids in the presence and absence of lipopolysaccharide (LPS). Using proteome arrays, our results demonstrate that CBD and CBG effectively and differentially alter macrophage function. Specifically, we identified a reduction in soluble intercellular adhesion molecule-1 (sICAM-1) secretion, a key regulator of immune signaling. To characterize this effect, we explored the dose-response effect of phytocannabinoids by quantitating sICAM-1 secretion via ELISA. Our results confirm a reduction in sICAM-1 secretion upon co-stimulation of J774.1 macrophages with LPS and CBD. These studies provide valuable insights into the role of phytocannabinoids in lessening inflammation and modulating immune cell function.

106*

Brain glycogen does not reduce severity of pilocarpine-induced seizure in mice

Mathilda A. Geyer , Clayton J. Harry, and Bartholomew A. Pederson

Epilepsy is a condition characterized by recurrent and involuntary seizures that can cause harm to the individual. While treatments are available, many people have treatment-resistant epilepsy, necessitating additional treatment options. Seizure requires significant energy and brain glycogen is the only appreciable stored energy source in the brain. Thus, brain glycogen could fuel seizure, potentially increasing severity. Conversely, brain glycogen could provide fuel that aids neuronal survival during seizure. This study aimed to determine if reduction of brain glycogen levels impact seizure severity. Wild-type mice were compared to mice genetically engineered to lack GYS1, the enzyme responsible for synthesizing glycogen. A pilocarpine-induced seizure model of epilepsy was used to determine if seizure outcomes were affected by the amount of brain glycogen present. After intraperitoneal pilocarpine injection, mice were observed for two hours post injection, in order to record the behavioral stages of seizure reached, and two days following the seizure, the brains were harvested and preserved. We found that brain glycogen levels did not have an effect on seizure severity. Future studies will analyze neuronal cell stress and degeneration to determine if brain glycogen has an impact.

107

Evaluating Antioxidant Status of a Ginger- and Curcumin-Supplemented Pesco-Vegetarian Diet Intervention

Annastasia Hutchings, Kaitline Martin, Olivia Terry, Dr. Hisako Masuda

Free radicals are among one of the leading factors that contribute to aging and human disease. Oral consumption of antioxidants has been shown to decrease the amounts of free radicals in the blood cells. In this study, we investigate the effects of a pesco-vegetarian-based diet with the additional consumption of ginger and curcumin supplements on free radical scavenging capacity of blood. Participants between the ages of 18 and 45 were asked to be on the diet for one week. Concluding the weeklong studies, we asked a few participants to return to do a month-long study to gather more insightful data. The antioxidant capacity of blood serum was assessed by reaction with a free radical 2,2-diphenyl-1-picryhydrazyl (DPPH.) A fluorescent microscope was used to determine the extent of protection against DNA damage following the addition of hydrogen peroxide by measuring the intensive mobility of DNA fragments in low-melting-point agar. This presentation will discuss our current progress on these two assays.

108*	**Requirement of Microtubule Stability in Degradation of Aberrant Proteins** **Kaikeyi M. Paxton, Eric M. Rubenstein** Microtubules are cytoskeletal fibers that aid in cell division and in transportation of cellular components, such as proteins. Kar3 is a kinesin-14 motor protein that "walks" along microtubules to perform its primary characterized functions in cell division. Kar3 has recently been found to be required in the degradation of aberrant proteins at the endoplasmic reticulum (ER). Accumulation of such proteins is linked to worsened outcomes in illnesses such as Type II Diabetes or neurodegeneration. It is unknown if stable association with microtubules is required for Kar3's function in protein degradation. Since other functions of Kar3 are dependent upon normal microtubule dynamics, we hypothesize that microtubules are similarly required for Kar3's function in degrading aberrant proteins. In this project, we will determine how perturbing microtubule physiology impacts ER protein degradation in a Saccharomyces cerevisiae (budding yeast) model system. Microtubules will be depolymerized using nocodazole or stabilized using Taxol. Drug treatments will be followed by cycloheximide chase and Western blot experiments to analyze the rates of degradation of model aberrant ER proteins. If the hypothesis is supported, and Kar3's function in degrading aberrant proteins is dependent on microtubule structure and function, we degradation of aberrant proteins will be impaired in cells with destabilized or hyper-stabilized microtubules. This work will allow us to gain a better understanding of the mechanisms of protein quality control that influence outcomes of Type II Diabetes
109*	**DHX36/G4R1 Knockdown Rescues Stress Granule Density in C9orf72 ALS Neural Progenitor Cells** **Chance S. Creviston, Nana Akua Koranteng, Kelsey Slattery, Christiana Whittey, Abbey Wiggham, Dr. Peter K. Todd, Dr. James P. Vaughn, Dr. Yuh-Hwa Wang, Dr. Philip J. Smaldino** A repeat expansion (G_4C_2) mutation to C9orf72 is the most common genetic cause of amyotrophic lateral sclerosis (C9 ALS). The mutation forms extensive G-quadruplexes (G4s) in DNA and RNA. The additional G4 burden in C9 ALS can lead to C9orf72 haploinsufficiency, inhibit RNA metabolism, and produce toxic dipeptide repeat proteins (DPRs). Dysregulated stress granules (SGs) are another hallmark of ALS broadly, including C9 ALS. DHX36 is the primary G4 helicase that unwinds RNA G4s, including C9orf72 G4s, and promotes DPR production. DHX36/G4R1 decreases SG abundance in cancer cells, but it is unknown whether DHX36/G4R1 regulates SG assembly in C9 ALS or in neural progenitor cells. Based on previous work in cancer cells, we hypothesized that DHX36/G4R1 negatively regulates SG assembly in C9 ALS. To accomplish this, we used neural progenitor cells (NPCs) derived from ALS patient iPSCs (one healthy, two C9 ALS, one FUS ALS) to assess the effect of DHX36 knockdown on SG assembly in the presence of oxidative stress. We found substantial differences in cell size between mutant lines, and that mutant ALS lines displayed significantly different SG abundance when normalized to cell area (SG density). DHX36/G4R1 knockdown produced a significant, dose-dependent increase in SG density in one C9 ALS line, partially rescuing SG density to healthy levels. However, this effect was not observed in the non-G4 FUS ALS line. Surprisingly, DHX36/G4R1 knockdown did not significantly increase SG density in healthy NPCs. These data show that DHX36/G4R1 may play a role in SG abundance in neural progenitor cells only under G4 stress, further characterizing it as a potential therapeutic target for C9 ALS.

Poster Number	Poster Title, Author(s), & Abstracts
110*	Polycomb (Pc) and Polycomb group genes (PcG) regulate cardiac patterning by repressing trithorax (trx)-mediated Hox expression in the embryonic heart tube. **Md. Sayeed Abu Rayhan, Sumaiya Islam, Adam J. Farmer, Shaad M. Ahmad, and Kristopher R. Schwab** PcG genes repress the expression of important developmental genes, such as the Hox genes, and antagonize the transcriptional activity of TrxG genes. Recently, we identified trx as a positive regulator of Hox expression and anterior-posterior patterning within the Drosophila embryonic heart tube. For example, trx maintains the expression of abdominal-A (abd-A) in the posterior heart tube, while Pc represses ectopic abd-A expression within the anterior heart tube. Whereas Pc regulation of cardiac Hox expression has yet to be thoroughly investigated in either Drosophila or mammalian models of heart development. To determine the precise roles for trx and Pc activity in Drosophila embryonic heart development, a recombinant trx, Pc strain was generated and crossed to evaluate homozygous trx, Pc mutant embryos. Remarkably, the trx, Pc strain recapitulated the trx phenotype consisting of the absence of abd-A expression and heart-proper patterning. This data suggests that cardiac Hox activity absolutely requires trx-mediated transcriptional activation, whereas Pc activity is limited to repressing ectopic Hox activity. These results broadly implicate an important role for PcG family in cardiac Hox repression. PcG repression can be mediated by the Pc-repressive complex 1 (PRC1), PRC2, and other noncanonical repressive complexes. The investigation of PRC1 and PRC2 genes for aberrant cardiac Hox expression and patterning has identified Sex combs on midleg (Scm) and Polyhomeotic (Ph) as key PRC1 members responsible for anterior cardiac abd-A repression. In contrast, our preliminary screen of the PRC2 genes indicate that these genes may be dispensable for abd-A repression. These findings identify diverse roles of PcG activity regulating cardiac Hox activity and patterning in development.
111*	Reconstructing the Fox transcription factor-regulated modular subnetworks mediating distinct cardiac progenitor cell divisions **M. Rezaul Hasan, Rajnandani Katariya, Kuncha Shashidhar, Mofazzal K. Sabbir, Andrew J. Kump, Mackenzie Steinsberger, Fatih Akgul, Manoj Panta, Kristopher R. Schwab, Mark H. Inlow, Shaad M. Ahmad** Forkhead box (Fox) transcription factors orchestrate conserved cardiogenic processes in both mammals and Drosophila. In Drosophila, the Fox genes jumeau (jumu) and Checkpoint suppressor 1-like (CHES-1-like) coordinate three categories of cardiac progenitor cell division: asymmetric, symmetric, and cell divisions at an earlier stage. Previous work demonstrated that jumu regulates a pathway comprising Polo kinase and the kinesin Nebbish (Neb) to mediate symmetric and earlier-stage divisions independently of CHES-1-like. These findings raised two questions: whether jumu regulates additional effectors that mediate cardiac progenitor cell divisions, and whether such effectors mediate all three categories of cell division or specific subsets thereof. Comparative RNA-seq analysis of wild-type, jumu loss-of-function, and CHES-1-like loss-of-function mesodermal cells identified multiple genes exclusively activated by jumu. Phenotypic analysis of these genes showed that the anilin Scraps (Scra), the citron kinase Sticky (Sti), the kinesin Pavarotti (Pav), and the Rho GTPase Tumbleweed (Tum) are required for all three cell division categories. Notably, scra exhibits dosage-sensitivity; a minimal threshold level suffices for asymmetric division. Pairwise genetic interaction assays revealed that scra acts synergistically with jumu, polo, and neb, but not with CHES-1-like, positioning scra within a jumu- and polo-regulated subnetwork governing symmetric and earlier-stage cardiac progenitor cell divisions. Cardiac mesoderm- and heart-specific RNAi knockdown confirmed that scra functions autonomously within cardiac progenitors to mediate symmetric cell divisions. Furthermore, cardiac mesoderm-targeted ectopic expression of scra partially rescued all three cardiac progenitor cell division defects in jumu-deficient embryos, establishing that scra operates downstream of jumu. Ongoing pairwise genetic interaction

