Texas Academy of Science

129th ANNUAL MEETING

February 27-28th, 2026

University of Texas, Tyler

Meeting Notes and Poster Guidelines

Registration: Meeting registration will be held in the College of Pharmacy (WTB) and will be open from 9:00 a.m. to 5:00 p.m. Friday February 27th and again on Saturday February 28th from 8 a.m. until noon.

Parking: All large vehicles will need to park across from University Blvd at the Behavioral Health facility and will be shuttled over to campus. Regular vehicles that will fit in single parking spots can find open parking on campus.

Posters: Posters should be set-up in the hallways of the first and second floors of the College of Business (COB) starting at 11 a.m. and no later than 2 p.m. on Friday February 27th. Because of vendor requirements, posters must be taken down by 7:30pm Friday February 27th. Posters left up after that time will be discarded.

Distinguished Texas Scientist & Outstanding Texas Educator: These presentations will take place at the Constellation Ballroom, Holiday Inn Conference Center, 5701 S. Broadway Avenue Tyler, TX 75703.

Saturday Lunch: Lunch will be served Saturday (to those who indicated on registration) from noon-1p.m. in the COB. Must have selected this option when registering.

Saturday Reception and Banquet: The Reception and Awards Banquet will be held at the Constellation Ballroom, Holiday Inn Conference Center, 5701 S. Broadway Avenue Tyler, TX 75703.

UTTyler™
THE UNIVERSITY OF TEXAS AT TYLER

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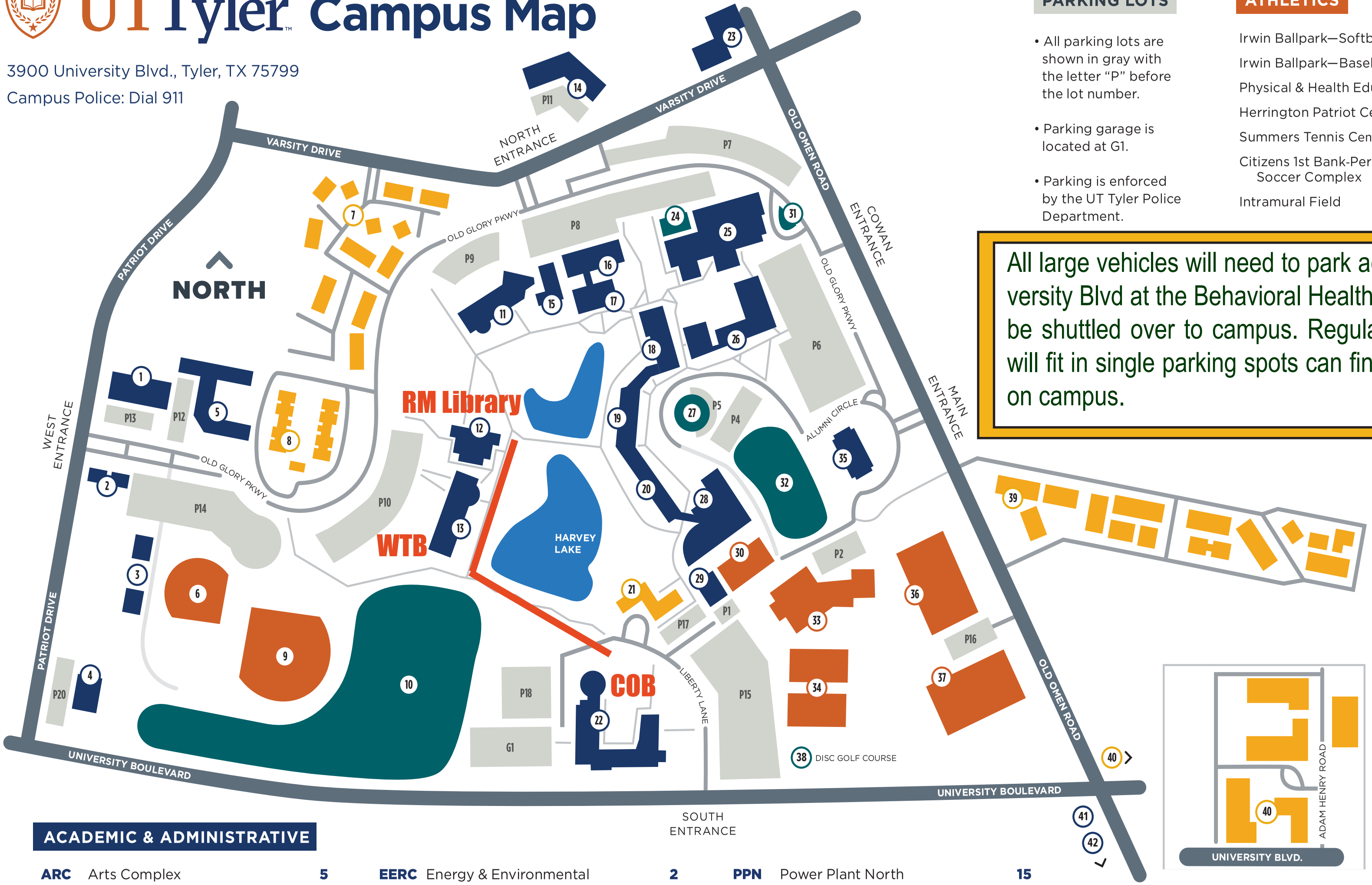
3900 University Blvd., Tyler, TX 75799
Campus Police: Dial 911



PARKING LOTS

- All parking lots are shown in gray with the letter "P" before the lot number.
- Parking garage is located at G1.
- Parking is enforced by the UT Tyler Police Department.

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All large vehicles will need to park across from University Blvd at the Behavioral Health facility and will be shuttled over to campus. Regular vehicles that will fit in single parking spots can find open parking on campus.

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ALH	Alumni House	35
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BEP	Biology, Education and Psychology Building/ College of Education & Psychology	18
BRB	David G. and Jacqueline M. Braithwaite Building/ School of Nursing	26
CMA	Center for the Musical Arts	25
CAS	College of Arts and Sciences	11
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Virtual Map

Local Hotels

Staybridge Suites Tyler University Area (IHG)
https://www.ihg.com/staybridge/hotels/us/en/tyler/tyrst/hoteldetail
+1 (903) 566-1100

Holiday Inn Express & Suites Tyler South (IHG)
https://www.ihg.com/holidayinnexpress/hotels/us/en/tyler/tyrcx/hoteldetail
+1 (903) 566-0600

La Quinta Inn & Suites Tyler - University Area (Wyndham)
https://la-quinta-inn-suites-university-area.tyler-tx-hotels.com/
+1 (903) 561-2223

Magnuson Grand Hotel & Conference Center - Tyler
Magnuson Grand Hotel Tyler www.magnusonhotels.com/magnuson-grand-hotel-and-conference-center-tyler/
+1 (903) 593-3600

Days Inn & Suites by Wyndham Tyler
www.wyndhamhotels.com/days-inn/tyler-texas/days-inn-and-suites-tyler-tx/overview
+1 (903) 705-4660

Comfort Suites Tyler South (Choice Hotels)
www.choicehotels.com/en-xl/texas/tyler/comfort-suites-hotels/tx767
+1 (903) 530-6105

Hampton Inn & Suites Tyler-South (Hilton)
Hilton Hampton Inn Tyler-South www.hilton.com/en/hotels/tyrtshx-hampton-suites-tyler-south/
+1 (903) 630-7272

Hilton Garden Inn Tyler
www.hilton.com/en/hotels/tyrtygi-hilton-garden-inn-tyler/
+1 (903) 509-1166

Homewood Suites by Hilton Tyler
www.hilton.com/en/hotels/tyrothw-homewood-suites-tyler/
+1 (903) 593-7880

Courtyard by Marriott Tyler
Marriott Courtyard Tyler www.marriott.com/en-us/hotels/tyrcy-courtyard-tyler/overview/
+1 (903) 509-4411

Restaurants Near UT Tyler (Near South Broadway Avenue)

Applebees Address: 5502 S Broadway Ave, Tyler, TX. Phone: (903) 509-4848 https://restaurants.applebees.com/en-us/tx/tyler/5502-s-broadway-ave-80018

Clear Springs Restaraunt Address: 6519 S Broadway Ave, Tyler, TX, Phone: (903) 561-0700 https://www.clearspringsrestaurant.com/tyler (Texas comfort food, seafood, catfish, steaks, world-famous onion rings)

Mama's Restaraunt Address: 7484 S Broadway Ave, Tyler, TX. https://www.tripadvisor.com/Restaurant_Review-g56797-d15841063-Reviews-Mama_s_Restaurant-Tyler_Texas.html (Mexican food, breakfast, variety menu)

Saltgrass Steakhouse Address: 7214 S Broadway Ave, Tyler, TX. Phone: (903) 561-8316. Saltgrass Steak House Tyler, TX

Chevy's Mexica Restaraunt Address: 5935 S Broadway Ave (Fountains of Chimney Rock development) https://www.chuys.com

Taco Bell Address: 3808 S Broadway Ave, Tyler, TX https://locations.tacobell.com/tx/tyler/3808-s-broadway-ave/restaurant.html

Texas Academy of Science 129th Annual Meeting 27 - 28 Feb 2026 *All times in CST*

Abbreviated Schedule

Friday, 27 February

8am

Board of Directors' Meeting (8am-11:30am)
College of Business (COB) 321

9am

Registration (9am-5pm)
College of Pharmacy (WTB) - Outside 134

10am

Science Jeopardy (10am-11:30am)
WTB 137

11am

Poster Setup (11am-2pm)
COB 1st/2nd Floor Hallways

11:30am

Section Chairs' Pre-Session Meeting (11:30am-12:30pm)
COB 307

12:30pm

Judges' Room
COB 350.55

Biomedical Sciences I (12:30pm-2pm)
COB 212

Chemistry & Biochemistry I (12:30pm-3pm)
COB 112

Conservation Ecology (12:30pm-2:30pm) & Section Meeting (2:30pm-2:45pm)
COB 111

Plant Biology (12:30pm-4pm) & Section Meeting (4-4:15pm)
COB 203

Science Education (12:30pm-1:30pm) & Section Meeting (1:30pm-1:45pm)
COB 214

2pm

Physics & Engineering (2pm-3pm) & Section Meeting (3pm-3:15pm)
COB 214

2:30pm

Coffee Break

2:45pm

Marine Science (2:45pm-4:30pm) & Section Meeting (4:30pm-4:45pm)
COB 111

3:15pm

Neuroscience (3:15pm-3:30pm) & Section Meeting (3:30pm-3:45pm)
COB 212

Systematics & Evolutionary Biology (3:15pm-4:45pm) & Section Meeting (4:45pm-5pm)
COB 112