	assays are investigating whether sti, pav, and tum are additional components of this subnetwork, with future qPCR and rescue assays aiming to define hierarchical relationships among these effectors. Collectively, these findings illustrate how a single regulator like jumu can generate diverse developmental outcomes by engaging distinct effector modules to control discrete cellular processes.
112	Investigating the Role of TRAF2 in Chemotherapy Resistance in T-Cell Acute Lymphoblastic Leukemia **Isabella Torres, Dr. James Olesen** T-cell acute lymphoblastic leukemia (T-ALL), a malignancy which stems from the uncontrolled proliferation of immature T-lymphocytes, has a relapse rate of 30% to 50% in adult cases. Chemotherapy resistance in affected individuals presents a difficult challenge for treatments. Approximately 60% of T-ALL diagnoses show an overexpression of T-cell acute lymphocytic leukemia protein 1 (TAL-1), a transcription factor which impairs cell differentiation, thus leading to malignancies. It has been suggested that TAL-1 may transcriptionally upregulate additional proteins that play a crucial role in an anti-apoptotic response to chemotherapy treatment. In order to ascertain the importance of TRAF2 in chemotherapy resistance, a Jurkat cell line will be used as an experimental model. This cell line is associated with T-ALL research because these cells ectopically express TAL-1. TRAF2 expression will be evaluated through quantifying Western blots of whole cell lysates taken from Jurkat cells treated with etoposide at concentrations of 0 μM, 1 μM and 5 μM. Preliminary data suggests that TRAF2 expression may increase in cells treated with 1 μM etoposide, and decrease in cells treated with 5 μM. This may indicate a potential anti-apoptotic role for TRAF2 at lower etoposide treatment, while TRAF2 has no sparing effect at higher etoposide treatment. When evaluating the involvement of TRAF2 on the apoptotic pathway of T-ALL, a better understanding of its innate chemotherapy resistance in T-ALL can be achieved. This project is being conducted to provide insights into potential and better targeted treatments for malignancies such as T-ALL.
113*	Establishing a Genetic Tool to Induce Multinucleated Polyploidy in Drosophila Tissues **Krista Cottom, Daniel Shappard and Takuya Akiyama** Mutations spontaneously occur in organisms due to the inherent instability of the genome. Germline mutations are passed on to offspring and exist in every cell in the progeny. In contrast, somatic mutations alter only the genetic information of a subset of individual cells within an organism, generating genetic heterogeneity within the tissue, known as somatic mosaicism. The acquisition of deleterious somatic mutations within single cells is the first step in many age-related diseases, including cancer and neurodegenerative disorders. Although recent advances in sequencing technology allow us to conduct single-cell whole-genome sequencing to investigate the degrees of emergence of somatic mutations, this strategy is still expensive and time-consuming. To quickly quantify somatic mutation rates at low cost, we recently established transgenic fruit fly lines carrying an exogenous lacZ gene encoding β-galactosidase as a mutation rate indicator at two locations on the second chromosome, and developed a polymerase chain reaction (PCR)-based protocol. In brief, first, we prepared genomic DNA from the mutation rate indicator transgenic lines and then performed PCR to amplify the lacZ fragment. This fragment was cloned into a plasmid vector, which was subsequently used to transform E. coli cells. While bacterial cells carrying the normal lacZ gene produced blue-colored colonies, disruption of β-galactosidase activity due to somatic mutations resulted in white colonies. By counting the number of white colonies relative to the total number of colonies, we calculated the mutation rates. As an initial key step, we examined how aging and gender affect the rate of somatic mutation. In the future, we can leverage this system to investigate how genetic and environmental factors impact genome integrity.
	Elucidating the Effect of Diet on Intestinal Stem Cell Division in the Drosophila midgut

114*	**Devyani Purohit and Takuya Akiyama** Cancer is a complex disease influenced by both genetic and environmental factors. Because two-thirds of cancer mutations arise from DNA replication errors in stem cells, environmental factors that cause tissue damage can act as risk factors by accelerating stem cell division to produce new cells that replace old ones. In the small intestine, the intestinal epithelium is directly exposed to the external environment and is constantly challenged by extrinsic factors, such as diet and the gut microbiome. Here, we used the Drosophila adult midgut to investigate how diet affects the rates of intestinal stem cell (ISC) divisions. The Drosophila midgut is analogous to the mammalian intestine and contains similar cell types. ISCs undergo either symmetric or asymmetric cell division to self-renew or differentiate into two functional intestinal cell types, secretory enteroendocrine cells and absorptive enterocytes. To examine dietary effects on ISC division, 5-6-day-old wild-type (Oregon R) female adult flies were fed seven diets: high-salt, artificial sweetener saccharin, high-sugar, catechin, caffeine, high-fat, and turmeric diets. After 10 days of feeding, the adult females were dissected and stained with an anti-phospho-Histone H3 antibody, a mitotic marker that visualizes stem cell division. While most of the diets did not alter the rate of ISC division, the saccharin and high-salt diets significantly increased ISC division by 1.5-fold ($p<0.05$) and 2.6-fold ($p<0.01$), respectively, compared with the control diet. Our preliminary results suggest that specific diets can modulate the rates of intestinal stem cell divisions, thus potentially acting as cancer risk factors. In the future, in addition to reconfirming our results, it would be interesting to explore how other extrinsic factors, including the gut microbiota and environmental contaminants such as PFAS, affect Drosophila intestinal stem cell division.
115*	Drosophila Spalt genes in heart development and their relevance to human congenital heart defects **Mofazzal K. Sabbir, Karim Zaher, M. Rezaul Hasan, Rajnandani Katariya, Kuncha Shashidhar, and Shaad M. Ahmad** Mutations in the human SALL1 and SALL4 genes, which encode zinc finger transcription factors, are linked to Townes-Brocks Syndrome and Duane-radial ray Syndrome (Okihiro Syndrome), respectively. Both disorders are characterized by congenital heart defects (CHDs), highlighting the essential roles of these transcription factors in cardiogenesis. To investigate the genetic basis of such CHDs, we are studying spalt major (salm) and spalt-related (salr), the Drosophila orthologs of SALL1 and SALL4, drawing on the conserved developmental pathways shared between fruit flies and mammals. A major challenge is distinguishing their individual functions, as salm and salr are adjacent paralogous genes with potential redundancy. To resolve this, we generated null mutations in each gene using CRISPR/Cas9 and combined these with the Df(2L)Exel6029 deficiency, which removes both loci, allowing us to examine their individual and combined roles more thoroughly. In wild-type embryos, the Drosophila heart forms as a tubular structure closed at the posterior end, consisting of two bilaterally symmetrical rows of myocardial cells that align precisely along the dorsal midline. In contrast, embryos lacking spalt activity exhibit striking abnormalities, including misalignment of myocardial hemisegments, aberrant curvature of the cardiac tube, atypical clustering of Tinman-expressing myocardial cells in abdominal segment seven, and incomplete posterior closure. These defects collectively suggest that salm and salr are required for the coordinated cell movements that give rise to a properly formed heart tube. To pinpoint the developmental origins of these defects, we plan to use real-time live imaging to track the spatiotemporal dynamics of cardiogenesis. By elucidating the cardiogenic functions of salm and salr, this work aims to uncover the evolutionarily conserved mechanisms underlying CHDs in Townes-Brocks and Duane-radial ray Syndromes, offering potential insights into the molecular etiology of these human disorders.

116*

Roles for jumeau and Checkpoint suppressor 1-like in alary muscle morphogenesis: expanding the cardiogenic functions of Fox genes

Kuncha Shashidhar, Rajnandani Katariya, M. Rezaul Hasan, Mofazzal K. Sabbir, Brady Matthew Verdon, Shaad M. Ahmad

The heart requires specialized support structures, such as the pericardial ligaments and diaphragm in mammals, to withstand mechanical stress and maintain stability and function. In the fruit fly Drosophila, the evolutionarily conserved analogs of these tissues, the Alary Muscles (AMs), anchor the Seven up-expressing pericardial cells (Svp-PCs) of the heart to the embryonic/larval body wall, ensuring mechanical stability, lumen integrity, and rhythmic function. Forkhead box (Fox) transcription factors are master regulators of heart development, with mutations in four Fox genes linked to human congenital heart disease. Previous studies from our laboratory revealed the conserved functions of two Drosophila Fox genes, jumeau (jumu) and Checkpoint suppressor 1-like (CHES-1-like), in regulating cardiac progenitor cell specification, division, differentiation, and spatial organization. Building on that work, we now find these two Fox genes are also essential for AM morphogenesis. Loss-of-function mutations in either jumu or CHES-1-like lead to truncated, incorrectly attached, or abnormally patterned AMs, suggesting defects in founder cell specification, myoblast fusion and elongation, or attachment site selection. Similar AM phenotypes in embryos mutant for the jumu-activated kinase-encoding gene back seat driver (bsd) suggest these three genes may function in a shared pathway essential for AM development. To elucidate the mechanisms underlying these defects, we propose three hypotheses: (1) incorrect specification of AM founder cells, (2) impaired myoblast fusion and elongation, and (3) defective positioning of AM attachment sites (Svp-PCs) due to errors in Fox-mediated cardiac progenitor cell division. Using phenotypic analyses, genetic interaction assays, and fixed and live imaging with transgenic reporters, we aim to determine which hypothesis is correct. Understanding how Fox genes coordinate cardiac support tissue development in Drosophila will provide insight into conserved pathways that maintain heart integrity in mammals and reveal how subtle defects in pericardial ligaments, the pericardium, or diaphragm may contribute to sudden cardiac failure.

117*

Unraveling the mechanism of Fox transcription factor-driven Polo kinase activation during cardiac progenitor cell division

Rajnandani Katariya, Brelin Dickerson, Abbigayle J. Gamble, Selma Akgul, M. Rezaul Hasan, Kuncha Shashidhar, Mofazzal K. Sabbir, Dr. Shaad M. Ahmad

Forkhead box (Fox) transcription factors are essential for heart development in both mammals and Drosophila. We previously showed that the Drosophila Fox gene jumeau (jumu) mediates cardiac progenitor cell division by upregulating Polo kinase activity. However, transcriptional profiling of flow cytometry-sorted mesodermal cells from wild-type embryos and jumu null mutants revealed that jumu does not transcriptionally regulate polo, suggesting that Fox-mediated activation of Polo occurs post-transcriptionally. A critical step in the posttranscriptional activation of Polo is its phosphorylation by the serine-threonine kinases Aurora B (AurB) and Back seat driver (Bsd). Intriguingly, both aurB and bsd, the genes encoding these kinases, are transcriptionally activated by Jumu, making them promising candidates for mediating Polo activation. While AurB has well-established mitotic roles, Bsd had previously been characterized only in postmitotic Polo activation for somatic muscle morphogenesis, leaving open the possibility that it also functions in cardiac progenitor mitosis. If Jumu utilizes AurB and Bsd to activate Polo for cardiac progenitor cell division, then aurB and bsd mutants should exhibit cardiac defects similar to those seen in jumu and polo mutants. Here, we show that loss-of-function mutations in aurB and bsd reproduce the cardiac progenitor cell division defects observed in jumu and polo mutants, consistent with our hypothesis. To determine whether aurB and bsd mediate Polo activation downstream of jumu, we are conducting genetic interaction and rescue assays. If Jumu utilizes these genes, they should exhibit synergistic genetic interactions with both jumu and polo. Further investigation revealed that bsd does indeed interact synergistically with jumu to mediate cell division. Additionally, cardiac-specific ectopic expression of the candidate gene should partially rescue defects in jumu mutants but not in polo mutants. These experiments will define the mechanism by which Jumu governs cardiac progenitor cell division and advance our understanding of Fox-dependent regulation of Polo kinase activity.

118	p53 inhibits 2-chloroethyl ethylsulfide (2-CEES)-induced centrosome amplification in human osteosarcoma cells (Saos2) **Richard A. Bennett, Jonathon D. Fulkerson** Mustard gas (MG) is a small molecule that was first used as a chemical weapon in World War I. As a powerful vesicant and alkylating agent, it causes painful blisters and macromolecule damage, including DNA, proteins, and lipids, respectively. The DNA damaging properties of MG have been associated with increased cancer morbidity in those exposed to it either on the battlefield or in mustard gas factories. Our previous work (Bennett et al, 2014) shows that MG also disrupts the cells ability to regulate centrosome number. Centrosomes are small, non-membrane bound organelles that direct the equal segregation of chromosomes during mitosis. Cells with more or less than two centrosomes during mitosis can segregate chromosomes unequally, resulting in chromosome instability. We have shown that Saos-2 cells treated with 2-chloroethl ethylsulfide (2-CEES), a MG surrogate, incur a higher level of centrosome amplification and chromosome instability when exposed to subtoxic levels. In this work, we show that the observed centrosome amplification can be inhibited if p53 is reintroduced into the Saos2 cells before treatment with 2-CEES. These data further our studies of 2-CEES-induced centrosome amplification, and may help to shed light on the mechanisms that drive MG-induced cancers.
119*	Assessing the impact of Nicotine during coronary artery vessel development in mice **Kenneth Reed, Dr. Bikram Sharma** Nicotine is a highly addictive stimulant found in tobacco consumed by people worldwide. Nicotine is known to affect cardiovascular health. Most importantly, Nicotine is known to aggravate CAD in adult. However, its role in the cardiovascular development; and in particular, how nicotine impacts coronary vessel development at embryonic stage is unclear. Our lab focuses on elucidating developmental programs that regulate coronary vessel formation and leveraging them to stimulate vessel regeneration in adults. Specifically, we utilize in vivo transgenic mouse models to study molecular mechanisms that drive coronary vessel growth from Sinus Venosus (SV)- and Endocardium-derived progenitors. Our preliminary data show that nicotinic-acetylcholine receptors (nAchRs) are expressed by coronary arteries during developmental stages. However, it is unknown whether nAchR regulates coronary vessel development . We hypothesize that the nAchRs impact the smooth muscle recruitment into developing coronary arteries. In this study, we will test whether nicotine consumption affects the smooth muscle lining, and if so, to what extent. To test this, we will analyze smooth muscle coverage by immunostaining arteries with anti-smooth muscle myosin heavy chain antibody in developing mouse hearts isolated from control (n =5) and nicotine (vape inhalation, n = 5) pregnant dams. We will co-stain samples with VE-Cadherin (to visualize coronary endothelium) and DAPI (nuclei). Immunostaining will be performed in cryosection samples of isolated hearts at two developmental stages: E14.5 (early stage) and E16.6 (late stage). Results from our study will enable us to determine whether nicotine consumption during pregnancy impact cardiovascular development.

Poster Number	Poster Title, Author(s), & Abstracts
120*	**Differential Signaling and Functional Outcomes of APELIN and ELABELA in Venous and Arterial Endothelial Cells** **Rupak Parajuli and Dr. Bikram Sharma** Coronary artery disease (CAD) remains the leading cause of mortality globally, highlighting the need for the development of novel therapies. The apelinergic system, comprising the APJ receptor and its two ligands, APELIN and ELABELA, is a critical regulator of angiogenesis and cardiac development. However, the distinct functional contributions and downstream molecular pathways activated by each ligand remain poorly defined. In this study, we investigated the hypothesis that APELIN and ELABELA elicit divergent signaling profiles through the APJ receptor, leading to differential angiogenic outcomes in endothelial cells. We used human umbilical vein endothelial cells (HUVECs) and human coronary artery endothelial cells (HCAECs) as in vitro model systems to test this hypothesis. First, we analyzed APJ expression in HUVEC and HCAECs using qRT-PCR analysis and found robust APJ expression in HUVECs, but weak expression in HCAECs, demonstrating dominant APJ expression in venous endothelial cells compared to arterial endothelial cells. Furthermore, cAMP assay confirmed that both ELABELA and APELIN stimulate APJ in ECs in vitro and transmit intracellular signaling via $G\alpha_i$-mediated signaling. Using Transwell migration and scratch assays, we observed that 100 nM APELIN and 500 nM ELABELA increased HUVEC migration, in contrast combined ligand treatment reduced the cell migration. Upon single and combined ligand treatment in HCAECs, cell migration was reduced. Western blot analysis further characterized this divergence: APELIN elevated p-$ERK_{1/2}$ in HUVECs, whereas combined ligand treatment reduced $ERK_{1/2}$ activation. In HCAECs, ELABELA elevated p-Akt, while combined treatment reduced Akt phosphorylation. Our preliminary data show similar signaling output via ELABELA and APELIN in ECs. However, we observed differences in APJ-mediated signaling output between venous versus arterial endothelial cells. These findings advance our fundamental understanding of the Apelinergic system and its regulation of endothelial cell biology.
121*	**Oxidative Stress Reveals Distinct Roles of FSHR-1 and its Ligands in C. elegans** **Joshua R. Gerber, Alexandra Alva, Jennifer R. Kowalski** Oxidative stress is due to the build up of reactive oxygen species (ROS) which occurs when the body cannot detoxify them efficiently. ROS are produced by both normal metabolic processes and immune responses. Oxidative stress contributes to tissue aging, particularly in the nervous system, and can lead to neurodegenerative disorders, such as Alzheimer's and Parkinson's disease. While the body has oxidative stress response systems to protect cellular function, their molecular pathways remain incompletely understood. We are investigating how neuromuscular function is regulated under oxidative stress in the model roundworm C. elegans. We found that FSHR-1, a receptor protein that regulates both oxidative stress responses and neuronal function in many organisms, is required for maintaining normal neuromuscular function under both normal and oxidative stress conditions. Two glycoproteins, GPLA-1 and GPLB-1, which have homologs in humans, are known ligands for FSHR-1 and may bind as a heterodimer. We hypothesized FSHR-1 works with GPLA-1 and GPLB-1 to promote neuromuscular function. Here, we show gpla-1,gplb-1, and fshr-1 work in a common pathway to regulate neuromuscular signaling, measured via body bending in liquid, under normal physiological conditions. However, under chronic, low-level oxidative stress, gpla-1 appears to work in a separate pathway from fshr-1 and gplb-1. Together, these data support a model in which FSHR-1 may

interact with distinct ligand combinations under different physiological conditions. Future studies will explore the mechanisms for this differential regulation, which may provide insight into stress-related hormonal control of nervous system function in humans.

122*

Intestinal regulation of neuromuscular function by the glycoprotein hormone receptor, FSHR-1

Lillian Groves, Areesha Qureshi, Lillian Rademacher, and Jennifer R. Kowalski

Neuronal communication requires a tight balance between excitatory and inhibitory signals (E:I balance), which either increase or decrease the likelihood that receiving neurons will fire additional signals. Misregulation of E:I balance occurs in many neurological and neurodegenerative disorders. Caenorhabditis elegans are used for investigating E:I balance regulation because these microscopic roundworms contain similar neuronal genes and pathways to humans. Our prior data show FSHR-1, the only C. elegans ortholog of vertebrate glycoprotein hormone receptors, is necessary and sufficient in the intestine to promote neuromuscular function. However, the mechanism FSHR-1 uses to signal from the intestine to the neuromuscular junction is unknown. We hypothesize that intestinal FSHR-1 alters neuromuscular signaling by promoting the release of peptides that act on excitatory motor neurons to cause muscle contraction. To test this hypothesis, we performed swimming experiments following tissue-specific depletion of intestinally secreted peptides using feeding RNA interference (RNAi) in wild type worms and in animals overexpressing FSHR-1 in the intestine. RNAi-mediated depletion of several insulin-like intestinal peptides, ins-31, ins-35, and ins-3, leads to reduced motor function even in the presence of intestinal FSHR-1 overexpression. We are now testing if the knockdown of other non-insulin peptides will also cause reduced swimming behavior. Additionally, we are measuring intestinal peptide release in animals with intestinal FSHR-1 over- or under-expression by imaging fluorescently tagged versions of the intestinal peptides. Results of this work can help us understand more about gut-brain interactions and inter-tissue regulation of the nervous system which may be relevant to humans.

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Targeted Silencing of DHX36/G4R1 in C9orf72 ALS/FTD and Impacts on Stress Granule Abundance.

Nana Akua O. Koranteng, Chance S. Creviston, Kelsey Slattery, Abbey Wiggam, Christiana Whittey, Peter K. Todd, James P. Vaughn, Yuh-Hwa Wang, Philip J. Smaldino

Amyotrophic lateral Sclerosis (ALS) and Frontotemporal Dementia (FTD) are two fatal neurodegenerative diseases often with a common genetic cause consisting of a G_4C_2 hexanucleotide repeat expansion (HRE) in the C9orf72 (C9) gene. This expansion at the DNA and RNA levels forms extensive G-quadruplex (G4) structures that sequester RNA-binding proteins and generate toxic dipeptide repeat (DPR) proteins through repeat-associated non-AUG (RAN) translation. DHX36/G4R1 is the major G4 helicase in human cells. DHX36/G4R1 regulates stress granule formation by targeting and unwinding endogenous G4s. Stress granules are membraneless organelles that form when cells are exposed to stress such as oxidative stress, ER stress or heat shock. Disruption of stress granule dynamics is increasingly implicated in a diverse set of neurodegenerative diseases, including ALS and FTD. We have previously shown that downregulation of DHX36/G4R1 inhibits the production of toxic C9 DPRs, however, its impact on stress granule formation in C9 ALS/FTD remains unknown. This study aims to evaluate the efficiency of DHX36 knockdown on stress granule abundance in C9 ALS/FTD patient-derived neural progenitor cells (NPC). We hypothesize that DHX36/G4R1 knockdown will increase stress granules abundance following ER stress in C9 ALS/FTD cells. Results obtained from the study will help inform the development of DHX36/G4R1-targeted therapies for C9orf72-linked ALS/FTD.

124*

Oncogenic Ras Induces Biomechanical Stress-Mediated EMT in the Drosophila Wing Disc

Kaleigh Kelley*, Ella Moustgaard*, Takuya Akiyama

Carcinoma arises from epithelial cells and is the most common cancer. Epithelial-Mesenchymal Transition (EMT) is a pivotal process that switches benign to malignant tumors, during which epithelial cells lose the cell adhesion protein E-Cadherin, detach from the epithelial tissue, and acquire mesenchymal-like properties. Using the Drosophila wing disc as a model epithelial tissue, we identified a non-canonical action of Ras oncogenic mutations that may facilitate EMT in a unique way. Conventionally, Ras oncogenic mutations promote cell proliferation, thereby increasing the likelihood of accumulating additional mutations that facilitate EMT. In contrast, in the wing disc, Ras mutations only altered the tissue architecture by inducing cysts without affecting cell proliferation. Because apical mitotic rounding during cell division is crucial for sufficient physical space for the chromosomes to align correctly during mitosis, we hypothesized that aberrant biomechanical forces emerging from cyst curvature led to insufficient rounding, resulting in defects in cell division. Consistent with this hypothesis, we frequently observed spindle misorientation and cell death within the cyst. Surprisingly, when the cell death pathway was genetically suppressed, these mitotic defects did not result in the elimination of mutant cells but instead, triggered delamination of mutant cells from the epithelial layer, resembling EMT. To examine whether these delaminated Ras tumor cells acquire mesenchymal cell characteristics, we performed immunostaining to visualize expression of the epithelial marker E-Cadherin and the mesenchymal cell marker matrix metalloprotease 1 (MMP1) in the mutant cells. We found that delaminated Ras mutant cells lost E-cadherin expression, whereas some cells expressed MMP1. Our results suggest that, when the cell death pathway is compromised, structural abnormalities caused by Ras oncogenic mutations can drive EMT-like phenomena and thus potentially promote cancer development independent of cell proliferation.

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Elucidating the Molecular and Cellular Mechanisms of Ras-Induced Cyst Formation in the Drosophila Wing Disc

Jaxon Howell, Aliyah Thuis, Nevena Zivadinovic, and Takuya Akiyama

Mutations in tumor suppressor genes and proto-oncogenes within epithelial tissues often lead to cyst formation, suggesting that cysts may be an early morphological hallmark of carcinoma. Although many cysts are benign, their persistence within tissues could contribute to tumor progression. In the Drosophila wing disc epithelium, the Ras Q61H mutation, but not G12V, induces cysts. We recently demonstrated that Ras-induced cysts can promote EMT-like phenotypes, linking structural abnormalities to cancer development. Nevertheless, the molecular and cellular mechanisms by which Ras Q61H oncogenic mutations trigger cyst formation remain unclear. To address this question, we employed inducible Drosophila lines to introduce Ras oncogenic mutations under endogenous regulatory control, generating clones of wild-type control, Ras G12V, and Ras Q61H mutant cells in the wing disc. Our analyses revealed that only Ras-Q61H mutatnt clones exhibit elevated E-Cadherin expression. Based on this observation, we hypothesized that discontinuous E-Cadherin expression contributes to cyst formation. E-Cadherin, a key adherens junction protein responsible for maintaining epithelial integrity, is often found to be elevated in ovarian cancer cysts. Furthermore, gene amplifications and deletions of E-Cadherin, which can produce discontinuous expression patterns, are common in various cancers. Thus, to test our hypothesis, we are currently preparing experiments in which we induce the clones of cells ectopically overexpressing E-Cadherin and examine if its overexpression is sufficient to cause cysts. Given their frequent occurrence across different epithelial tissue contexts, cyst formation may be a widespread, yet underrecognized, driver of tumorigenesis.

Pathways of Protein Degradation and Stress Tolerance During Translocon Clogging

Hailey J Barton, Eric M Rubenstein

126*

Conserved mechanisms of protein quality control that prevent the accumulation of aberrant proteins are important for cellular growth and health. One class of aberrant protein are those that clog endoplasmic reticulum translocons. Translocon clogging arising from translational errors or premature folding disrupts cellular function and has been linked to diseases such as diabetes. The conserved enzymes Hrd1 (an E3 ubiquitin ligase) and Ste24 (a zinc metalloprotease) play important roles in translocon unclogging and protein degradation. We investigated whether the vacuole contributes to cellular homeostasis under conditions of translocon clogging (e.g. by degrading translocon-clogging proteins). Our results indicate that the vacuole does not protect cells against translocon-clogging stress, even in the absence of Hrd1 and Ste24, as loss of vacuole function did not worsen growth defects caused by high-level expression of translocon-clogging proteins. During the course of these studies, we discovered that yeast lacking Ste24 and Hrd1 exhibit a profound growth defect that was worsened at elevated temperatures. Translocon modifications that slow translocation rescued this growth phenotype. Taken together, these results suggest that the vacuole is not a major degradation pathway for translocon-clogging proteins, and that slowing translocation alleviates stress in the absence of pathways that clear clogged translocons. These results are significant for understanding the cellular pathways that clear translocons to possibly discover therapeutic methods for diabetes.