3:30pm

Mathematics & Computer Science (3:30pm-4:30pm) & Section Meeting (4:30pm-4:45pm)
COB 214

4pm

Coffee Break

5pm

Graduate Fair
COB 2nd Floor Lounge

Posters-Anthropology (P1-P7)
COB 1st/2nd Floor Hallways

Posters - Biomedical Science (P8-P18)
COB 1st/2nd Floor Hallways

Posters - Cell & Molecular Biology (P19-P44)
COB 1st/2nd Floor Hallways

Posters - Chemistry & Biochemistry (P45-P73)
COB 1st/2nd Floor Hallways

Posters - Conservation Ecology (P74-P81)
COB 1st/2nd Floor Hallways

Posters - Freshwater Science (P82-P88)
COB 1st/2nd Floor Hallways

Posters - Geoscience (P89-P92)
COB 1st/2nd Floor Hallways

Posters - Marine Science (P93-P99)
COB 1st/2nd Floor Hallways

Posters - Mathematics & Computer Science (P100-103)
COB 1st/2nd Floor Hallways

Posters - Neuroscience (P104-P114)
COB 1st/2nd Floor Hallways

Posters - Physics & Engineering (P115-P116)
COB 1st/2nd Floor Hallways

Posters - Plant Biology (P117-P127)
COB 1st/2nd Floor Hallways

Posters - Science Education (P128-P137)
COB 1st/2nd Floor Hallways

Posters - Systematics & Evolutionary Biology (P138-P150)
COB 1st/2nd Floor Hallways

Posters - Terrestrial Ecology & Management (P151-P164)
COB 1st/2nd Floor Hallways

7pm

Poster Tear Down (7pm-7:30pm) - Posters left after this time will be discarded!
COB 1st/2nd Floor Hallways

Saturday, 28 February

7am

Fellows' & Past Presidents' Breakfast
COB 350.55

Continued from **Saturday, 28 February**

8am

Registration
College of Pharmacy (WTB) - Outside 134

Cell & Molecular Biology (8am-10:30am) & Section Meeting (10:30am-10:45am)
COB 111

Chemistry & Biochemistry II (8am-11:15am) & Section Meeting (11:15am-11:30am)
COB 112

8:30am

Anthropology (8:30am-9:15am) & Section Meeting (9:15am-9:30am)
COB 214

Freshwater Science (8:30am-10am) & Section Meeting (10am-10:15am)
COB 212

9:30am

Coffee Break
COB

10am

Geosciences (10am-11:15am) & Section Meeting (11:15am-11:30am)
COB 214

10:30am

Biomedical Sciences II (10:30am-11:45am) & Section Meeting (11:45-noon)
COB 212

Terrestrial Ecology & Management (10:30am-11am) & Section Meeting (11am-11:15am)
COB 203

12pm

Boxed Lunch
COB 112

1pm

Graduate Student Oral Presentation Competition
Robert R. Muntz Library (401)

2:30pm

Post-Section Chairs' Meeting
COB 307

4pm

Commute to Holiday Inn Conference Center for Awards Banquet

4:30pm

Outstanding Texas Educator - Mrs. Jamie Flint
Constellation Ballroom, Holiday Inn Conference Center

5:15pm

Distinguished Texas Scientist - Dr. Rusty Towell
Constellation Ballroom, Holiday Inn Conference Center

6pm

Awards Banquet
Constellation Ballroom, Holiday Inn Conference Center

Holiday Inn
BY IHG

Address : 5701 South Broadway. Tyler TX 75703
Phone: 1-903-561-5800
* Free parking is available for Registered TAS Attendees

Courtesy of JasonLLocklin photography

Welcome from the Program Chair

For over 12 years I have attended and brought students to the Texas Academy of Science. The value it brings to not only the students, but the state of Texas is powerful. At this conference, you get to be a part of something special. You get to be a part of watching generations of STEM experts interact with and mentor new emerging professionals who will pave the way as leaders and innovators of tomorrow.

Throughout this weekend, you will witness the breadth of expertise and knowledge that Texas scientists and mathematicians contribute to their fields. You will also get to witness the dedication of numerous volunteers who give up their time and energy so that a new generation may one day take the helm.

Thank you for investing your weekend to this conference.

Craig Younce, Ph.D

Program Chair & President-Elect, Texas Academy of Science
Associate Dean and Professor of Biology
Holland School of Science and Mathematics
Hardin-Simmons University

Welcome from the TAS President

We are delighted to bring the 129th Annual Meeting of TAS to the University of Texas at Tyler, a distinguished scientific institution in Tyler, Texas. This year's meeting features exceptional programming, including our keynote lectures from Dr. Rusty Towell, nominee for the 2026 Distinguished Texas Scientist Award (Professor of Engineering and Physics, Abilene Christian University, Abilene, Texas), and Jamie Flint, recipient of the 2026 Outstanding Texas Educator Award (Spring Woods High School, Spring Branch, Houston, Texas). Our program offers rich opportunities for professional development and connection. Networking events during the poster sessions will help our student members—the future of Texas science—forge meaningful connections for their promising careers. You'll also enjoy the intellectual energy of our Graduate Student Oral Presentation Competition, the always-popular Science Jeopardy, and Saturday evening's Awards Banquet. We look forward to celebrating the diverse research being conducted across the Lone Star State and reconnecting with colleagues, collaborators, and friends both new and familiar.

This meeting succeeds because of an extraordinary team of volunteers. Please join me in thanking our local host, Dr. Shawana Tabassum, Ph.D., and the entire team at the University of Texas at Tyler for their exceptional hospitality and creativity. Special recognition goes to TAS President-Elect Dr. Craig Younce, who meticulously crafted this standing program and will assume the presidency at Saturday's Awards Banquet. Our Treasurer, Dr. Kathy Wood, has provided invaluable leadership throughout the year. Dr. Dipak Singh, TAS Director of Information Technology, deserves particular thanks for the technical expertise essential to this meeting's success.

Courtesy of Maria Burns

The entire Board of Directors, Section Chairs, Vice Chairs, and additional volunteers performed admirably in reviewing abstracts and award nominations. We especially recognize colleagues completing their Board service at this conference—your contributions will be celebrated at our Awards Banquet. Finally, heartfelt thanks to the mentors statewide who guided our student authors in producing an impressive collection of almost 300 oral and poster presentations.

TAS has strengthened its fundraising efforts under the leadership of Development Chair Dr. Gerald Mulvey. Your financial support directly enables us to promote STEM excellence in Texas through student travel grants, research awards, enhanced annual meetings, and programs across the state. We celebrate the generosity of our donors: Friend (any amount), Supporter ($100–$199), Bronze ($200-$599), Silver ($600-$1999), Gold ($2000-$4999) and Platinum ($5,000+). Donor recognition appears in the printed program, meeting app, and on our website. I encourage all professional members to consider contributing at www.texasacademyofscience.org/donate. Serving as your TAS President this year has been a profound honor. Thank you for your support and trust. I look forward to continuing to contribute to the Academy's growth in my next role as Immediate Past President.

Maria Burns, Ph.D

President, Texas Academy of Science
Director and Faculty, Technology Leadership and Innovation Management Program
Cullen College of Engineering, University of Houston
Honorary Member, Lifetime Award, U.S. Coast Guard Auxiliary

Donate to TAS
Today!

Courtesy of JasonLLocklin photography

Welcome from the TAS Treasurer

It is a great pleasure to welcome all of you to our 129th Annual Conference for the Texas Academy of Science! It has been a good year financially for the Academy – we have successfully maintained our budget and financial standing as well as being able to recognize many students that have done outstanding research at various institutions.

One of the things that I really appreciate about TAS is that it is an organization completely run by volunteers. Most of these volunteers already have a "day job" that keeps them extremely busy so they really don't need to add anything else to their to-do list. And yet they spend hours making sure that TAS can be one of the premier organizations supporting research in our state.

Speaking of volunteers, we are always looking for new people like you to make TAS even better. There are positions every year that we need to fill from our membership so I hope that even now you might consider volunteering for one of these positions. For example, every year the Board of Directors needs at least one additional Non-Academic Director, one Academic Director, a Student Representative, and a new Vice-President. The Vice-President position actually begins a 4-year "track" – the Vice-President transitions into the President-Elect, followed by the President, and finally followed by the Immediate Past President. So, if you find yourself interested in getting involved like this, talk with our President about it and let's see if we can put you to work!

As I just mentioned, students are not only sharing their research at our Annual Meeting, but they are also sharing their ideas on our Board of Directors. If you are wondering what a Student Representative might be doing on our Board, they are the ones that actually plan and execute the immensely popular Science Jeopardy that we have every year at our Annual Meeting. So, if you have a student that you think would make a great Student Representative because they are full of ideas and can be relied upon to get things done, let us know! Our Immediate Past President is always looking for those kinds of students for that position.

It is an honor to serve as the Treasurer of TAS and I'm looking forward to continued association with an organization that I have grown to love and respect. I hope you enjoy this year's meeting!

Kathy Wood, Ph.D

Treasurer,
Texas Academy of Science

THE TEXAS JOURNAL OF SCIENCE

Welcome to Tyler and to the 129th annual meeting of the Texas Academy of Science. As Managing Editor of the Texas Journal of Science (TJS), I am delighted to welcome you and wish you a productive and enjoyable weekend of presentations, conversations, and connections with colleagues from across the state.

As the official journal of the Texas Academy of Science, TJS continues to serve as a venue for sharing high quality research conducted by our members and colleagues working in and around Texas. We are currently accepting manuscripts for consideration and encourage you to submit your work. The journal is fully open access, which increases the visibility and reach of the research we publish and ensures that it is accessible to a broad scientific audience.

To better support authors and streamline the publication process, we have recently modified our editorial staffing structure to include additional manuscript editors, Dr. Andy Kasner and Dr. Kathryn Perez. Both Andy and Kathryn have served Texas Academy of Science and the journal for many years. Their coming back on as TJS Manuscript Editors allows us to handle reviews more efficiently to reduce the time from submission to publication. Once an article is accepted, it is published online immediately so that new research is available without delay.

Because the journal is now published exclusively online, page charges are no longer being collected. Instead, a flat article processing charge is in place. In addition, color figures and photographs can now be published without any additional fees, allowing authors greater flexibility in how their work is presented.

Thank you for being part of the Texas Academy of Science and for your continued support of the Texas Journal of Science. I hope you enjoy your time in Tyler and have a great meeting.

Sincerely,

Jason L. Locklin, Ph.D.

Managing Editor
Texas Journal of Science

Texas Journal of Science

THE TEXAS JOURNAL OF SCIENCE

Call for Manuscripts

The Texas Journal of Science is the peer-reviewed publication of The Texas Academy of Science. The goal of the Journal is the timely dissemination of research results and scientific information to the scientific community. Scholarly papers reporting original research results in any field of science, technology, or science education will be considered for publication.