127*

Beyond the Proteasome: Hidden Sources of Peptide Degradation

Cole J. Shifferly, Nhan V.T. Huynh, Mawuli Nevis, Henry Giesel, Mason J. Naaman, William S. Keeling, Walter R.P. Novak, Erika B. Sorensen

Protein homeostasis (proteostasis) describes how cells maintain a balance between functional and damaged proteins. Enhanced proteostasis is associated with longevity, whereas decreased proteostasis results in the accumulation of dysfunctional proteins, which contribute to neurodegenerative diseases. One way that organisms clear dysfunctional proteins is using a cellular machine called the proteasome. We studied proteasome activity in C. elegans, a nematode worm that serves as a widely used model for aging and neurodegenerative disease. We assessed proteasome activity using fluorogenic peptide substrates in lysates derived from mutant animals reported to have elevated proteasome activity at high temperatures and from wild type (normal) worms. We found that peptide degradation was elevated at higher temperatures regardless of genetic background; however, we suspected that some of this degradation was due to small proteolytic enzymes (proteases) rather than the proteasome because we could fully inhibit cleavage in lysate using a protease inhibitor cocktail (PIC). We identified four potential candidate proteases responsible for this non-proteasomal cleavage and tested their contribution using gene depletion (RNAi) or knockout mutants. Our fluorogenic peptide cleavage assays confirm reduced peptide cleavage when some of these enzymes are compromised. Moreover, qRT-PCR analysis reveals that mutant worm lysate with the highest fluorogenic protein cleavage activity exhibit increased expression of these proteases. Clarifying how proteases and proteasomes differentially contribute to peptide cleavage will help guide researchers using peptide-based assays to measure proteasome activity.

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Who's Cleaving What? Defining the Enzymes Behind CT-L Activity in C. elegans

Hugh T. Ford, Walter R.P. Novak, Erika B. Sorensen

Healthy cells maintain protein homeostasis (proteostasis) by balancing protein synthesis and degradation to prevent the accumulation of damaged or misfolded proteins, a hallmark of age-related diseases such as neurodegeneration. Using C. elegans, a nematode model widely used in aging studies, we measured chymotrypsin-like (CT-L) proteolytic activity in whole-animal lysates using a fluorescent peptide substrate. Consistent with previous work, we observed that mutant animals exposed to high temperatures exhibited increased CT-L activity relative to wild type worms. This activity was fully inhibited using either a proteasome inhibitor (Bmib) or a protease inhibitor cocktail (PIC). By testing individual PIC components, we determined that the majority of observed CT-L activity in lysate was likely due to serine proteases. Using bioinformatic analysis, we identified four candidate serine proteases that we predicted could

	cleave the CT-L substrate: lonp-2, svh-1, tpp-2, and K12H4.7. To determine if these enzymes can directly cleave the CT-L substrate independent of other cellular factors, I amplified each gene using PCR and cloned each into the pET-28a+ expression vector for recombinant protein expression. Using these clones, I will express these proteases in E. coli and purify them using nickel-affinity chromatography. Lastly, I will test purified enzymes individually for their ability to cleave the CT-L substrate. These experiments will clarify the source of CT-L activity in C. elegans lysate and enhance our interpretation of
129*	Determining whether hypoxia stimulates DHX36 and SOX17 expression in coronary endothelial cells **Kendra Eller, Rupak Parajuli, Bright Afranie, Ken Reed, Alyx Panoncillo, Lorena Barb, Dr. Bikram Sharma** Coronary artery diseases remain a leading cause of mortality worldwide, and one promising therapeutic approach involves repairing and regenerating damaged coronary vessels. Achieving this goal requires a deep understanding of the cellular and molecular programs that regulate coronary vessel growth. Research has shown that coronary vessels originate from multiple progenitor stem cell pathways stimulated by unique molecular programs. Our lab focuses on elucidating these developmental programs and leveraging them to stimulate vessel regeneration in adults. Specifically, we utilize in vivo transgenic mouse models to study molecular mechanisms that drive coronary vessel growth from Sinus Venosus (SV)- and Endocardium-derived progenitors. One of the key projects in our lab is understanding the mechanistic interactions between hypoxia, DHX36, and SOX17 in the regulation of coronary angiogenesis. We use VHL knockout transgenic mouse to generate hypoxia gain-of-function. Previous work has shown stunted coronary angiogenesis in SOX17 knockout mice and the activation of SOX17 within the hypoxic regions of the developing mouse hearts. In this study, we will test directly whether SOX17 is activated by hypoxia in the VHL cKO hearts. To study this, we will measure SOX17 expression in hypoxia gain-of-function (VHL cKO) and control hearts. Our preliminary data show that DHX36 is involved in the regulation of coronary angiogenesis. However, its exact mechanism is not known. We hypothesize that DHX36 interacts with hypoxia mediated signaling in a positive feedback manner. In this study, we will test whether hypoxia stimulates DHX36 and SOX17 expression in the developing mouse hearts. We have established the necessary transgenic mouse colony and have successfully optimized the genotyping protocols for CRE, VHL flox, and DHX36 flox mouse lines. We expect to see that hypoxia gain-of-function stimulates both DHX36 and SOX17 expression to regulate coronary angiogenesis in developing mouse hearts.

Poster Number	Poster Title, Author(s), & Abstracts
130	The pseudo-kinase EphB6 receptor can act as a "loser" gene in human cancer cell competition **Masaru Nakamoto, Autumn Underwood, Jelena Kolundzija, Jessica Lumakovska, Chizu Makino-Nakamoto** During cancer development, cancer cells and neighboring non-cancer cells interact with each other and compete for survival. If cancer cells "lose" the competition, they would be eliminated through induction of programmed cell death by surrounding non-cancer cells. Therefore, mechanisms that help cancer cells "lose" the competition for survival are promising targets for future cancer therapeutics. EphB6 is a unique member of the Eph family of receptor tyrosine kinases, in that its kinase domain is catalytically-defective (pseudokinase). Decreased expression of EphB6 is correlated with aggressive tumor characteristics and poor prognosis in many cancers, including colorectal, prostate, breast, and non-small cell lung cancers, malignant melanoma, and neuroblastoma. However, the molecular mechanisms of EphB6-mediated suppression of tumor progression remain largely unknown. In this study, we investigated the function of EphB6 in cancer cell competition. By using human colorectal (COLO-320) and prostate (LNCaP) cancer cells that lack detectable endogenous EphB6, cell lines that stably express wild-type (wt-EphB6) or mutant EphB6 receptors were established and tested in in vitro cell competition assays. When established cell lines were cultured individually (e.g. wt-EphB6–expressing cells only), few cells undergoing apoptosis were observed. In contrast, when wt-EphB6–expressing cancer cells were co-cultured with mock-transfected cells, wt-EphB6–expressing cells facing mock-transfected cells showed significantly increased apoptosis. Cancer cells expressing a truncated EphB6 lacking the cytoplasmic domain or a mutant EphB6 in which all the cytoplasmic tyrosine residues were altered survived without showing increased apoptosis. These results suggest that EphB6 exerts tumor-suppressor functions by acting as a "loser" gene in cancer cell competition and its tyrosine-phosphorylation plays important roles in "loser" signal transduction.
131*	Investigating the Molecular Mechanisms of Ras Tumor Cell Regression in the Drosophila midgut **Dreama Cronin, Connor Wilson, Takuya Akiyama** Mutations in the Ras proto-oncogene are prevalent across various cancers. As a small GTPase, Ras regulates downstream signaling pathways that control cell growth, proliferation, differentiation, and cytoskeletal remodeling. Cancer genome sequencing shows that certain Ras mutations appear more frequently in specific tissues. Nevertheless, the mechanisms driving this tissue selectivity remain elusive. To rigorously examine allele-specific effects in vivo, we generated inducible Drosophila lines to introduce Ras oncogenic mutations under endogenous control. This approach uncovered striking allele-dependent differences in mutant cell dynamics in the adult midgut. Ras G12V mutant cells exhibited a growth advantage over wild-type cells and ultimately took over the intestine. When we induced the Q61H mutation, the mutant cells hyper proliferated and rapidly occupied almost the entire intestinal tissue. However, unlike G12V mutant cells, Q61H mutant cells were subsequently eliminated from the gut epithelium. Our transcriptomic analyses identified two highly expressed genes in Q61H mutant cells: the cGAS-like receptor cGlr1 and Mov10, which encodes a component of the microRNA gene-silencing complex. Based on these findings, we hypothesized that 1) elevated Mov10 expression in the mutant midgut promotes the formation of R-loops, three-stranded structures consisting of DNA-RNA hybrids and displaced ssDNA, by downregulating the expression of Top3β, a key R-loop-resolving enzyme, and 2) R-loop-derived RNA-DNA hybrids activate the innate immune cGAS-STING pathway, leading to mutant cell death. As a key first step, we reconfirmed increased cGlr1 and Mov10 expression in the midgut carrying Q61H mutant cells using RT-qPCR. We are currently examining Mov10 protein expression in the midgut. Although further studies are required to elucidate the molecular basis of Ras-driven tumor cell regression, our findings demonstrate that distinct oncogenic mutations within the same protooncogene can drive divergent outcomes. These differences may contribute to the tissue-dependent Ras mutation patterns and may influence early-stage cancer development.

132*

Establishing a Genetic Tool to Induce Multinucleated Polyploidy in Drosophila Tissues

Haley Lorey, Takuya Akiyama

Both endopolyploidy and multinucleated polyploidy are common features of many cancers. Polyploidy is often associated with tumor progression and poor survival by conferring a fitness advantage, such as enhanced stress tolerance and drug resistance. Nevertheless, how these cellular states provide a fitness advantage to tumor cells remains poorly understood. Further, while a cell with endopolyploidy contains one large nucleus, multinucleated polyploid cells share the same cytoplasm among multiple nuclei. Because the nucleus is generally the largest and most rigid organelle in the cell, these two distinct cellular properties may influence tumor progression in different ways. To rigorously investigate how these two polyploidy states influence tumor development, we use a genetically tractable model, the fruit fly Drosophila. Using the Gal4/UAS overexpression system, we can induce endopolyploidy in Drosophila tissues by overexpressing fizzy-related (fzr). fzr encodes a positive regulator of the Anaphase Promoting Complex/Cyclosome, and its overexpression is sufficient to switch from the mitotic cycle to the endocycle, producing endopolyploid cells. In contrast, due to the lack of a genetic tool, generating multinucleated polyploidy has been challenging. Here, we are generating a new transgenic line to induce multinucleated polyploid cells by overexpressing FAST, a 125-amino-acid Fusion-Associated Small Transmembrane protein from reovirus. Previous studies have demonstrated that exogenous overexpression of FAST promotes cell fusion in mammalian tissue culture systems. We first synthesized a codon-optimized FAST cDNA based on reovirus amino acid sequences. After performing PCR using the synthesized DNA, we are currently cloning the construct into pUAST attB using EcoRI and KpnI restriction enzyme sites for PhiC31-mediated site-specific transgenesis. Following transgenesis, using the GAL4/UAS system, we plan to induce endopolyploidy or multinucleated polyploidy in Ras mutant cells by overexpressing Fzr or FAST, respectively. Our future studies will provide new insights into how distinct polyploid cellular architectures contribute to Ras tumor progression.

133*

Cellular Characterization of Mesenchymal-like Cells Derived from Ras-induced Biomechanical Stress-mediated EMT in the Drosophila Wing Disc

Phillip Bilby, Cameron Jackson, Dr. Takuya Akiyama

Cancer metastasis accounts for approximately 90% of cancer-related deaths. A critical driver of metastasis is the epithelial-mesenchymal transition (EMT), during which tumor cells acquire migratory and invasive properties. Defining the molecular and cellular mechanisms underlying EMT is therefore essential for developing strategies to inhibit metastatic progression. We recently demonstrated that non-canonical effects of oncogenic Ras mutations can promote an EMT-like process in the Drosophila wing imaginal disc. Conventionally, Ras oncogenic mutations are thought to drive tumor progression primarily by stimulating cell proliferation, thereby increasing the likelihood of acquiring additional mutations that confer migratory and invasive abilities. In contrast, in the wing disc, Ras oncogenic mutations only induced cyst formation without affecting the cell cycle. Further, we found that the mutant cells in these cysts frequently exhibited spindle misorientation and elevated cell death. Surprisingly, when the cell death pathway was genetically blocked, these mitotic defects triggered delamination of mutant cells from the epithelial layer, resembling EMT. We are currently characterizing the proliferative and migratory properties of this delaminated cell population using anti-phosphorylated Histone H3 to assess mitotic activity and Sir-Actin to visualize Actin cytoskeletal remodeling. Our ongoing and future studies will demonstrate that Ras-induced structural abnormalities can function as an oncogenic driver that facilitates EMT-like behavior, highlighting a previously underappreciated link between oncogenic mutations, tissue architecture, and epithelial cell plasticity.

Regulation of SYD-2/Liprin Alpha in GABA motor neurons

Sarah Daly, Adalaid Scott, Anna Pressel, Jennifer R. Kowalski

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The balance of excitatory and inhibitory signals is important for proper nervous system function. These signals, which occur at neuronal junctions called synapses, either promote or inhibit neural communication and thus are tightly regulated by many different proteins. Our goal in this study is to determine how a critical synaptic scaffolding protein SYD-2 (Liprin-alpha in humans) is regulated in inhibitory motor neurons in C. elegans. Prior work indicates one potential regulator, the Anaphase Promoting Complex (APC), a conserved cellular enzyme that regulates cell division and neuronal function, may be responsible for the ubiquitination, or protein marking, of SYD-2 for degradation. Another SYD-2 regulatory molecule, UNC-43 (CAM Kinase II in humans), may also regulate SYD-2 synaptic abundance or localization. Prior data suggests UNC-43 might regulate SYD-2 directly or indirectly via association with the APC. We hypothesize SYD-2 in inhibitory neurons is negatively regulated by the APC and/or its associated enzyme UNC-43. We are using biochemical protein analysis and fluorescence microscopy to test effects of these regulators on GFP-tagged SYD-2 levels and ubiquitin tagging in inhibitory motor neurons. Ubiquitinated SYD-2 has been isolated from C. elegans, and we are confirming binding specificity. Additionally, worms lacking unc-43 have a higher density ($p = 0.02$) but lower intensity ($p = 0.04$) of SYD-2::GFP at synapses, suggesting UNC-43 regulates SYD-2 localization rather than abundance. Future experiments will assess APC effects on SYD-2 ubiquitination and the specificity of UNC-43 regulation. Results should provide insight into neuronal regulating

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The Role of Dfm1 in the Hrd1 Translocon Quality Control Pathway

Sudhee Bommineni, Kaikeyi Paxton, James Avaala, Dr. Eric (VJ) Rubenstein

In cells, protein degradation plays an important role in quality control of abnormal proteins. One way in which proteins can behave aberrantly is by clogging endoplasmic reticulum translocons, which can lead to negative effects such as cell sickness, dysfunction and even cell death. Unresolved translocon clogging can worsen diseases like diabetes. Cells have two conserved mechanisms to degrade translocon-clogging proteins. These two mechanisms are mediated by the ubiquitin ligase Hrd1 and protease Ste24. Recent data indicate an ER protein called Dfm1 is required for translocon-clogging protein degradation in the Ste24 pathway. It is not yet clear if Dfm1 is also required in the Hrd1 pathway. In the project, we investigated whether Dfm1 plays a role in the Hrd1 pathway in a Saccharomyces cerevisiae model system. Cycloheximide chase and western blot experiments were conducted to determine the abundance and degradation rate of translocon-clogging proteins that are normally targeted by Hrd1 in yeast lacking Dfm1. We found that yeast lacking Dfm1 showed similar degradation rates as the wild type cells. These results suggest that Dfm1 is not required in a Hrd1 pathway for protein degradation. Identifying proteins that are required for cell degradation may guide the development of improved treatments for diseases like diabetes.

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Elucidating the Molecular Mechanisms Underlying Tumor Cell Expansion in Drosophila Myoblasts

Woasifur Rahman Chowdhury

Oncogenic mutations drive tumorigenesis not only through enhanced proliferation but also by enabling mutant cells to eliminate neighboring wild-type cells based on relative fitness, a phenomenon known as super-cell competition. Ras GTPase regulates cell proliferation, differentiation, and survival, and its oncogenic mutations are prevalent across various cancers. Drosophila myoblasts reside in the adepithelial layers of the notum region of the wing disc and later differentiate into adult flight muscles, providing a genetically tractable in vivo model for sarcoma-like tumorigenesis. We previously showed that oncogenic Ras mutations G12V and Q61H induce super-cell competition in the myoblasts. However, the mechanisms by which these mutations trigger super-cell competition remain elusive. Here, we investigated mechanisms underlying Ras-driven super-cell competition in myoblasts. First, we examined whether metabolic adaptation accompanies clonal expansion. Since rapid expansion may require increased energy, we hypothesized that Ras mutant cells might alter mitochondrial number or induce the Warburg effect marked by elevated Lactate Dehydrogenase (LDH) to meet energy demand. To test this, we employed MitoTracker Red staining

and an LDH-GFP reporter. However, neither MitoTracker Red staining nor an LDH-GFP reporter revealed no difference between wild-type and Ras mutant cells. These results suggest that Ras mutant myoblasts expand and eliminate wild-type cells through distinct mechanisms, prompting us to consider another scenario that Ras mutation may increase cell motility to efficiently spread and expand their territory. Intriguingly, our immunostaining using anti-Matrix Metalloproteinase 1 (MMP1) revealed that 2 or 3 Ras mutant cells within the myoblasts occasionally exhibit an elevated MMP1 expression. As MMP1 degrades extracellular matrix components and is often upregulated in invasive tumors, increasing MMP1 expression even in a few cells may be sufficient to facilitate Ras tumor cell expansion through extracellular remodeling. To explore this further, we are optimizing the live imaging technique to monitor the mutant cell dynamics in myoblasts.

137*

Retinal Vasculature Changes in a Model of Papilledema

Maggie Evans, Nasim Shafiee Nejad, Teri Belecky-Adams

Papilledema is when optic disc swells as a result of elevated intracranial pressure, which can be seen in hydrocephalus, and may lead to progressive vision loss. Complications such as enlargement of the optic disc, venous engorgement, and retinal ganglion cell loss are present in human patients, which are believed to result from buildup of molecules also known as axoplasmic stasis. Some studies have shown the association between vision loss and choroidal neovascular membrane formation, which is demonstrative of the role neovascularization plays in the progressive vision loss often accompanying papilledema. In this study, vasculature changes were assessed on retinal flat mounts at post-natal day 45. Eyes were removed, fixed in 4% PFA, dissected to create 4 petals, and retinas were kept at −20 C in methanol until used for immunohistochemistry. Primary antibody Isolectin-GS IB4, was used to stain vasculature. The retinas were scanned using the Nikon AXR confocal microscope, and z stacks were taken in the central and peripheral retina for each petal. The Isolectin-GS IB4 results were analyzed using NIS Elements software, including GA3 analysis and thresholding using Artificial Intelligence. In animals post-natal day 45, a slight reduction in vasculature volume was observed; however, a larger sample size is required to perform statistical analysis.

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Putting the Puzzle Together: Hyperadhesive Desmosome Protein Complexes in Early Vertebrate Embryonic Ectoderm

Rochelle M. Maxson, Emma Chavira, Gregory F. Weber

Desmosomes are highly specialized cell-cell adhesion complexes required to withstand mechanical stress in tissues constantly facing mechanical load such as the epidermis, the intestine, and the myocardium. Hyperadhesive desmosomes are a specialized intensely strong adhesive form of desmosomal adhesion, uniquely resistant to calcium chelation. These adhesions have been found in mature, differentiated cells and tissues, with impacts to processes of wound healing and various disease states, including pemphigus vulgaris and certain types of cancer.8,24 The existence and potential role of hyperadhesion in proliferative undifferentiated embryonic tissues is largely unknown and would provide mechanistic insight about their formation and regulation. Hyperadhesion can be identified using immunofluorescent staining and microscopic imaging of key protein markers, including heat shock protein 27 (Hsp27) and spectrin. Using embryonic ectodermal tissue from the African clawed frog, Xenopus laevis, Hsp27 and spectrin were found to colocalize with keratin and actin cytoskeletal filaments. These associations persist when hyperadhesive desmosomes are the only cell adhesions present, with at least spectrin becoming concentrated at the hyperadhesive contact. While hyperadhesive desmosomes are considered highly stable protein complexes linked primarily to keratin intermediate filaments, colocalization of Hsp27 and spectrin with both actin and keratin filaments in embryonic tissues suggests that the transition from classic cadherin adherens junctions to desmosomes to hyperadhesive desmosomes is a highly dynamic process and remains reversible. Further, the existence of these linkages and adhesions in an embryonic tissue reveals the complex nature of their structure,

139*	Effect of Lipid Chain Length on Structural Dynamics of ABC Transporter Sav1866 **Divya Rajendran, Emmanuel Osei, Dr. Horia Petrache** Phospholipid membranes, consisting of hydrophilic headgroups and hydrophobic fatty acid chains in a bilayer structure, are semipermeable structures that separate a cell's internal components from its surrounding environment and enable critical cell functions. Though membranes have been widely studied for their biochemical implications, they have unique potential as biological materials due to their physical properties. At typical human body temperatures, they are classified as being in the liquid-crystal phase, exhibiting both fluid and solid properties. These physical aspects facilitate the function of various cellular processes, including the transport of substrates (e.g., lipids, drugs, and ions), cell signaling, and fission. Bacterial ATP-binding cassette (ABC) transport proteins have significant implications on membrane dynamics, contributing to overall membrane asymmetry by translocating lipids to the membrane surface. In this study, we focus on the structural dynamics of the ABC transport protein Sav1866, found in Staphylococcus aureus bacterial cells, in five separate lipid membrane environments of varying chain lengths (DOPC, DLPC, DMPC, DPPC, and DOPE) to understand the effect of lipid chain length on membrane structural dynamics. These membranes were synthesized using CHARMM-GUI software, and all-atom nanoscale molecular dynamics (NAMD) simulations were performed at a timescale of 500 nanoseconds at 30 °C using the Big Red 200 supercomputer at Indiana University. Simulations of lipid-only systems served as a baseline for comparison. Parameters such as membrane curvature, thickness, and order profiling were measured; analyses of the root mean square fluctuation/deviation (RMSF/RMSD) and spatial phosphorus atom position indicated that membranes with shorter chain lengths exhibited increased flexibility and curvature. Membrane thickness gradually increased over time, suggesting transporter-induced asymmetry. Order parameter profiling indicated that the systems exhibited more disorder as chain lengths decreased. These results signify that membrane structural dynamics can be optimized to enhance cellular functions such as drug absorption.