The Journal is actively seeking manuscripts

The Journal is online and open access. Accepted papers are published immediately.

Old issues (1949-2010) are also available online for free from the Biodiversity Heritage Library through the Texas Journal of Science website.

If all authors are TAS members at the time an article is submitted and published, article processing charges will be waived for the manuscript. We invite you to submit your latest manuscript at www.texasjournalofscience.org.

Courtesy of JasonLLocklin photography

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Texas State University
Vice Chair: Theresa de Cree
Texas State University

Biomedical Science
Chair: Joni Ylostalo
University of Mary Hardin-Baylor
Vice Chair: Rachael Carroll-Craig
University of Mary Hardin-Baylor

Cell & Molecular Biology
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University of Houston-Downtown
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Chemistry & Biochemistry
Chair: Darrell Fry
Stephen F. Austin State University
Vice Chair: Bidisha Sengupta
Stephen F. Austin State University

Conservation Ecology
Chair: Wendi Wolfram
Purdue Global University
Vice Chair: Andrea Jensen
University of Mary Hardin-Baylor

Freshwater Science
Chair: Mary Kay Johnston
Concordia University
Vice Chair: Cynthia Bashara
Southwestern University

Geoscience
Chair: Michael Read
Stephen F. Austin State University
Vice Chair: Mindy Faulkner
Stephen F. Austin State University

Graduate Student Oral Paper Competition
Chair: Travis LaDuc
University of Texas Austin

Marine Science
Chair: Annie Mowry
McLennan Community College
Vice Chair: Jennifer Hunt
University of Texas Permian Basin

Mathematics & Computer Science
Chair: Todd Dole
Hardin-Simmons University

Nueroscience
Chair: Seena Mathew
University of Mary Hardin-Baylor
Vice Chair: Danielle Grove
Texas Lutheran University

Physics & Engineering
Chair: Bryant Wyatt
Tarleton State University
Vice Chair: Brian Flowers
University of Texas Permian Basin

Plant Biology
Chair: Kevin Eddy
Texas Lutheran University
Vice Chair: Matt Allen
Wayland Baptist University

Science Education
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Vice Chair: Dustin Perez
University of Houston

Systematics & Evolutionary Biology
Chair: Matt Greenwold
University of Texas Tyler
Vice Chair: Thornton Larson
Sul Ross State University

Terrestrial Ecology & Management
Chair: Eli Hartung
Texas State University
Vice Chair: Richard Patrock
Texas A&M Kingsville

DISTINGUISHED TEXAS SCIENTIST

Dr. Rusty Towell

Director of NEXT Lab
Professor of Engineering and Physics
Abilene Christian University

Dr. Rusty Towell is the founding director of ACU's Nuclear Energy eXperimental Testing (NEXT) Lab which is building the first university advanced reactor in the country. Rusty has a BS degree in Engineering Physics from ACU where he has been a professor for the past 25 years. He earned a Ph.D. in nuclear physics from The University of Texas. He served in the U.S. Navy as an instructor at the Naval Nuclear Power School and completed a postdoctoral research fellowship with Los Alamos National Laboratory working at Brookhaven National Lab. For the past 37 years, Rusty has worked at many different national labs on several international research projects. His over 500 publications have been cited more than 50,000 times.

Outstanding Texas Educator

Mrs. Jamie Flint

Jamie Flint is a National Board–Certified Teacher with a Bachelor of Science in Biomedical Science from Texas A&M University and a master's degree in Chemical Education from South Dakota State University. She has taught AP Chemistry and Honors Chemistry for 21 years at Spring Woods High School in Houston, Texas, and has served as the school's National Honor Society sponsor since 2021.

Mrs. Flint has been an AP Chemistry Exam Reader since 2015 and became a Table Leader in 2025. Deeply passionate about chemical education, she regularly attends and presents at chemistry conferences, continually seeking innovative strategies to enhance student learning. She is an active member of the American Association of Chemistry Teachers (AACT), the Science Teachers Association of Texas (STAT), and the Associated Chemistry Teachers of Texas (ACT2), where she served on the board from 2010 to 2022.

Mrs. Flint believes the role of a teacher is to ignite curiosity, not just deliver information. As William Butler Yeats wrote, "Education is not the filling of a pail, but the lighting of a fire." Chemistry can be intimidating for many students, but she meets that fear head-on through engaging demonstrations, interactive lessons, and her classroom motto, "Chem-Is-Try." When students begin to doubt themselves, she reminds them that success in chemistry comes from persistence and the courage to ask questions. Her classroom is a place where mistakes are expected and progress is celebrated.

Teaching at a Title I campus, Mrs. Flint is committed to ensuring that limited funding never limits student opportunity. She actively pursues grants to support professional development and classroom innovation. In 2024, she was selected as a Shell Science Lab Regional Challenge High School Winner and awarded $10,000 in laboratory equipment. In 2025, she received a $5,000 Burns & McDonnell STEM Grant, which allowed her to purchase probeware used across all chemistry courses. These tools enable students to physically experience scientific concepts, such as pressure changes, while simultaneously visualizing real-time data and graphs. These tools deepen conceptual understanding and build transferable STEM skills.

Mrs. Flint's dedication and excellence in science education have earned her numerous honors, including Spring Branch ISD Teacher of the Year (2012), the H-E-B Excellence in Education Leadership Award (2018), the ACS Southwest Regional Award for Excellence in High School Science Teaching (2022), and the Ernest and Sarah Butler Award for Science Teaching at the High School Level (2024). She was also named a Texas State Finalist for the Presidential Awards for Excellence in Mathematics and Science Teaching in both 2023 and 2025.

Awards Banquet Agenda

Welcome from TAS	Dr. Maria Burns, TAS President
Welcome to UT Tyler	Dr. Shawana Tabassum
Outstanding Texas Educator Award	Dr. Maria Burns, TAS President
Distinguished Texas Scientist Award	Dr. Maria Burns, TAS President
Undergraduate Poster Section Awards	Dr. Alyx Frantzen, TAS Collegiate Academy
Undergraduate Oral Presentation Awards	Dr. Alyx Frantzen, TAS Collegiate Academy
Sammy Ray Marine Science Award	Annie Mowry, Marine Science Section Chair
Amir-Moez Award for Excellence in Mathematics	Todd Dole, Mathematics & Computer Science Section Chair
Graduate Student Presentation Competition Awards	Dr. Travis LaDuc, TAS Graduate Academy Counselor
Student Research Grants	Dr. Travis LaDuc, TAS Research Grants
Recognition of Outgoing Board Members	Dr. Maria Burns, TAS President
Recognition of New Board Members	Dr. Maria Burns, TAS President
Introducing the New President of TAS	Dr. Maria Burns, TAS President
Next Year’s Conference & Final Comments	Dr. Craig Younce, Incoming TAS President

Graduate Student Competition

Courtesy of JasonlLocklin photography

February 28th, 1pm-2:30pm
Robert R. Muntz Library, Room 401
Chair: Dr. Travis LaDuc

#001-GC Comprehensive insights into mosquito species diversity and habitat-specific host selection patterns in Cameron Park Zoo, Waco, Texas.

Dhivya Rajamanickam [1], Jason Pitts [1] (1. Baylor University)

The coexistence of native and non-native animals in zoological environments creates a unique ecological setting that can influence mosquito host–vector interactions. Blood-fed mosquitoes act as direct indicators of host selection and provide key insights into potential zoonotic mosquito-borne disease transmission cycles. The major objective of this study is to improve the efficiency of conventional odor-baited mosquito traps to increase mosquito collection, thereby enhancing mosquito species identification and understanding host preferences within the zoo environment. From 2023 to 2025, we conducted a three-year odor-baited mosquito surveillance at Cameron Park Zoo. We deployed three types of traps: CO_2-baited BG-PRO light traps; ten BG-Sentinel traps (five baited with BG lure only, and five baited with BG lure plus CO_2 from dry ice); and two CDC gravid traps baited with hay infusion. Mosquito species and their blood-meal hosts were identified using DNA barcoding, and pooled samples were analyzed via Oxford Nanopore Technology. To estimate the minimum flight distances of mosquitoes, we mapped blood-fed mosquito locations relative to the positions of captive animal enclosures using a Geographic Information System (GIS). BG-Sentinel traps baited with both CO_2 and lure caught significantly more mosquitoes than traps using lure alone. Blood-meal analysis revealed strong ornithophilic tendencies in Culex species and more generalist feeding behavior in Aedes species. Overall, our findings suggest that the confined zoo environment influences mosquito host-seeking behavior, likely driven by host availability and the short-distance dispersal of adult mosquitoes.

#002-GC Potential Disruptors of the Acoustic Habitat of the Carolina Wren and the Implications for Reproductive Isolation

Zachary Seidel [1], Diane Neudorf [1] (1. Sam Houston State University)

Birdsong is a culturally transmitted trait in the oscine passerines that is highly plastic in the early life history of many species, but is generally aplastic in adults. Because of this mechanism of inheritance, the song repertoire of a given adult is heavily influenced by the songs present in its acoustic habitat during the song learning phase of life. When barriers to transmission of songs, such as isolation on islands, form, these disparate populations can form unique dialects that render the reproductive signal carried by the song mutually unintelligible. A novel technique for using citizen science data to determine if dialects are forming in the Carolina wren (Thryothorus ludovicianus) and model the probable causes of those dialects was evaluated, and a field study was conducted to evaluate whether a non-native song type would elicit a territorial response in male Carolina wrens. Preliminary results indicate that the major influences on song type distribution are elevation and tree canopy density, which form major dispersal barriers for juvenile wrens and would restrict the amount of cultural exchange that is possible between populations. The field study also indicated that male Carolina wrens are more likely to react with a territorial response when presented with a familiar song type than a novel song type and are overall more reactive during the spring, their breeding season, than the fall. These results indicate that cultural song inheritance may act as a mechanism of reproductive isolation, and furthermore that citizen science is useful in modeling diverging cultural traits.

#003-GC The impact of nutrition on insecticide resistance and gene expression in Aedes aegypti

Esmeralda Rosas [1], Sarah Maestas [1], Jason Tidwell [2], Christopher Vitek [1] (1. University of Texas Rio Grande Valley, 2. USDA-Agricultural Research Service)

The development of insecticide resistance in Aedes aegypti, a major vector of medically important arboviruses such as dengue virus, Zika virus, and chikungunya virus, poses a significant challenge to vector control efforts worldwide, especially in urban and endemic regions like South Texas. Insecticides remain a common method for mosquito management; however, their widespread use has accelerated the evolution of resistance mechanisms, particularly metabolic resistance mediated by cytochrome P450 enzymes. Previous studies have demonstrated that environmental factors, such as larval nutrition, may influence mosquito physiology and the expression of resistance-associated genes, but this relationship is still poorly understood. Our study aims to investigate how varying nutritional conditions during the larval stage affect the expression of key cytochrome P450 genes (CYP6 and CYP9 families) linked to pyrethroid resistance in Aedes aegypti. Larvae were fed one of five different food treatments with varied ratios of lipids and proteins. Once mosquitoes emerged as adults, they were exposed to permethrin using the CDC bottle bioassay. Known susceptible and resistant strains were tested alongside South Texas field-collected populations for comparison. Surviving mosquitoes were tested for enzymatic activity using quantitative PCR. We hypothesize that treatments containing the highest amount of carbohydrates relative to protein will show the highest gene expression of cytochrome P450. These data will ideally provide insights into how nutrition shapes resistance, and to inform more effective strategies for vector management, including the potential manipulation of food resources to enhance the impact of control efforts.

#004-GC Influence of Mint and Basil Phytochemicals against Bacterial Biofilm Formation

Cephus Bess-Grunewald [1], Bidisha Sengupta [1] (1. Stephen F. Austin State University)

Bacterial biofilms present a persistent challenge in environmental and public health systems due to their intrinsic resistance to antimicrobial treatments. Identifying safer, biologically derived agents that can disrupt biofilm formation is therefore essential. This study investigates the effects of phytochemical-rich methanolic extracts from mint (peppermint, spearmint, chocolate mint) and basil leaves on biofilms formed by Bacillus thuringiensis in treated wastewater from the Nacogdoches, Texas wastewater treatment plant. Plant extracts were prepared through maceration in methanol, ultracentrifugation, and fine filtration. Biofilms were grown on silica discs at a 50:50 (v/v) ratio of treated wastewater and Luria broth, followed by treatment with 0.3% methanolic extracts. Optical density of the post-biofilm supernatants (OD600) and scanning electron microscopy (SEM) were used to evaluate bacterial growth and structural biofilm changes. Both phytochemical extracts and methanol reduced biofilm-associated growth relative to untreated samples, with mint and basil extracts demonstrating stronger antimicrobial activity than MeOH alone. Spearmint exhibited the most consistent reduction in OD600 and visibly decreased biofilm density in SEM images, suggesting enhanced disruption of extracellular matrix integrity. Imaging further revealed discontinuous vertical biofilm growth in MeOH-treated samples, likely attributed to alcohol-induced membrane alterations, while phytochemical extracts produced pronounced structural degradation consistent with flavonoid- and polyphenol-mediated membrane disruption. Overall, the findings highlight the potential of mint- and basil-derived phytochemicals as natural, safer alternatives for mitigating biofilm formation in treated wastewater systems.

Detailed Schedule

Key
U = undergraduate presentation
G = graduate presentation
H = high school presentation
N = professional presentation

Friday, 27 February

8am **Board of Directors' Meeting (8am-11:30am)**
College of Business (COB) 321

9am **Registration (9am-5pm)**
College of Pharmacy (WTB) - Outside 134

10am **Science Jeopardy (10am-11:30am)**
WTB 137

11am **Poster Setup (11am-2pm)**
COB 1st/2nd Floor Hallways

11:30am **Section Chairs' Pre-Session Meeting (11:30am-12:30pm)**
COB 307

12:30pm **Judges' Room**
COB 350.55

12:30pm **Biomedical Sciences I (12:30pm-2pm)**
COB 212
Chaired by: Dr. Joni Ylostalo

12:30pm **#001-U Mirtron-5010 Enhances Stemness and Iron Accumulation in Aggressive Breast Cancer Cells**
» Noah Padilla, Reagan Farrell, Maya Vaela, Alejandro Ruiz, Trevor Jones, Dr. Kuan-Hui Ethan Chen

12:45pm **#002-U Screening Compounds for Their Anti-Cell Proliferation Properties**
» Tina Prajapati, Dr. Vaishali Chaubal, Dr. Rachna Sadana

1pm **#003-U Histological Characterization of Cardiovascular Malformations in a Chick Model of Maternal Phenylketonuria**
» Desarey Reyna Gaytan Robles, Danny Gutierrez, Dr. Nikki J. Seagraves, Dr. Adriana P. Visbal, PhD

1:15pm **#004-U The Skin Microbiome & Acne: How Common Skincare Ingredients Affect Bacteria and Inflammation**
» Alanis Cotto, Irene Perry

1:30pm **#005-U Cytotoxicity of Freebase Nicotine and Its Analogs Using Cellular and Statistical Methods**
» Kiera Griffin, Taylor Jefferis, Dominic Pruss, Mohana Sengupta, Dr. Rodney Sturdivant, Dr. Amanda Charlton-Sevcik, Dr. Robert Strongin, Dr. Christie Sayes

1:45pm **#006-G Production of 3-cyanopyridine upon vaping nicotinamide and evaluating the toxicological effects of individual and combined exposures via isobologram-based analysis**
» Taylor Jefferis, Mohana Sengupta, Kiera Griffin, Dr. Robert Strongin, Dr. Christie Sayes

12:30pm **Chemistry & Biochemistry I (12:30pm-3pm)**
COB 112
Chaired by: Dr. Darrell Fry

12:30pm **#007-U Boron Is Special: Unique Role of Boron in C-B Bond Forming Reactions**
» Avree Fields, Dr. John Gary

12:45pm **#008-U No Ring Required: Constraints for Organic Components in Redox Cooperativity**
» Emma Patton, Dr. John Gary

1pm **#009-U Battle of the Geometries: Square Planar Versus Tetrahedral Geometry for Electronic Communication**
» Aiyana Gonzalez, Dr. John Gary

1:15pm **#010-U The Great Shape Debate: How Geometry and Electron Count Affect Electronic Communication**
» Sophia Myers, Dr. John Gary

1:30pm **#011-U The Crystal Clear Truth About Salts: A Dive into Characterization of Global Salt Samples**
» Katelyn Jones, Dr. Alyx Frantzen, Dr. Julie Bloxson

Continued from **Friday, 27 February**

1:45pm **#012-U In Situ Characterization of HIMARS Launch Sites: A Proof of Concept for Portable XRF Screening**

» Aaron Beavers, Dr. Kiley Miller

2pm **#013-U IMAC protein purification via Ni(II)-NTA and histidine tags: A computational approach of incremental binding energies**

» Kaci Thomson, Dr. Brian Barngrover

2:15pm **#014-U Growth of Bismuth Nanoparticles from BiCl Salts Using DFT**

» Barbie Adams

2:30pm **#015-N The chemistry of the Si-Ge bond, 2**

» Dr. Keith Pannell

2:45pm **#016-N Designing Strategies of H-Bonded Chemosensors for Molecular Recognition**

» Prof. Rashid Mia

12:30pm Conservation Ecology (12:30pm-2:30pm) & Section Meeting (2:30pm-2:45pm)

COB 111

Chaired by: Dr. Wendi Wolfram

12:30pm **#017-U Wanted Dead, Not Alive: Using eRNA:eDNA ratios to assess viability of invasive apple snail (Pomacea maculata)**

» Kylie Allemeier, Katelin Pilarski, Dr. Romi Burks, Dr. Matthew Barnes

12:45pm **#018-U Examining angiosperm conservation methods through the diet of Bombus pensylvanicus**

» Gabriel Ramos, Dr. Christopher Randle, Dr. Justin Williams

1pm **#019-U Where Could This Moth Go? Predicting Future Distribution Using SDMs**

» Zyra Johnson, Dr. Christopher Randle

1:15pm **#020-U Effects of Invasive Chinaberry Tree Fruits on Invasive Asian Clams**

» Amy Lowe, Dr. Chris Distel

1:30pm **#021-G Comparing the efficacy of three crayfish sampling methods on two Texas SGCN Procambarus species during different seasons**

» Matthew Blow, McKenzie Adkins, Jared Dickson, Katrin Kellner, Dr. Archis Grubh, Dr. Matt Greenwold

1:45pm **#022-G Comparative physiology and thermal biology of sympatric toad species**

» Peter J. Babcock, Dr. William I. Lutterschmidt

2pm **#023-G Monitoring the effects of environmental variations on nesting success of Eastern Bluebirds (Sialia sialis) on a university campus**

» Gwendolyn Nichols, Jessica Coleman, Dr. Matt Greenwold

2:15pm **#024-G Environmental influences of eDNA detection and persistence inform sampling protocol**

» Dr. William I. Lutterschmidt, Kyra S. Woytek

12:30pm Plant Biology (12:30pm-4pm) & Section Meeting (4-4:15pm)

COB 203

Chaired by: Dr. Kevin Eddy

12:30pm **#025-U Comparative Analysis of Anti-Hemolytic Properties in Ilex Species: A Study of Plant Extracts against Streptococcus and Enterococcus Bacteria**

» Atlanta Williams, Hanna Erfanian

12:45pm **#026-U Diquat Herbicide-Induced Effects on Cherry Tomatoes**

» Yamilex Hernandez, Dr. Honey Golden

1pm **#027-U Gene flow between 'races' of the annual wildflower Mentzelia pectinata (Loasaceae) based on multiple microsatellite loci**

» Gisela Guerrero, Ana Rodriguez, Hannah Anthony, Amy Osborn, Dr. Joshua Brokaw

Continued from **Friday, 27 February**

1:15pm	**#028-U Microhabitat variation influences streambed plant diversity at the Independence Creek Preserve** » Edmundo Avalos, Olivia Fischer, Dr. Matthew Allen
1:30pm	**#029-U Development of new microsatellite loci to study geneflow in the annual wildflower Mentzelia pectinata (Loasaceae).** » Ana Rodriguez, Hannah Anthony, Gisela Guerrero, Dr. Joshua Brokaw
1:45pm	**#030-G Shedding Light on Plant and Soil Sciences with Synchrotron-Based Spectroscopy** » Caleb Shackelford
2pm	**#031-N Microbial Strategies to Promote Legume Tolerance to Soil Alkalinity** » Dr. Ahmad Kabir
2:15pm	**#032-N Preserving the Biodiversity of the UT Permian Basin Kurtz Herbarium by Inclusion in the Texas Oklahoma Regional Consortium of Herbaria (TORCH)** » Irene Perry
2:30pm	**#033-N Expert in a Dying Field? Botany's Decline in Tuition-Dependent Colleges and Universities** » Dr. Joshua Brokaw
12:30pm	**Science Education (12:30pm-1:30pm) & Section Meeting (1:30pm-1:45pm)** *COB 214* Chaired by: Woody Cox
12:30pm	**#034-N Navigating Human Values and Motives in STEM Education: Insights from the Preteen Years** » Dr. Sajid Bashir, Dr. Jingbo Liu
12:45pm	**#035-N The successful application of WOKE funding to STEM progress** » Dr. Keith Pannell
1pm	**#036-N A Pedagogical Experiment: Repackaging Introductory Biology Labs and Research Classes Into Professional Skills Courses** » Dr. Chris Distel
2pm	**Physics & Engineering (2pm-3pm) & Section Meeting (3pm-3:15pm)** *COB 214* Chaired by: Dr. Bryant Wyatt
2pm	**#037-U A Novel Multiphysics Simulation Engine for Modelling High-Enthalpy Plasma-Surface Interactions in Hypersonic Flight Regimes** » John-Ryan Lawrence, Dr. Sajid Liu, Dr. Jingbo Liu
2:15pm	**#038-G Benchmarking Transformer Models for the Classification of Gravitational-Wave Detector Glitches** » Rudhresh Manoharan, Brian Phillips, Tanish Chettiar, Dr. Gerald Cleaver
2:30pm	**#039-N From Discovery to Application: Engineering Atomic-Ternary Semiconductors into TRL-4 Resilient Power Modules** » Dr. Jingbo Liu, Dr. Sajid Bashir
2:30pm	**Coffee Break**
2:45pm	**Marine Science (2:45pm-4:30pm) & Section Meeting (4:30pm-4:45pm)** *COB 111* Chaired by: Annie Mowry
2:45pm	**#040-U Impact of Topology on Coral Larvae Settlement on Concrete Matrices** » Jennifer Hunt, Dr. Matthew Barnes, Dr. Brian Flowers, Dr. Thomas Ready