Poster Number	Poster Title, Author(s), & Abstracts
140*	Targeting CPSF73 to Inhibit Adenovirus Replication **Cal Swartzendruber, Lorenzo Serra, Molly Patterson, Dr. Alexander Price** Viral infections cause 81.7% of upper respiratory infections, and it particularly impacts children under 5 and the elderly. Adenovirus is one of the most common causes of respiratory infections and has limited treatment and prevention options. We sought to use two novel drugs to prevent adenovirus replication: JTE607 and KK149. They both inhibit CPSF73, a key part of the polyadenylation complex in humans. To do this, we infected A549 cells with Adenovirus 5. Using qRT-PCR, we quantified the mRNA expression of 4 target genes: E1A, E2B, Fiber, and the Major Late Promoter (MLP). E1A, Fiber, and MLP all had spliced and unspliced variants of primers. Western blots were used to determine protein expression of the same genes. We found 5uM added at 1 hour post infection (hpi) was the most effective method of treatment for KK149. JTE607 at 5uM added 1hpi was partially effective, reducing expression of the spliced mRNA at multiple concentrations but not reducing protein expression. Our findings suggest KK149 has potential to be used in clinical trials.
141*	Effect of simulated microgravity on Candida albicans resistance to caspofungin and fluconazole **Kendall Carter, James Livengood, Gracie Holt, Liwia Zachara and Patrice Bouyer** Candida Albicans (C. albicans) is an opportunistic commensal fungus that can alter its behavior under low-shear modeled microgravity by exhibiting phenotypes associated with increased virulence. For instance, it has been previously reported that microgravity increased C. albicans resistance to amphotericin B, but did not change its resistance to caspofungin. Here, we investigated how microgravity (5 and 6 days) influences the resistance of two C. albicans strains (SC5314 and NCCLS11) to fluconazole (25 µg) and caspofungin (5 µg). Drug susceptibility was assessed by measuring the zone of inhibition (ZOI) around the treatment discs after 24 hours of exposure under microgravity and gravity conditions. A clinostat was used to simulate a microgravity environment. Five days pre-exposure to microgravity on Mueller-Hinton agar significantly increased NCCLS11 sensitivity to 25 µg fluconazole 508.2±30.2 (n=28) mm^2 versus 352.1±40.7 mm^2 (n=26), P =0.003 (unpaired t-test), which reverted after 6 days 411.7±19 (n=24) mm^2 versus 396.5±.20.8 (n=23), P =0.59 (unpaired t-test). No change in sensitivity was observed to 5 µg caspofungin with or without gravity. Similarly, using SC5314 strain and YEPD agar medium we found no change in fluconazole sensitivity. Our results suggest that drug sensitivity during microgravity varies depending on the agar medium and C. albicans strains.
142*	Effect of estrogen on Candida albicans filament growth in the presence and absence of an epithelial layer **Matthew Gaetano, George Gundelach, Mackenzie Sorrell, Dr. Patrice G Bouyer** Candida albicans is a commensal fungus with pathogenic potential. In its filamentous form, it can invade the host and cause systemic infection. Work by others suggests that increased estrogen levels may be responsible for filament growth. In our study, we investigated the effect of short-term exposure to 1 nM estrogen on C. albicans filament growth. C. albicans cells (200,000) were added to a 24-well plate containing one the three substrates: either T84 cells, Caco2 cells, or no cells (HPBSS = saline solution alone) for various times. Estrogen or its solvent (DMSO) was added to cells simultaneously with C. albicans. Images were captured using an Olympus microscope and a 40× objective. Filament length was measured using Cellsense software (Olympus). When C. albicans (yeast form) were

	exposed to HPBSS (no cells), over the course of 105 minutes, we measured a significant difference in filament length: 6.0 ± 0.5 μm n = 24 at 60 min, 9.5 ± 0.6 μm n = 46 at 90 min and 15.6 ± 0.7 μm at 105 min, with $p \leqslant 0.01$ for 60 versus 90 min and $p \leqslant 0.001$ for 90 versus 105 min). When comparing filament lengths at 90 minutes across substrates, the presence of T84 cells caused significantly longer filaments (16.7 ± 0.8 μm) when compared to either the presence of Caco2 cells (11.1 ± 0.7 μm, $p < 0.001$) or in the absence of cells (9.5 ± 0.6 μm, $p \leqslant 0.001$). Filaments length between the Caco2 and HPBSS is not statistically significant ($p = 0.3$). We also found estrogen to cause no significant increase in filament length across any conditions. In summary, acute exposure to estrogen does not seem to have a significant effect on the filamentation lengths, but we notice that cell lines do have a profound effect.
143	Translocation of Pus7 within C. albicans **Taylor Smith, Doug Bernstein** Candida albicans, an opportunistic pathogen, can cause invasive infections among hospitalized patients. Antifungal drug resistance within C. albicans is increasing making it the fourth most isolated organism in invasive yeast infection cases. New antifungal drug targets need to be discovered to treat these rising infections. Pseudouridination is an RNA modification that is a potential target for drug treatments. Pus7 aids in the process of Pseudouridination of different RNA molecules, such as tRNA, mRNA, snRNA. This RNA modification allows for the control of gene expression among many organisms. In other organisms, Pus7 can translocate into the nucleus to perform its role of modifying mRNA sequences. It is unknown if Pus7 can translocate into the nucleus of C. albicans. Engineered plasmids that contained a Pus7-GFP sequence were digested and transformed into C. albicans cells. This research is still being investigated. Current work is understanding how to improve the transformation protocol for C. albicans. Future investigations will look at PCR confirmation of successful transformations within C. albicans and Fluorescence Microscopy to confirm the location of Pus7.
144*	Identification of Candida albicans Mutants that can Filament in the Presence of Hygromycin B **Vivana Bhagat, Summer Davis, Sanaa Kulkarni, Dr. Douglas Bernstein** Candida albicans is an opportunistic fungal pathogen capable of switching between yeast and filamentous forms, a process closely linked to virulence. The reference strain SC5314 is highly invasive and exhibits robust filamentation relative to many other isolates, making it a valuable model for studying morphogenesis. We have found that hygromycin is a potent inhibitor of C. albicans filamentation, but the underlying molecular mechanisms behind this phenotype are unknown. In this study, C. albicans SC5314 cultures were exposed to UV irradiation and selected on hygromycin-containing media to isolate mutants that could filament in the presence of hygromycin. Colonies were evaluated across increasing hygromycin concentrations on Spider media to assess changes in growth and filamentation patterns. A clear irradiation-dependent gradient of phenotypes was observed: minimal UV exposure produced predominantly yeast-form colonies, intermediate exposure (4-6 seconds) yielded wrinkled colonies with mixed pseudohyphal growth, and higher irradiation favored primarily pseudohyphal or hyphal phenotypes. These observations indicate that UV-induced mutations can differentially impact regulatory pathways governing morphogenesis under translational stress. Because hygromycin inhibits protein synthesis, persistent filamentation under drug pressure may arise from mutations in stress-response or morphogenesis regulators. In the future, transcriptional analyses will be used to identify gene expression changes associated with these filamentation phenotypes.
	Comparative Analysis of Gene LDH, and MDH in the Puerto Rican Parrot, and Chicken **Mariana Berdugo, Alexis Cantrell, Zoe Hogue, Sarah Justice, Don Paetkau, Alondra Diaz Lameiro, Juan Carlos Martinez-Cruzado**

145*

Background: The Puerto Rican parrot (Amazona vittata) is an endangered species and the only parrot protected under U.S. jurisdiction. It faces several threats to its survival, including low reproductive success. A major challenge captive breeding programs are currently facing is the fragility of the eggshells, which results in a high rate of embryo death.

Eggshell formation is a complicated biological process shaped by both genetic and environmental influences. In chickens, the most well characterized bird species, ~1,200 genes related to calcium regulation, collagen production, and mineralization have been correlated with eggshell development. However, the specific genes responsible for eggshell weakness in A. vittata remain unknown. Because the species has a very small population and limited genetic diversity, factors that complicate conservation efforts, it is essential to identify any genetic mutations that contribute to this problem.

Methods: This project builds on work initiated at the University of Puerto Rico, Mayaguez, in partnership with the Genomics Education Partnership (GEP). Computational gene annotation and comparative genomics were used to identify potential mutations in lactate dehydrogenase (LDH) and malate dehydrogenase (MDH), complexes that were found to be differentially expressed in chicken uterus. After manual annotation of each gene in A. vittata, sequences were compared across closely related bird species to identify potential causative mutations in the parrot.

Future directions: Next steps of this project include cloning wildtype LDH/MDH genes into plasmids. Mutagenesis will be used to modify sequences to create mutations found in A. vittata. LDH and MDH will be purified, and enzyme kinetics will be performed to compare activity in mutant vs. wildtype enzymes. These data will help identify genes involved in eggshell formation. Gaining a clearer understanding of these genetic factors could improve the management of breeding programs and offer new insights into avian reproductive biology.

146*

Developing DNA Barcodes for Species Identification of North American Azaleas

Alexis Cantrell, Mariana Berdugo, Zoe Hogue, Elizabeth Hasenmyer, Dr. Sarah Justice

Introduction: North American Azaleas are understudied members of the Rhododendron genus. These species remain unexplored due to the lack of availability of published whole-genome sequences. Our long-term goal is to sequence the genomes of the North American Azalea species in the Whipple Azalea Garden at Taylor University. One of the primary challenges in obtaining the complete genome sequence is species identification. This study develops a DNA barcoding strategy to accurately identify subspecies beyond the Rhododendron genus.

Methods: The initial stages of this process include using existing barcode sequences for plants against four genes: ITS4, ITS2, matK, and psbA-trnH. Unfortunately, not all of the barcode sequences are publicly available for the Azalea species in the garden. Existing literature shows that due to the genetic similarity of these species, these four barcodes by themselves are not sufficient to accurately determine species. Once we have all four barcodes sequenced for the ten species in the Azalea garden, we will develop a new barcode sequence using existing genomes from Asian azaleas.

Results: Our preliminary data shows that we can consistently identify the Azaleas as Rhododendron, but there is too high of a degree of sequence identity to differentiate using the canonical barcodes. Current efforts include sequencing and publishing on NCBI the canonical barcodes for all 10 species and determining candidate sequences for new barcodes.

Conclusions: Upon successful development of these new barcodes, we will use whole genome sequencing of individuals from each of the ten species and some interspecies hybrids from the garden. In addition to the molecular work being completed at Marian, collaborators at Taylor University are collecting phenotypic data from the garden.

	Completion of these genomes and analysis comparing genotype and phenotype data will permit future studies on the genetics of flower color, bloom time, and other Azalea traits.
147*	The effects of abnormal temperature patterns on Batrachochytrium dendrobatidis density and size in vitro **Megan Lawson, Jonathan Lopez, Kurt Lutz, Dr. Catherine Searle** Amphibian species throughout the world have been declining at increasing rates due to infections from the fungal pathogen, Batrachochytrium dendrobatidis (Bd). Bd is found on every continent that has amphibians, and has adapted to a wide range of temperatures with maximum growth rates between 17°C - 25°C. As global temperatures increase and fluctuate, it is important to consider how these shifts can influence the survival and growth of Bd. Organisms can increase their tolerance range of an abiotic factor, such as temperature, through an increase in phenotypic plasticity, gaining the ability to survive in a larger temperature range. To evaluate Bd growth in hypothetical scenarios of warming and fluctuating climates, the pathogen's growth rate and size were measured in varying temperatures. Over the course of 10-11 days, Bd samples in liquid media were exposed to four temperature treatments: constant temperatures at 22°C or 26°C, and fluctuating temperatures from 20°C to 24°C and 24°C to 28°C. Temperatures of the fluctuating treatments were changed every 24 hours. Following the exposure period, Bd zoospores were quantified and compared to the original zoospore count prior to treatment. Samples were preserved, and zoospore and zoosporangia size were measured using fluorescence microscopy. Results are expected to show that when exposed to fluctuating temperatures at a higher range (24°C to 28°C), Bd samples will have higher zoospore densities compared to those kept at a constant temperature outside of the pathogen's preferred range (28°C). Bd zoospores exposed to higher temperature ranges are expected to be larger in size, but at lower densities, compared to those in lower temperature ranges. When exposed to temperatures within the preferred range, Bd zoospores are expected to be smaller in size, but at higher densities.
148	Agricultural Microbes as a Source of Antimicrobials **Mana Shahrokhi, Dr. John McKillip** The rapid emergence of antimicrobial resistance (AMR) has created an urgent need for new antimicrobial compounds from underexplored natural sources. Environmental bioprospecting remains a powerful strategy for identifying microorganisms capable of producing structurally diverse and biologically active secondary metabolites. In this study, environmental samples were collected from agricultural settings with high microbial diversity, including dairy farms, to isolate bacteria with antimicrobial potential. Bacterial isolates were recovered using selective and non-selective culturing methods and initially screened for antimicrobial activity using agar-based inhibition assays against multiple bacterial targets, including members of the ESKAPE pathogen group. Active isolates were scaled up using liquid fermentation, with nutrient conditions adjusted to enhance bioactive metabolite production. Several isolates showed consistent antimicrobial activity, suggesting the production of bioactive metabolites. Molecular and biochemical analyses identified several active isolates as Bacillus spp., including Bacillus pumilus. Crude metabolite extracts prepared from selected isolates retained inhibitory activity, supporting their potential as sources of antimicrobial compounds. These findings demonstrate agricultural environments as valuable reservoirs of antimicrobial producing bacteria and the effectiveness of environmental bioprospecting in antimicrobial discovery. Future efforts focus on improving metabolite production and characterization to assess the novelty and antimicrobial potential of these compounds.

149*	Widespread Multi-drug-Resistant Bacteria and Resistance Genes in Indiana's Reservoirs **Ashley Durnil, Eshaan Patel, Samina Akbar, PhD** Background: Antimicrobial resistance (AMR) is a critical public health crisis, yet the role of urban wetlands as environmental reservoirs remains poorly characterized. Urban freshwater systems serve as interfaces where human and agricultural antibiotics usage converge, potentially creating a "hidden resistome." This study investigated the prevalence and persistence of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs) within the Upper White River Watershed in Indiana, specifically focusing on urban wetland ecosystems as potential sinks for multidrug-resistant (MDR) organisms. Methods: Samples were collected from the Nina Mason Pulliam Ecolab, Eagle Creek Reservoir, and Geist Reservoir. Samples were processed via membrane filtration (0.45 μm) and cultured on MacConkey and Nutrient agar. Purified isolates (n = 310) were identified using 16S rRNA sequencing. Phenotypic resistance was determined via Kirby–Bauer disc diffusion and Minimum Inhibitory Concentration (MIC) assays against seven antibiotic classes. Molecular screening for ARGs (including Cephamycinase-2 (CMY-2), Cefotaximase (CTX-M), Klebsiella Pneumoniae Carbapenemase (KPC), New Dehli Metallo-β-lactamase (NDM) and Sulfhydryl Variable (SHV)) and Type 1 integrons were performed using gene-specific PCR and multiplex PCR assays. Results: This process recovered isolates from 19 genera, primarily Escherichia, Pseudomonas, Klebsiella, and Serratia. Approximately 95% of isolates exhibited MDR phenotypes, with the highest resistance frequencies observed against aminopenicillins (77%), cephalosporins (73%), and ciprofloxacin (43%). Molecular analysis confirmed a high abundance (97%) of clinically significant ARGs, including carbapenemases (KPC, NDM, and OXA variants) and extended-spectrum β-lactamases (CTX-M and TEM). The presence of Type 1 integrons suggests a high potential for horizontal gene transfer within these aquatic habitats. Conclusions: These findings demonstrate that interconnected urban freshwater systems and wetlands function as significant environmental reservoirs for high-priority gram negative bacterial pathogens. Establishing these baseline phenotypic and genotypic profiles is essential for source-tracking AMR, informing public health policy and environmental stewardship in Indiana.

Poster Number	Poster Title, Author(s), & Abstracts
150*	Evaluation of Antibiotic Resistance and Species Identification of Gram-Negative Bacteria from the Geist Reservoir **Kiley Wardwell, Ashley Durnil, Dr. Samina Akbar** **Background:** Urbanization has accelerated the spread of antibiotic-resistant (AR) bacteria in Marion County waterways, establishing environmental reservoirs for antimicrobial resistance genes and posing significant public health risks. Aquatic surveillance provides critical data on resistance transmission pathways, particularly given that many human pathogens originate from environmental sources. The White River watershed, including Geist Reservoir—a heavily utilized recreational site—receives substantial urban and agricultural runoff, making it a high-priority target for resistance monitoring. **Objective:** To isolate gram-negative bacteria from Geist Reservoir water samples, identify bacterial species via 16S rRNA gene sequencing, and determine antibiotic susceptibility profiles using Kirby-Bauer disk diffusion assays. **Methods:** Water samples were sequentially vacuum filtered through 5 µm, 1.2 µm, and 0.45 µm membrane filters to concentrate bacteria. Filters were incubated on MacConkey agar to select for gram-negative organisms, and 84 individual colonies were purified through serial subculturing. Genomic DNA was extracted using the GenElute® Bacterial Genomic DNA Kit and submitted for 16S rRNA gene sequencing. Antibiotic resistance profiles are being determined using disk diffusion assays against a panel of clinically relevant antibiotics. **Results:** Members of the Enterobacteriaceae family—including Escherichia, Shigella, and Klebsiella—were identified alongside other potentially pathogenic genera. Antibiotic susceptibility testing is currently in progress. **Conclusion:** This study will characterize the diversity and antibiotic resistance profiles of gram-negative bacteria in the White River watershed. The detection of recognized human pathogens in a popular recreational water source underscores the urgent need for ongoing environmental surveillance. Elucidating resistance mechanisms and tracing the origins of resistance determinants in this watershed will inform evidence-based public health strategies to mitigate community exposure risks.
151	Characterizing PUG1 mutants in the opportunistic fungal pathogen Candida auris **Summer Davis, James Carty, Dr. Doug Bernstein** Candida auris is an opportunistic fungal pathogen that is characterized by its distinct ability to thrive on skin and medical devices. When an individual becomes sick or severely injured, Candida auris can cause a bloodstream infection called invasive candidiasis. Invasive candidiasis, paired with the weakened immune system, leads to a mortality rate of about 30-60%. C. auris has also evolved to be multi-drug resistant, meaning many strains do not respond to at least two of the three major classes of anti-fungals available today. Candida auris contains a protein called PUG1, which is responsible for breaking down the RNA modification pseudouridine in Candida species. PUG1 is absent in both humans and Saccharomyces cerevisiae, making it a possible target for future anti-fungals to treat invasive candidiasis. Using CRISPR-Cas9 technology, we have successfully knocked out PUG1 from the two of the four major clades of Candida auris. Our aim is to knockout PUG1 from the remaining Candida auris clades and examine its growth and ability to infect model organisms. Preliminary data from the first two clades shows that the loss of PUG1 negatively effects C. auris' ability to grow under stress conditions.

152*

Efficacy of MCP-1 in C. neoformans killing by CITED1 Knockout Macrophages

Garrett Roberts, Dr. Erin McClelland

Background: CITED1 is a transcriptional coregulator involved in the macrophage innate immune response and specifically enhances pro-inflammatory gene expression in response to IFNγ. Previously, two CITED1 knockout strains (Δ 6 and Δ 9) and two control strains (scrambled and overexpressing) were infected with the fungal pathogen Cryptococcus neoformans. CITED1 knockouts were ineffective at clearing the C. neoformans infection. Here, we tested whether the lack of killing was due to lack of the cytokine monocyte chemoattractant protein-1 (MCP-1) in these strains. MCP-1 initiates an inflammatory response, increasing oxidative stress through production of reactive oxygen species, which help kill C. neoformans. Thus, we tested whether cells without CITED1 could better kill C. neoformans in the presence of exogenous MCP-1.

Methods: Mouse macrophages were infected with C. neoformans with or without MCP-1 and washed every 6 hours to remove excess yeast. After 24 hours, macrophages were lysed, and intracellular C. neoformans were plated onto YPD plates. CFU/mL was determined after 36 hours.

Results: The Δ6 strain better killed C. neoformans compared to that that of the Δ9 and the Scrambled control. The first trial showed more killing in the presence of MCP-1 in the knockout strain, though not statistically significant. The second and third trials showed no difference in killing. The observed killing in the first trial was likely due to accidently using a higher concentration of MCP-1, whereas the second and third trials used physiological levels of MCP-1.

Conclusions/Future directions: These data suggest that MCP-1 may be involved in the mechanism of CITED1 killing of C. neoformans, though more research is needed. Future experiments include a MCP-1 does response curve to determine the best MCP-1 concentration to use and testing the CITED1 overexpressing strain to assess whether there is a difference in killing with or without MCP-1 when CITED1 is overexpressed.

153*

CITED1 Effect on Macrophage Apoptosis when Exposed to Cryptococcus neoformans

Claire Kinder, Dr. Erin McClelland, Dr. Arathi Subramani, Dr. David Nelson

Background: Cryptococcus neoformans is an environmental fungal pathogen that primarily affects immunocompromised individuals. Macrophages, innate immune cells that phagocytose foreign particles, are the first line of defense against C. neoformans. Macrophages can be classically activated (M1) via IFNγ which increases interferon-stimulated gene (ISG) expression, resulting in proinflammatory cytokine expression and production of reactive oxygen and reactive nitrogen species that promote clearance of cryptococcal infections. CITED1 is an ISG that enhances the expression of a variety of ISGs. Macrophages can also be alternatively activated (M2) via IL-4, which induces an anti-inflammatory state associated with resolution and "clean up" of an infection. H99S C. neoformans induces a change in cytokine production associated with M2 macrophages, constituting a more suitable environment for growth of the pathogen.

Methods: To investigate if CITED1 promotes the survival of host macrophages, Raw264.7 murine Δ6 CITED1 knockout, Δ9 CITED1 knockout, and scrambled CITED1 control classically and alternatively activated macrophages were infected with H99S C. neoformans for 24 h. Cytosolic and mitochondrial cellular fractions were collected to quantify the amount of apoptosis that occurred after infection, including levels of cytochrome C and the presence of cleaved caspases 3 and 7 in the cytosol. Fractions were separated by SDS-PAGE and probed with antibodies against cytochrome C, cleaved caspase 3, and cleaved caspase 7.

Results: Both control and C. neoformans-infected macrophages showed cytochrome C and cleaved caspases 3 and 7 in the cytosol, suggesting apoptosis was occurring in all cell lines. Thus, these data were not consistent with a conclusive change in apoptosis between Δ6, Δ9, and scrambled cell lines in M1 and M2 macrophages.

Conclusion: CITED1 does not appear to play a role in inducing apoptosis in C. neoformans-infected macrophages.

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A Potential Role for DHX36/G4R1, a G4 helicase, in Genomic Maintenance in C9orf72 ALS/FTD

Kelsey Slattery, Quinn Anderson, Joesph Gumina, Dylan Seiler, Chance Creviston, Omar Habous, Nana Akua Koranteng, Abbey Wiggam, Christiana Whittey, Peter K. Todd, James P. Vaughn, Yuh-Hwa Wang, Philip J. Smaldino

Genomic instability and accumulation of DNA damage are emerging as molecular hallmarks of neurodegenerative diseases, including C9orf72-linked amyotrophic lateral sclerosis and frontotemporal dementia (C9 ALS/FTD). C9 ALS/FTD is most commonly caused by an inherited hexanucleotide (G4C2)n-repeat expansion (HRE) mutation, which results in excessive formation of G-quadruplex (G4) DNA and RNA structures. G4 structures are stable secondary structures that modulate replication, transcription, translation, and are associated with genomic instability if left unresolved. In C9 ALS/FTD the GGGGCC-repeat codes for toxic repeat RNAs and dipeptide repeat (DPR) proteins that further exacerbate DNA damage. Previous in vitroand in vivo studies suggest that reduction of the G-quadruplex helicase, DHX36/G4R1, reduces toxic DPRs in C9 ALS/FTD, representing a potential therapeutic target. However, DHX36 plays a vital role in resolving G4 DNA structures during replication and transcription, suggesting that its loss may compromise genomic stability in central nervous tissues. To investigate this, we generated a CNS-specific DHX36/G4R1 knockout model. To do this we crossed DHX36/G4R1fl/fl mice with a transgenic mouse line in which Cre expression is driven by the Nestin gene promoter, restricting knockout to CNS tissues. Genotypical analysis revealed a stark absence of homozygous CNS deletion of DHX36/G4R1, demonstrating an essential role for DHX36/G4R1 during embryonic CNS development. Behavioral analysis of heterozygous DHX36/G4R1 knockout mice revealed significantly increased grip strength by two months of age, indicating an alteration of neuromuscular functionality following this reduction. Ongoing molecular analysis of brain and spinal cord tissue, including qRT-PCR and ELISA aim to determine whether DHX36 loss increases markers of DNA damage. Collectively, this work establishes DHX36 as a critical regulator of embryonic CNS development and motor function and provides further exploration of targeting DHX36 as a potential therapeutic target in C9 ALS/FTD.

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Using LUHMES cells to measure MST-312's impact on Herpes Simplex Virus Latency

Kayli Liles, Prajakta Pradhan, Dr. Marie L. Nguyen

Herpes simplex virus (HSV) often causes diseases in healthy individuals and poses a danger to the lives of newborns and immunosuppressed populations with symptoms varying from cold sores to encephalitis. Herpesvirus infections are difficult to treat due to their unique tendency to trigger repeated illness, necessitating extended use of antivirals. This ability comes from the formation of latency within neuronal cells.