Continued from **Friday, 27 February**

3pm **#041-U The Role of Symbiotic Status of Exaiptasia diaphana in Serratia marcescens Pathogenesis**

» Amy Joffrion, Dr. Tanya Brown

3:15pm **#042-U Abundance and Disease Status of Starlet Corals in Roatán, Honduras**

» Gloria Dominguez, Ashley Tejada, Kaylee Aguilar, Xaile Garza, Ana Quintanilla, Leon Rosales, Annie Mowry, Ashlyn Kennedy, Matthew Hicks, Racheal Gomez, Traesha Robertson, Dr. Stephanie Lockwood, Jacqueline Dove, Stephanie Randell

3:30pm **#043-U The Diversity of West Caribbean Octocorals in Roatán, Honduras**

» Harrison Wolf, Christopher Allovio, Hannah Dawson, Zoe Hilliard, Traesha Robertson, Annie Mowry, Ashlyn Kennedy, Jacqueline Dove, Dr. Stephanie Lockwood, Stephanie Randell

3:45pm **#044-U A Longitudinal Study of Macroorganism Associations and Health Status of Demospongiae Species in Roatán, Honduras**

» Cambria Blanton, Caden Helona, Ashlyn Kennedy, Anne Mowry, Traesha Robertson, Jacqueline Dove, Dr. Stephanie Lockwood, Naomi Hammond, Stephanie Randell

4pm **#045-U Rope Sponge Diversity and Health Status in Roatán, Honduras**

» Yuto Goto, Nicholas Mischtian, Tafadzwa Duri, Juliusz Bachleda-Curus, Traesha Robertson, Annie Mowry, Ashlyn Kennedy, Jacqueline Dove, Dr. Stephanie Lockwood, Stephanie Randell

4:15pm **#046-G From Anemone to Coral: Establishing Nematostella vectensis as a Translational Model for Coral Disease Research**

» James Campbell, Dr. Tanya Brown

3:15pm **Neuroscience (3:15pm-3:30pm) & Section Meeting (3:30pm-3:45pm)**

COB 212

Chaired by: Dr. Seena Mathew

3:15pm **#047-N Effects of Transcranial Photobiomodulation on Cognitive Processes, Anxiety Symptoms, and Brain Hemodynamics**

» Adrian Nguyen, Laura Gamboa, Isabelle Rose, Jordan Schwartz, Nicole J. Moore, Dr. Douglas Barrett, Dr. F. Gonzalez-Lima

3:15pm **Systematics & Evolutionary Biology (3:15pm-4:45pm) & Section Meeting (4:45pm-5pm)**

COB 112

Chaired by: Dr. Matt Greenwold

3:15pm **#048-U Gene Currents: Understanding Genetic Diversity of Apple Snails in Northern and Southern Belizean Watersheds**

» Johun Reyes, Gage Mallo, Dr. Romi Burks

3:30pm **#049-U Opercularis Muscle in Facultatively Metamorphic Eurycea sp. A Comparison between Paedomorphs and Metamorphs**

» Kelsey M. Malousek, Joseph Humphrey, Dr. Ruben U. Tovar, Dr. Thomas J. Devitt, Dr. David M. Hillis, Dr. Dana M. Garcia

3:45pm **#050-G Comparative morphology of the American and Houston Toad**

» Lauren N. Scherrer, Dr. Juan D. Daza, Dr. William I. Lutterschmidt

4pm **#051-G Diversity and Mitogenomics of Archinominae Species (Annelida: Amphinomidae) From Marine Biodiversity Hotspots**

» Bernard Mbithi, Dr. Fernando Calderón-Gutiérrez, Dr. Utpal Smart, Dr. Beatriz Yáñez Rivera, Dr. Elizabeth Borda

4:15pm **#052-G Adaptation to Acidic Environments Potentiates Pathogenicity of Bacteria**

» Kingsley Amoateng, Wei-Chin Ho

4:30pm **#053-GMorphological variation in the molar dentition of a population of Neotoma micropus from Chaparral Wildlife Management Area, La Salle County, Texas**

» Stacie Skwarcan, Christopher Bell

Continued from **Friday, 27 February**

3:30pm **Mathematics & Computer Science (3:30pm-4:30pm) & Section Meeting (4:30pm-4:45pm)**
COB 214
Chaired by: Todd Dole

3:30pm **#054-U Standardizing Academic Syllabi Using Artificial Intelligence**
» Daniel Antonio, Prof. Dipak Singh

3:45pm **#055-U In Silico Design of Peptides to Prevent Insulin Aggregation**
» Thanh Tien Dao, Dr. Bidisha Sengupta

4pm **#056-N Reasoning from the Code Image of a Graph**
» Dr. Paul Feit

4:15pm **#057-N Category Theory or How to Talk Easily about Hard Things**
» Dr. Paul Feit

4pm **Coffee Break**

5pm **Graduate Fair**
COB 2nd Floor Lounge

5pm **Posters-Anthropology (P1-P7)**
COB 1st/2nd Floor Hallways

P1-U Evaluating bone strength in press-fit versus cement-fit arthroplasty via micro-CT
» Theresa de Cree, James Myrick, Dr. Daniel Wescott

P2-G Can low-resolution imaging be used to assess living activity level in skeletal remains? A comparison of imaging modalities using the Texas State Donated Skeletal Collection (TXSTDSC)
» ChristiAna Dunham, Dr. Elaine Chu

P3-U Evaluation Of Sunscreen Properties Of Ancient Maya Body Paints
» Jessi Loyd

P4-U The importance of projectile trauma analysis training for undergraduate students
» Javier Garcia, Theresa de Cree

P5-G Forensic analysis of hacksaw paint transfer in dismemberment
» Muthoni Thuku, Sanjib Thapa, Dr. Rizalia Klausmeyer, Rohil Kayastha, Dr. Bernd Zechmann, Dr. Zhenrong Zhang, Dr. Joseph Ferraro

P6-U Recognizing Intimate Partner Violence in Forensic Anthropological Trauma Analysis: A Literature Review
» Sara Medeiros

P7-G Osteometric Measurements for Reassociating and Pair-Matching of Commingled Tali and Naviculars
» Susanna Jones

5pm **Posters - Biomedical Science (P8-P18)**
COB 1st/2nd Floor Hallways
Chaired by: Dr. Joni Ylostalo

P8-U Gene Expression Changes in Parkinson's Disease
» Serena Ylostalo, Dr. Joni Ylostalo

P9-G Enhancing Monascus pigments production and application as a natural alternative to sodium nitrite in pork sausages compared with traditional food colorants.
» Lakshmi Devi Chittepu, Minji Jang, Behiye Ebru Sahiner, Krithika Maki, Boluwatife Ajayi, Dr. Md Ariful Haque, Dr. Md Abdur Razzak, Dr. Hye Kim, Dr. Wesley Osburn, Dr. Mathew Taylor, Dr. Seockmo Ku

P10-U Optimization of PVA, Ag Hydrogels: Effects of Heating and Freeze Thaw Crosslinking on Antibacterial Activity Against E. coli
» Ethan Yager, Dr. Milka Montes

Continued from **Friday, 27 February**

P11-G Diversity and Prevalence of Non-Tuberculosis Mycobacteria in Texas

» Maritza Estrada, Dr. Jennifer Honda, Dr. Joshua Banta

P12-U Pedigree of a Rare Variant of the MYH7 Gene Associated with Cardiomyopathy

» Danielle Felice Galon, Pheben Abebe, Dr. Joshua Brokaw

P13-U Screening Compounds for their Potential to Inhibit Growth of Leukemia cells (Molt-4)

» Jiya Desai, Tina Prajapati, Dr. Rachna Sadana

P14-U Discovering potential inhibitors of New Delhi metallo-β-lactamase 1 (NDM-1) using Computational Docking

» Laura Jung, Dr. Josh Beckham

P15-U Evaluation of Cranberry-Loaded Hydrogels for Antibacterial Activity

» Shayna Oliver

P16-H The Impact of BT2-Modulated BCAA Reduction as a Novel Therapeutic for Alzheimer's Disease

» Shriya Sreeju, Tanisha Makam, Lara Makkapati

P17-U Exploring natural anti-microbial and anti-virulence compounds with their mechanism of actions to combat drug-resistant pathogens

» Nathaniel Pyenta, Dr. Santosh Kumar

P18-H Inhibitron-LC - A Novel Multitarget Drug with Nanoparticle Precision for Triple-Negative Breast Cancer

» Nikila Swaminathan

5pm **Posters - Cell & Molecular Biology (P19-P44)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Adriana P. Visbal, PhD

P19-U Regulation of RumAB Mutagenic Activity by the Putative R391 Lon Protease

» Caleb Hammons, Dr. Martín González

P20-U Role of DENN Domain-Containing Protein 5b (dennd5b) During Early Embryonic Development of Zebrafish

» Khaled Mohamed Nassar, Alicia Mendoza, Magdalen Marston, Andre Gil, Dr. Sharmin Hasan

P21-U Discovery of potential novel inhibitors of Mycobacterium tuberculosis InhA (MtInhA) with virtual screening

» Shriya Mukkavilli, Dr. Josh Beckham

P22-U Novel DKNR Compounds Inhibit Proliferation in Triple-Negative Breast Cancer Cell Line

» Ashley Espinoza

P23-H Validating the Specificity of Novel Primers for a Biofilm Study

» Shijay Sivakumar, Dr. Athenia Oldham

P24-U Formin Binding Protein 1l (fnbp1l) plays an important role during early embryonic development of zebrafish (Danio rerio)

» Ty Franklin, Michael La Fontaine, Alicia Mendoza, Dr. Sharmin Hasan

P25-U CUDC-970 induces epigenetic reprogramming and AKT dephosphorylation in peripheral T-cell lymphoma

» Braden Samples, Alex Rodmanac, Marco Maples, Sophia Myers, Adam Chaudhary, Dr. Mamta Gupta

P26-U Requirement of Hippo signaling for larval crawling muscle development in Drosophila.