Our laboratory's prior research demonstrated that MST-312, a telomerase inhibitor, exhibits antiviral activity on the lytic phase of the HSV life cycle. In this project, we initiated studies to test the effect of MST-312 on the latent phase of the infection. To accomplish this, Lund human mesencephalic (LUHMES) cells, which are immortalized human embryonic neuronal precursor cells that can be differentiated into neuronal cells, were used. LUHMES cells have recently been shown to support the latent phase of HSV-1 strain 17syn+. Our initial aim was to confirm the MST-312 antiviral activity in this HSV-1 strain.

Experiments were performed by infecting Vero cells with HSV-1 strain 17syn+ in the presence and absence of MST-312. The next day, virus was harvested, and plaque formation was measured. We found that MST-312 is effective at inhibiting viral 17syn+ replication. Next, LUHMES neuronal cell differentiation was confirmed by identification of βIII-tubulin and synaptophysin upregulation through western blot analysis. Finally, differentiated LUHMES cells were infected with HSV-1 strain 17syn+. MST-312 was added during the establishment and reactivation of latency. Virus samples were collected at various timepoints. Inhibition of HSV-1 reactivation by MST-312 was not observed in preliminary LUHMES cell experiments, however further research is needed to complete the assessment of the potential antiviral effects during latency.

The Effect of Fetal Alcohol Spectrum Disorders on Development of the Hippocampus in Relation to ADHD-Like Behaviors

Ash Bishop, Allison Velie

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Fetal Alcohol Spectrum Disorders encompass a range of neurodevelopmental issues caused by prenatal alcohol exposure, with approximately 13.5% of pregnant women worldwide reporting alcohol consumption during pregnancy. This is a worldwide issue and prenatal alcohol exposure increases the risk of attention-deficit hyperactivity disorder (ADHD) by nearly 40%. The mechanism by which prenatal alcohol exposure contributes to ADHD is largely unknown. This study focused on two classes of genes implicated in several behaviors disrupted by prenatal alcohol exposure, namely dopaminergic and cadherin genes. Seventy rats were assigned to three diet groups: ad libitum, pair-fed, and ethanol-exposed. Brain tissue was collected in adolescence, and we measured changes in dopamine receptor genes (D1-D5) and N-cadherin expression in the hippocampus, with plans to analyze the striatum and prefrontal cortex. It is expected that both dopaminergic and N-cadherin expression will significantly decrease in brain regions of rats that have been exposed to alcohol during development, and that these changes in expression will correlate with ADHD-like impulsive behaviors measured in a separate cohort of rats. The findings of this study

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Dose-Dependent Inhibition of hRSV and Clinically Relevant Pathogens by Mānuka Honey Without Cytotoxic Effects

Grant Ipsen, Jessica Paulson, Dr. Dia Beachboard, Dr. Ashlee Tietje, Dr. Christopher Stobart

Mānuka honey, produced from the nectar of Leptospermum scoparium, is recognized for its medicinal properties and characterized by its Unique Mānuka Factor (UMF) rating. While its bioactive potential is widely acknowledged, the influence of UMF variation on antiviral and antimicrobial efficacy remains poorly characterized. This study evaluated the impact of Manuka honey at varying UMF grades (5+ to 25+) on HEp-2 and DBT cell viability and investigated its antiviral activity against mammalian cells and clinically relevant pathogens. Cytotoxicity assays were first conducted using HEp-2 and DBT cell lines to ensure the absence of adverse effects. Furthermore, immunofluorescent microscopy was performed to assess mitosis, apoptosis, and cytoskeletal rearrangement. Results demonstrated no statistical differences in cell viability or cytoskeletal integrity across all UMF grades, clarifying a favorable safety profile for therapeutic application. Antiviral activity against human respiratory syncytial virus (hRSV) and was then examined through inactivation and growth curve studies. In the inactivation experiments, Mānuka-treated samples showed UMF and concentration-dependent inhibition, with complete hRSV inactivation achieved at higher grades (15+ to 25+). Growth curve analysis confirmed that all UMF grades significantly reduced viral replication compared to water and forest honey controls. Finally, antimicrobial activity was evaluated against clinically relevant bacteria and fungi. Growth inhibition was quantified using OD_{600} measurements across multiple concentrations. Together, these results provide mechanistic insight into how UMF variation influences pathogen inactivation and replication kinetics, supporting the therapeutic potential of Mānuka honey as a safe, antimicrobial agent.

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Analysis of Previously Reported SARS-CoV-2 3CLpro Inhibitors for Broad Neutralizing Activity Against the 3CLpro of Human Common Cold Coronavirus Strain HKU1

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The emergences of highly pathogenic coronaviruses in the recent past including SARS-CoV (2003), MERS-CoV (2012), and SARS-CoV-2 (2019) along with the potential for new emerging human coronaviruses highlights the urgent need for identification and development of broad-spectrum antivirals for coronaviruses. In this study, we examine the efficacy of various antiviral agents which have been shown previously to inhibit the 3CLpro protease of SARS-CoV-2 to inhibit the 3CLpro protease of human coronavirus HKU1. To test these inhibitors, a chimeric mouse hepatitis virus (MHV) coronavirus expressing the 3CLpro protease of HKU1 was treated with a panel of 5 inhibitors: GC376, tideglusib, rosmarinic acid, cefadroxil, and tanshinone I. While varying levels of cytotoxicity were observed in the DBT-9 cells used in this study, most of the inhibitors evaluated showed selective virus inhibition at significantly lower concentrations than where cytotoxicity was observed. Notably, GC376 demonstrated a very low EC_{50} of 32.98 nM. Additionally, a therapeutic window was also observed for the cephalosporin antibiotic, cefadroxil, which was able to inhibit the HKU1-containing MHV strain. Collectively, these data shed light on the potential of these various

	antiviral substances to serve as broad-spectrum coronavirus antivirals in the event of new emerging human coronavirus of clinical concern.
159*	SARS-CoV-2 3CLpro Inhibitors Exhibit Neutralizing Activity Against the 3CLpro of Human Common Cold Coronavirus Strain OC43 **Aarish Sakib, Sahar Atmar, Andrew Burdette, Gracie Walls, Cora Zilinski, Jayden Doster, Mackenzie Yurchiak, Ethan White, Kara Selesky, Angelena Donovan, Matthew Demshuk, Jacob Moehlenkamp, Stefania Farha, George Papadeas, Cameron Harrison, Dia Beachboard, Christopher Stobart** The recent emergence of SARS-CoV-2 highlights the continued potential for new human coronavirus strains of clinical concern. 3CLpro, the main protease of coronaviruses, has a critical and indespensible role in the mediating replication complex formation for coronaviruses. In this study, we examine the efficacy of several antiviral agents that have demonstrated inhibition against the 3CLpro protease of SARS-CoV-2. Using a chimeric mouse hepatitis virus (MHV) strain expressing the OC43 3CLpro (O5-MHV), we tested GC376, Tideglusib, Rosmarinic Acid, Cefadroxil, and Tanshinone I initially for cytotoxicity and morphological impacts on DBT-9 cells, a murine astrocytoma cell line that is permissive to MHV infection. Subsequent inhibition assays were performed to determine the EC_{50} of each putative inhibitor against O5-MHV. We found that GC376 exhibited the greatest therapeutic potential with significant inhibition (EC_{50} = 12.7 nM) against the virus. In addition, Cefadroxil was found to exhibit low micromolar inhibition, whereas Rosmarinic Acid and Tideglusib failed to demonstrate significant inhibitory activities and Tanshinone I induced high cytotoxicity which prevented a therapeutic window for investigation. In addition to reporting inhibition data, we conclude by describing ongoing efforts to characterize potential escape mutation pathways following sub-lethal exposure to GC376. These studies collectively offer insight into the efficacy of several characterized coronavirus inhibitors as pan-coronaviral antiviral agents.

Poster Number	Poster Title, Author(s), & Abstracts
160	The Role of RIP1 in T-Cell Acute Lymphoblastic Leukemia Chemoresistance **Katelyn Ellison, Dr. James Olesen** T-cell Acute Lymphoblastic Leukemia (T-ALL) is an aggressive blood cancer affecting the development of normal T-cells. Nearly 12-15% of all newly diagnosed ALL cases occur in pediatric patients, and it is noteworthy for its unique clinical and biological features thought to be caused by the ectopic expression of certain proteins. Of importance to this study is the function and expression of RIP1 and its potential role as an anti-apoptotic protein. Previous research has shown that RIP1 is crucial for mouse survival, as mice lacking RIP1 experienced extensive apoptosis in lymphoid tissue, leading researchers to believe that RIP1 is important for T-cell survival. We believe that RIP1 will be an ideal target for understanding how it works both in resisting apoptosis and in promoting TCR-induced proliferation responses. To assess RIP1 expression, whole cell lysates were created from Jurkat cells either treated with 1 μM or 5 μM etoposide or left untreated (0 μM). Western blot analyses were completed, and the expression data collected indicated that RIP1 expression increased as the concentration of etoposide increased. This suggests that cells might upregulate the expression of RIP1 to counter the induction of apoptosis by etoposide treatment. In the end, we hope to have a better understanding of the role of RIP1 in T-ALL and how better, targeted therapies might be developed against this survival factor.
161*	Defining supporting structures: the Back seat driver kinase orchestrates the development of heart-anchoring alary muscles. **Brady Matthew Verdon1,2, Kuncha Shashidhar1,2,3, Rajnandani Katariya1,2,3, M. Rezaul Hasan1,2,3, Mofazzal K. Sabbir1,2, Shaad M. Ahmad1,2,3** **Abstract Text:** The back seat driver (bsd) gene encodes a serine/threonine kinase that regulates gene expression epigenetically and is essential for larval somatic muscle development in Drosophila. Previous studies indicate that Bsd preserves muscle identity by preventing the fusion of somatic myotubes derived from distinct lineages. Its human ortholog, VRK1 (vaccinia-related kinase 1), is a proto-oncogene whose expression increases under pathological conditions such as vascular injury and cancer, hinting at a conserved role in regulating cellular organization and proliferation. In our study of bsd null mutants, we observed a striking defect in alary muscle formation. Alary muscles are a subset of somatic muscles that anchor the Drosophila heart tube to the body wall, providing structural support analogous to human pericardial ligaments. Disruption of these muscles often leads to heart tube collapse and impaired cardiac stability. In bsd deficient mutants, over 70% of the embryos exhibited severe disruption of alary muscles, and approximately 60% lacked at least one alary muscle, indicating that Bsd is essential for their proper development and organization. Based on the known role of Bsd in restricting cross-lineage myotube fusion, we hypothesize that the missing or disrupted alary muscle phenotypes arise from inappropriate fusion events between developing alary muscle myotubes and adjacent somatic muscle myotubes, resulting in hybrid or incorrectly patterned muscle fibers. To test this, we plan to employ MHC-tau-GFP in combination with an alary muscle-specific marker to visualize all somatic and alary muscles myotubes simultaneously. This strategy will reveal if other muscle types occupy the positions of missing alary muscles in bsd mutants and will determine if lineage mixing causes this phenotype. Collectively, our results establish Bsd as a key factor in maintaining the architecture and function of alary muscles that are critical for heart support.
	Physics begets biophysics, from the early 1900s to the 1950s. Its role in the birth of twentieth century molecular biology, with a focus on Nobel laureates and legendary Hoosiers who made crucially important contributions **Dr. Paul Todd, Dr. Rex Bickers**

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164	An Indiana History of Solar Eclipses: Connecting Science to Community **Sarah J. Reynolds** Solar eclipses have a long history of capturing attention and stimulating scientific interest as people seek to understand this spectacular, and sometimes unsettling, phenomenon. Recently the solar eclipses of 2017 and 2024 have provided special opportunities to consider how Indiana and its people have been impacted by eclipses over the years. Developments in the scientific study of eclipses can be traced through the work of Indiana astronomers such as Theophilus Wylie, Wilbur Cogshall, and brothers Earl and Vesto Slipher, up to the present day. Indiana newspapers and other popular media show the ways that everyday "Hoosiers" engaged throughout the years with such scientific developments. Examining these accounts especially highlights the role that new technologies have played in both capturing and communicating about eclipses around the world. Furthermore, certain historical eclipses, such as the 1806 eclipse that Shawnee prophet Tenskwatawa (brother of Tecumseh) used to challenge territorial governor William Henry Harrison or the 1778 eclipse that marked George Roger Clark's crossing of the Falls of the Ohio (River) on Indiana's southern border with a Revolutionary War militia, illustrate how scientific knowledge has been used for a variety of societal purposes and can impact our communities in myriad ways.
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