» Kevin Hernandez

P27-G An Expressional and Functional Study of PDZ and Lim Domain Paralogs in Danio rerio

» Andre Gil, Alicia Mendoza, Dr. Sharmin Hasan

Continued from **Friday, 27 February**

P28-U New Protocol for Genotyping Casper Zebrafish Mutants Using RT-PCR in a University Genetics Course

» Pheben Abebe, Danielle Felice Galon, Dr. Joshua Brokaw

P29-U Screening Synthetic Compounds for Impact on Cell Viability of Pancreatic Cell Line

» Vivian Do Nguyen, Tina Prajapti, Dr. Rachna Sadana

P30-U Calibration matters: Refining protocols for reliable dose-response data

» Noah Dyson

P31-G Expression and Functional Analysis of MTSS2 Isoforms (mtss1la/mtss1lb) During Early Embryonic Development in Zebrafish

» Danielle Duncan, Braulio Sandoval, Andre Gil, Samira Alam, Alicia Mendoza, Amira Manry, Dr. Sharmin Hasan

P32-U Evaluating Synthetic Compounds for Inhibition of Cell Proliferation in Lung Cancer Cell Line

» Huriel Bautista, Dr. Rachna Sadana, Tina Prajapati

P33-G The protective role of oncomodulin from stress induced mitochondrial damage in auditory cells

» Janith Halpage, Dr. Santha Ranganathan, Dr. Dwayne Simmons

P34-U Dimethyl Terephthalate Effects on Adipogenesis in an OP9 Cell Model

» Gustavo Zamora, Klarissa Martinez, Prof. Jennifer Heitmeyer, Dr. Danielle Grove

P35-U Post-translational Regulation of the MucA□□B Error-Prone DNA Polymerase

» Paige Djurdjevic, Dr. Martín González

P36-U Troubleshooting GSK3β Purification and Optimizing Virtual Screening for Inhibitor Discovery

» Xiya Chen, Saikrishna Gundlapalli, Dr. Josh Beckham

P37-U The Adipogenic Effects of Butylparaben on OP9 Mouse Cells

» Natalie Osina, Caitlin Roach, Prof. Jennifer Heitmeyer, Dr. Danielle Grove

P38-U Effects of p-Phthalate Dimethyl Terephthalate on OP9 Mouse Mesenchymal Stem Cells

» Klarissa Martinez, Gustavo Zamora, Prof. Jennifer Heitmeyer, Dr. Danielle Grove

P39-U OP9 Mouse Stem Cell Differentiation When Treated With Two Specific Types of PFHxS (PFAS)

» Ryan Trevino, Nicole Bloodgood, Prof. Jennifer Heitmeyer, Dr. Danielle Grove

P40-U Microbiological Determination of Folate in Fermented Asparagus Using HPLC

» Sanjana Rachala

P41-U Differential Gene Expression in Human Bronchial Cells after Exposure to 3D-printer Emitted Aerosols

» Dominic Pruss, Mahmud Shojiv, Taylor Jefferis, Dr. Jon Beard, Charli Worth, Dr. Joseph Taube, Dr. Mary Lauren Benton, Dr. Christie Sayes

P42-U Assessing the Adipogenic Effects of 1H,1H,2H,2H-PFHxS and PFHxS Using the OP9 Mouse Cell Line

» Nicole Bloodgood, Ryan Trevino, Prof. Jennifer Heitmeyer, Dr. Danielle Grove

P43-G Visualizing Non-Centrosomal Microtubule-Organizing Centers in Drosophila Muscle Using Fluorescent Tools

» Cody Griffin, Dr. Mardelle Atkins

P44-U The microtubule network is altered prior to cachexic wasting in a Drosophila larval model

» Chrislynn Harris, Dr. Mardelle Atkins

5pm **Posters - Chemistry & Biochemistry (P45-P73)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Darrell Fry

Continued from **Friday, 27 February**

P45-U Impact of azadiradione on DNA oxidation

» Julia Jurewicz, Mariah Saenz, Dr. Mary Brintha Croos

P46-U Improving temperature control for myoglobin oxidation kinetic studies

» Eva Zohne, Nwankwo U. Dickson, Zechariah Hall, Destini Eidman, Dr. David E. Thompson

P47-U Discovering Novel Inhibitors for 3-Oxoacyl-(Acyl-Carrier-Protein) Reductase (FabG) in Plasmodium falciparum

» Sam Vargas, Dr. Josh Beckham

P48-U Comparing Dynamics of Fermentation and Probiotic Properties with American Kimchi

» Justy Chung, Jairus Wenzel, Sehyeon Song, Dr. Seockmo Ku

P49-U Shifting Geometries: Octahedral Geometry and Electron Count Affect Electronic Communication

» Jordan Ruppert, Dr. John Gary

P50-U Biochar Production Through Microwave Pyrolysis: A Study of the Structure of Activated Carbon and Graphite Carbon.

» Jemima Estrada, Jessica Villarreal

P51-U The Use of Microwave-Promoted Heating in an Undergraduate Organic Lab Activity: The Cannizzaro Reaction

» Hayden Tolbert, Dr. Russell Franks

P52-U Exploring thermal selectivity for portable SERS-based methamphetamine detection in soil

» Michaela Henson, Alicia Cortez, Samantha Martinez, Chizzy Obietikponah, Dr. David E. Thompson

P53-U Reflective Analysis of Inorganic Pigments

» Clayton Engler, Holdin Price, Dr. Corey Thompson

P54-U Pharmaceutical Contaminant Analysis in the Nacogdoches Wastewater Treatment Process using SPE-UHPLC-MS/MS

» Brandon Lovell, Dr. Kefa Onchoke, Dr. Mike Ojemaye, Dr. Michael Janusa, Kadin Green, Dr. Jamie Humphries

P55-U Thermally-controlled bypass valves for selective SERS detection of methamphetamine in soil

» Samantha Martinez, Alicia Cortez, Michaela Henson, Chizzy Obietikponah, Dr. David E. Thompson

P56-U GC-MS Analysis of Castor Oil

» Anthony Ramos, Dr. Darrell Fry

P57-U Fluorescent polarization is superior to BIOMOL® for measuring RecA binding affinity

» Emma Scott, Dr. Robert Moore

P58-U Analysis of contaminant metals in tampons and evidence for metal mobility

» Sage Bartlett, Naomi Moody, Dr. Alison Bray

P59-U Green Synthesis of a Cross-linked Polymerized Hydrogel Containing NDGA-Capped Gold Nanoparticles for Skin Lesion Treatment

» Areej Khodair, Dr. Milka Montes

P60-U Pyranone Generation By Way of Substituted Oxetanes

» Denali Rubio, Dr. Michael Ruane, Sheldon Peters

P61-U Phytochemical Modulators of Cancer Metabolism: Docking Analysis of Flavonoid Interactions with 6-Phosphogluconate Dehydrogenase

» Alicia Trejo, Thanh Tien Dao, Georgetta Zuo, Dr. Bidisha Sengupta

P62-U Flavoring chelation properties influence the quantity of metals in vaping aerosols

» Anna Perez, Dr. Clancy Collom, Dr. Gregory Smith

Continued from **Friday, 27 February**

P63-U Investigation of Naturally Fluorescent Materials Using Fluorescent Microscopy

» Ian Cortez

P64-U Tuning Hydrogen Bonding for Designing Colorimetric Sensor for Heavy Metals

» Andrew Do, Prof. Rashid Mia, Jack Weeks

P65-U Delta-8 or Delta-9? Testing the Truth Behind THC Gummies

» Abby Henderson, Dr. Dennis Gibson

P66-G Innovative and Timely Cell-Free Assays: A Novel Approach/ Methodology in Toxicity Testing

» Sabrina Shahjabeen Alam, Dr. Christie Sayes, Dr. Amanda Charlton-Sevcik

P67-U Utilizing Free Fatty Acids to Inhibit Bacteria in Eyedrops

» Bethany Blair, Bailey Nobles

P68-U Investigating Various Deep Eutectic Solvent Solutions in Chitin Extraction

» Addysage Seay, Dr. Dennis Gibson, Dr. Philips Agboola

P69-U Virtual Screening–Driven Identification of Inhibitors Targeting MtFabG in Mycobacterium tuberculosis

» Manal Saad, Mahdia Rahman, Sharon Rong, Dr. Josh Beckham

P70-U PEG-BSA hydrogels: release and diffusion studies

» Averi Felan, Jenna Slussler, Dr. Jacques Jean-Francois

P71-U Are FTIR and mass changes a good way to determine the degradation of plastics?

» Kirstin Van Nostrand

P72-U Redox-Sensitive GFP to Monitor the Impact of Carbon Monoxide on Cellular Redox Status in Saccharomyces cerevisiae

» Jessica Villarreal, Dr. Nin Dingra

P73-U Discovering novel inhibitors of D-alanine D-alanine ligase in Yersinia pestis

» Raina Patel, Mahitha Simhambhatla, Dr. Josh Beckham

5pm **Posters - Conservation Ecology (P74-P81)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Wendi Wolfram

P74-U Foraging Responses of Hummingbirds to Nectar Concentration in an Andean Cloud Forest

» Mercy Nnaeme, Andres Vasquez, Dr. Mark Brown, Dr. Joshua Banta

P75-U Comparison of Bird Species in Various Habitats in Weston Ranch

» Natalie Garcia

P76-G Investigating the Conservation Statuses of Native Texas Crayfish Species Through Distribution Analysis and Ecological Niche Modeling

» Ms. Elizabeth Croft, Jared Dickson, Dr. Archis Grubh, Dr. Ryan Shartau, Dr. Joshua Banta

P77-G Aggregation and collation of Texas crayfish museum specimens to determine their current conservation statuses

» Adrian Alvarez, Dr. Archis Grubh, Dr. Joshua Banta, Dr. Ryan Shartau

P78-G Environmental tolerances and habitat association of three critically imperiled crayfish species in Texas

» Andy Walker, Dr. Ryan Shartau, Dr. Joshua Banta

P79-N Resilient Biodiversity: Guadalupe River Flooding Update

» Dr. Chris Distel

Continued from **Friday, 27 February**

P80-U Utilization of an eDNA ddPCR assay on two SGCN mayfly species.

» Jace Douglas, Matthew Blow, James York, Marsha Williams, Dr. Archis Grubh, Dr. Lance Williams, Dr. Matt Greenwold

P81-G Life histories of two SGCN Procambarus Species in East Texas

» McKenzie Adkins, Matthew Blow, Katrin Kellner, Dr. Matt Greenwold, Jared Dickson

5pm **Posters - Freshwater Science (P82-P88)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Mary Kay Johnston

P82-U Playing by the numbers: Comparing microplastic estimates from summation and extrapolation

» Sarah Berver, Emma Flores, Jordan Emerson, Dr. Romi Burks, Andre Felton

P83-U Thermal Sensitivity Patterns in Urban and Rural Austin Streams

» Jaalah Shand, Amber Clark, Dr. Mary Poteet

P84-G Spatiotemporal analysis of metazoan community from the subterranean estuaries of the Yucatan Peninsula and Cozumel island through metagenomics

» Danielle Bragg, Dr. Elizabeth Borda, Dr. Fernando Calderón-Gutiérrez

P85-U Phenotypic Diversity of Escherichia coli from Water Samples in North and East Texas

» Christian Buford, Wei-Chin Ho

P86-U Using Grass Shrimp to Evaluate Mercury Concentrations of Texas Lake Systems

» Robert Albin, Dr. T.J. Boyle

P87-U Assessing white bass (Morone chrysops) population characteristics in two central Texas lakes across season and size classes

» Caleb Fry, Yessenia Edgecomb, Caroline Vanderburg, Mervin Narito, Dr. Jason Locklin

P88-U Signs of Decline in Texas? Zebra Mussel Population Density and Condition Across Invasion Timelines

» Kaylyn Wolf, Mervin Narito, Peyton Sen, Dr. Jason Locklin

5pm **Posters - Geoscience (P89-P92)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Michael Read

P89-U Visualizing the First Flush Temperature Effect in Austin, Texas

» Rhianna Saini, Dr. Mary Poteet

P90-U Characterizing the K-Pg Boundary in Central Arkansas, USA

» Matthew Smith, Dr. Mindy Faulkner

P91-G Evaluating Sulfate-Reducing Potential of Native Wetland Plant Species in a Coal Ash Disposal Area, Panola County, Texas, USA

» Cari Mitchell, Dr. Mindy Faulkner, Dr. Jenny Rashall

P92-U Insights into the Large Mammal Fossils from Phillips Paleo Cave, Crockett County, Texas

» Angelica Reyes, Stacie Skwarcan

5pm **Posters - Marine Science (P93-P99)**

COB 1st/2nd Floor Hallways

Chaired by: Annie Mowry

P93-U Staging the embryogenesis of male-pregnant Gulf pipefish (Syngnathus scovelli) using optic development.

» Kimble Gould, Aniston Lovetinsky, Dr. Sunny K. Scobell

Continued from **Friday, 27 February**

P94-U Characterizing embryonic development in the pregnant male pipefish, Syngnathus Scovelli, using snout formation as a morphological marker

» Aniston Lovetinsky, Kimble Gould, Dr. Sunny K. Scobell

P95-U A Longitudinal Study: The Abundance and Disease Status of Starlet Corals in Roatán, Honduras

» Gloria Dominguez, Ashley Tejada, Kaylee Aguilar, Xaile Garza, Ana Quintinilla, Leon Rosales, Annie Mowry, Ashlyn Kennedy, Matthew Hicks, Racheal Gomez, Traesha Robertson, Stephanie Randell, Dr. Stephanie Lockwood, Jacqueline Dove

P96-U The Role of Symbiodiniaceae Identity in Mediating Pathogenic Bacterial Effects on Exaiptasia

» Emily Ryan, Dr. Tanya Brown

P97-U Echinoderm Diversity in Roatán, Honduras

» Anna Contreras, Yuto Goto, Harrison Wolf, Sarah Lucas, Hannah Kaye Windwehen, Traesha Robertson, Annie Mowry, Ashlyn Kennedy, Jacqueline Dove, Dr. Stephanie Lockwood, Stephanie Randell

P98-U Association of Diversity and Health of Scleractinian Corals with Macroalgae in Roatan, Honduras

» Hannah Dawson, Zoe Hilliard, Harrison Wolf, Christopher Allovio, Traesha Robertson, Anne Mowry, Ashlyn Kennedy, Jacqueline Dove, Dr. Stephanie Lockwood, Stephanie Randell

P99-U Associations of algal species with sponge disease in Roatán, Honduras

» Paola Vallejo, Virginia Fuentes, Grettel E. Ramirez, Traesha Robertson, Annie Mowry, Ashlyn Kennedy, Jacqueline Dove, Dr. Stephanie Lockwood, Stephanie Randell

5pm **Posters - Mathematics & Computer Science (P100-103)**

COB 1st/2nd Floor Hallways

Chaired by: Todd Dole

P100-U MoRocco – A Secure Exam Operating System for Academic Integrity

» Rocco Guevara

P101-U Comparing the Effectiveness of Two Common Lichen Sampling Methods

» Courtney Shuman, Prof. Chad Cryer, Martha Hartt

P102-U GRACE – Gesture Recognition for Augmented Cultural/Religious Expression

» Daniil Kochkonbaev

P103-H Q-Safe: Mitigating Quantum Threats with Lattice-Based Cryptography

» Nikhitha Swaminathan

5pm **Posters - Neuroscience (P104-P114)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Seena Mathew

P104-U Location of AVT neurons within the seahorse and pipefish pituitary

» Rachel Ling, Dr. Sunny K. Scobell

P105-G Assessing Cell Death in a 6-Hydroxydopamine Zebrafish Model

» Yushe N Islam, Roha Qureshi, Nolawit Tilahun, Dr. Ayman Hamouda, Dr. Brent Bill

P106-U An analysis of the dopaminergic pathway in the brain and pituitary of male-pregnant pipefish and seahorses

» Madeleine Thomas, Dr. Sunny K. Scobell

P107-G Exploring the Role of Angiotensin Receptor Blockers in the Management of Traumatic Brain Injury: A Review of Mechanisms and Therapeutic Potential

» Manaal Salman, Kayley Stroupe, Dr. Lora Talley

Continued from **Friday, 27 February**

P108-U Investigating AHDC1 Loss and Retinal Development in a Zebrafish Model of Xia-Gibbs Syndrome

» Adedire Owulebaja

P109-G Prefrontal Transcranial Photobiomodulation in Autism Spectrum Disorder: Cognitive, Behavioral, and Neurophysiological Effects Across Age Groups

» Sarah Diaz, Hunter Dutkiewicz, Dr. Gabriela Guimaraes, Nicole J. Moore, Isabelle Rose, Dr. Douglas Barrett, Dr. F. Gonzalez-Lima

P110-U Investigation of the role of Drosophila gene CG12299 in the circadian controlled locomotive activity in fruit flies

» Annie Trinh, Aimalohi Edeghere, Dr. Yuan Yuan Kang

P111-U Blueprints of the Brain: Fetal Cortical Development and the Shadow of Gestational Diabetes

» Riya Jadeja

P112-G Effects of Repeated-Session Transcranial Photobiomodulation on Prefrontal Oxygenation and Impulse Control in Adults with Attention-Deficit/Hyperactivity Disorder

» Farzad Salehpour, Dr. Patrick O'Connor, Dr. Douglas Barrett, Isabelle Rose, Ayla Farzamnia, Monique Tran, Amir Emamian, Haeun Yeo, Dr. F. Gonzalez-Lima

P113-U Investigation of the role of Drosophila gene polyhomeotic proximal in the circadian controlled locomotive activity in fruit flies

» Pedro Rodriguez Navarro, Dr. Yuan Yuan Kang, Delwin Sunil

P114-U Antidepressants and Lung Toxicity: A Narrative Review

» Ariana Azimi, Elakiya Jayaramen

5pm **Posters - Physics & Engineering (P115-P116)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Bryant Wyatt

P115-H Can Deep Learning Models Trained on Cosmological Simulations Predict the Signatures of Early Supermassive Black Hole Seeds Formation Scenarios?

» Hitaishi Chillara, Dr. Ryan Farber

P116-U Using 3D Printing in a Research Lab

» Montserrat Menchaca, Dr. Rosa Cardenas, Ileana Lane

5pm **Posters - Plant Biology (P117-P127)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Kevin Eddy

P117-U Under the Soil: Effects of Diquat Herbicide on Tomato Root Complexity and AM Fungi Symbiosis

» Michaela Stelzer, Annabel Ferniza, Dr. Honey Golden

P118-U Heat stress response in Sorghum halepense: tolerance decreases with exposure time but is consistent across seasons

» Ashley Cantu, Mandy Payan, Daniel Odejimi, Dr. Michael Tobin

P119-U Modest increase in photosynthetic heat tolerance occurs across leaf developmental stages in Johnson Grass (Sorghum halepense)

» Mary Robles, Diana Diaz, Jacqueline Cervantes, Shaimaa Obaid, Dr. Michael Tobin

P120-U Heat-induced ion leakage curves similar across leaf developmental stages in Johnson grass (Sorghum halepense)

» Daniel Odejimi, Mandy Payan, Ashley Cantu, Jacqueline Cervantes, Dr. Michael Tobin

P121-U Sanger sequencing of microsatellite loci to characterize contributions of non-tandem indels to allelic diversity in Mentzelia pectinata.

» Hannah Anthony, Ana Rodriguez, Dr. Joshua Brokaw

P122-U Using database searches and new collections to document the floristic diversity of the Independence Creek Preserve, TX

» Olivia Fischer, Edmundo Avalos, Matt Allen

Continued from **Friday, 27 February**

P123-U Revisiting Zygnema: assessing diversity and systematics using publicly available sequence data

» Monserrat Alvarez, Dr. Anna Crowell

P124-U The use of the rbcL gene to identify relationships among Nitzschia palea strains (Bacillariophyceae)

» Ambivalencia Bonilla Love, Dr. Anna Crowell

P125-U Understanding Evolutionary History Within Genus Amphora Using the rbcL Gene

» Justino Gonzalez, Dr. Anna Crowell

P126-U Phylogenetic relationships among Sheathia species (Batrachospermales, Rhodophyta)

» Alfredo Aldana Lopez, Dr. Anna Crowell

P127-G Potential for Acorn Morphometric Analysis in Quercus Identification

» Zoe Matranga, Dr. Juan Daza

5pm **Posters - Science Education (P128-P137)**

COB 1st/2nd Floor Hallways

Chaired by: Woody Cox

P128-N AI/VR Digital Twin Prototypes for Supply Chain Operations Education

» Dr. Maria Burns, Dr. Suresh Kumar Peddoju

P129-U Improving Math Readiness for General Chemistry Through the Development of an Online Bootcamp

» Alfonso Lena Ordaz, Ariyana Fisher, Lindsey Niehof, Dr. Lance English

P130-U Bringing Biochemistry into Organic Chemistry through an LLPS-Based CURE Module

» Lila O'Donnell, Lindsey Niehof, Ariyana Fisher, Luis Rodulfo, Steven Whitten, Dr. Lance English

P131-G Engineering Lassi by Exploring How Common Ingredients Shape Fermentation and Quality

» Haran Prasad, Dr. Hye Kim, Dr. Md Ariful Haque, Dr. Jaehyun Ahn, Dr. Seockmo Ku

P132-U From Concept to Cosmos: Cultivating The Next Generation of Our Future Space-STEM Workforce

» Brett Jacobsen

P133-U Creek to classroom: Exploring biodiversity through hands-on ecological investigation

» Edmundo Avalos, Dr. Matthew Allen

P134-U Enhancing STEM Education Through Micro-Credentialing: Fostering Instrument Proficiency and Career-Ready Skills

» Corey Hobbs, Dr. Darrell Fry

P135-U Cost-Effective Spectrophotometry for K-12

» Victoriano Cooper, Dr. Dennis Gibson, Bobby Womack, Dr. Wade Ashby

P136-G Girl Scout STEM Education and Engagement through Field Activities

» Kendall Kinsey, Dr. Steven Koether, Dr. Diane Neudorf

P137-N Bridging the AI Literacy Gap: STEM Student Perspectives on Artificial Intelligence in Higher Education

» Dr. Wendi Wolfram, Liz Fitzgerald, Dr. Shama Grimmage, Dr. Jenna Odeh, Dr. Josh Lackey, Naseeba Abdeljaber

5pm **Posters - Systematics & Evolutionary Biology (P138-P150)**

COB 1st/2nd Floor Hallways

Chaired by: Dr. Matt Greenwold

P138-U A Taxonomically and Ecologically Diverse Marine Vertebrate Assemblage at the end of the Cretaceous in Texas (USA)

» Kieu Nguyen, Dr. Thomas Stidham

Continued from **Friday, 27 February**

P139-U Examining the survival and initial recovery of fish after the Cretaceous mass extinction of the Kincaid Formation in Texas.

» Diana Kettler, Emma Potts, Dr. Thomas Stidham

P140-U Morphological differences in among populations of Amphisbaenians from Puerto Rico

» Minji Kim, Dr. Juan Daza, Oscar Ospina, Camilo Linares-Vargas

P141-U Comparative study of male aggression of food generalists and specialists in Drosophila species

» Yuliana Santos Ventura, Abdulrahman Omar, Laurie Neuman, Dr. Yuan Yuan Kang

P142-U Spontaneous Mutations on Antibiotic Resistance in Escherichia coli

» Julian Ramirez, Brent Orji, Christian Buford, Natalie Zarate, Wei-Chin Ho

P143-U Fungal Genotyping and Phylogenetic Categorization of Lower Attine Ants Cyphomyrmex wheelri and Mycetosoritis hartmanni

» Lunden Hahn, Erin McFarland, Dr. Jon Seal, Katrin Kellner

P144-U The Effects of Historical Adaptation of Microbes in New Stressful Environments

» Ivan Mendez, Kingsley Amoateng, Sora Kim, Julian Ramirez, Natalie Zarate, Wei-Chin Ho

P145-G Resolving the Sphaerodactylus macrolepis species complex in the Puerto Rican bank

» Lilly Nguyen, Dr. Juan Daza, Dr. Alexandra Herrera Martinez

P146-U The role of Trachymyrmex smithii ants in structuring bacterial communities in their symbiotic fungus gardens

» Sorrel Estrada, Erin McFarland, Katrin Kellner, Dr. Jon Seal

P147-U Quantitative Trait Locus mapping and functional validation of genes regulating circadian controlled locomotion in Drosophila species

» Delwin Sunil, Dr. Yuan Yuan Kang, Benjamin Soibam, Pedro Rodriguez Navarro, Isabela Rodriguez Avila

P148-G Comparing cranial telescoping in select squamate groups

» Paige Donkers, Dr. Juan Daza

P149-G The Fungal Microbiome of Pheidole adrianoi, an ant that associates with mycorrhizae

» Erin McFarland, Dr. Jon Seal, Katrin Kellner

P150-U Assessing Male Mating Success Across Proto-Y Genotypes in Musca domestica

» Juan Fuentes, Alexis Hernandez, Lotus Ha, Landon Sanz, Tania Barcenast

5pm

Posters - Terrestrial Ecology & Management (P151-P164)

COB 1st/2nd Floor Hallways

Chaired by: Eli Hartung

P152-G Diet and parasites of newly documented Hemidactylus from south Texas, USA

» Kevin Green, Dr. Drew Davis

P153-U Investigating Post-Prandial Thermophily in a Fossorial Snake Species

» Julian Villanueva, Dr. William I. Lutterschmidt

P154-U Seasonal occurrences of mammals in Natchitoches parish Louisiana

» Blake Willey, Prof. Chad Cryer

P155-U Influence of ultraviolet light on the distribution of fluorescent lichen

» Layla Salina, Jordan Whittaker, Caleb Smith, Prof. Chad Cryer

Continued from **Friday, 27 February**

P156-U Arachnid Diversity at Firebase Libby and Callahan County
» Jacob Wooten, Dr. T.J. Boyle

P157-G The Impact of Social Isolation on Madagascar Hissing Cockroaches
» Asmau Shiyanbade, Dr. Diane Neudorf, Dr. Sibyl Bucheli

P158-U Influence of tree bark pH on lichen distribution
» Ruby Tapia, Jada Gosey, Cyah White, Alicia Hawkins, Prof. Chad Cryer

P159-U Nest Density of Atta texana in a Temperate East Texas Forest
» Megan Rhea, Erin McFarland, Dr. Jon Seal

P160-U Are they Fools, or Will they Learn? Behavioral adaptation in Physarum polycephalum
» Ella Johnson, Hannah Loya, Samuel De La Garza, Dr. Mary Kay Johnston

P161-U Nasal botfly prevalence in the 2025 hunting season of white-tailed deer
» Tyler Miller, Prof. Chad Cryer

P162-N Composting Polystyrene Using Superworms: Some Practical Applications
» Tara Hansler, Dr. Richard Patrock

P163-U Distribution of UV+ lichens on various tree species in Central Texas
» Jacquelyn Rios, Prof. Chad Cryer

P164-U Seed predation differs between native and exotic seed species, and across a latitudinal gradient
» Ana Caballero, Sage Gruver, Charlotte Savage, Yahida Soto, Will Bieker, Dr. Lana Bolin

7pm **Poster Tear Down (7pm-7:30pm) - Posters left after this time will be discarded!**
COB 1st/2nd Floor Hallways

Saturday, 28 February

7am **Fellows' & Past Presidents' Breakfast**
COB 350.55

8am **Registration**
College of Pharmacy (WTB) - Outside 134

8am **Cell & Molecular Biology (8am-10:30am) & Section Meeting (10:30am-10:45am)**
COB 111
Chaired by: Dr. Adriana P. Visbal, PhD

8am **#058-U Finding Novel Inhibitors of Francisella tularensis Enoyl-ACP reductase FabI (FtFabI) in Francisella tularensis**
» Yiming Chen, Dr. Josh Beckham

8:15am **#059-U Cancer Stem Cells as Mitochondrial Donors: Implications for Macrophage Polarization and Tumor Immune Evasion**
» Nicholas Pascuzzi, Luke Peck, Chris Uliberri, Diya Shah, Dr. Kuan-Hui Ethan Chen

8:30am **#060-U Investigating The Formation and Biological Impact of Oxysterol-RNA Adducts in Drosophila Melanogaster**
» Tyson Easterling, Miriam Andersen, Zoey Storch, Dr. Godwin Ifere

8:45am **#061-U Screening TZ62, TZ70, TZ71 and DKNR8, DKNR10, DKNR13 for Induction of Apoptosis and Inhibition of Metastasis**
» Maximiliano Perez, Tina Prajapati, Dr. Vaishali Chaubal, Dr. Rachna Sadana

Continued from **Saturday, 28 February**

9am **#062-G Exploring the Role of Lung cancer-associated Variants and Genes in DNA Damage Promotion**

» Maryam Vaziripour, Daniel Snyder, Christopher Amos, Yanhong Liu, Dr. Jun Xia

9:15am **#063-G Fibroblast Lineage Remodeling in Uterine Blood Reveals a Conserved Protumorigenic Trajectory in Endometrial Cancer**

» Bingru Feng, Dr. Jun Xia, Dr. Yusi Fu

9:30am **#064-G PAX6 in Mechanosensory Neuromasts of Salamanders and Zebrafish: A Molecular, Microscopic, and Computational Investigation**

» Nisa Sindhi, Nikhil Pawar, Dr. Ruben U. Tovar, Dr. Thomas J. Devitt, Dr. David M. Hillis, Dr. Dana M. Garcia

9:45am **#065-G Expression and Functional Analysis of Profilin Genes (pfn1, pfn2a, pfn2b) During Early Embryonic Development in Zebrafish**

» Samira Alam, Andre Gil, Alicia Mendoza, Dr. Sharmin Hasan

10am **#066-N Three left standing: Population wide investigation of histone missense mutation landscape reveals novel constraint pattern**

» Tiffany Bastos, Dustin Fetch, Dr. Wan Song, Natalie Redding, Marzieh Rouzbehani, Ava George, Ksenia Dydo, Juliannah Rua-Avendano, Gauri Raje, Dr. Alexey Soshnev

10:15am **#067-N Androgen regulation of the reproductive cycle in male-pregnant pipefishes**

» Dr. Sunny K. Scobell

8am **Chemistry & Biochemistry II (8am-11:15am) & Section Meeting (11:15am-11:30am)**

COB 112

Chaired by: Dr. Darrell Fry

8am **#068-U Ripe for Discussion: The Curious Case of Fungus on Wine Grapes and What It Means for Our Palates**

» Zachary Dennison, Dr. Alyx Frantzen

8:15am **#069-U Redox Cooperativity Analysis with Computational Chemistry: Role of 3d Versus 4d/5d Metals**

» Hadley Watts, Dr. John Gary

8:30am **#070-U The Grapes of Wrath: How to Store Wine Without Letting It Go Bad (and Other Oenological Adventures)**

» Ev Crowe, Dr. Alyx Frantzen

8:45am **#071-U Protective Effects of Mint Extracts Against Oxidative Stress in Human Serum Albumin Protein**

» Perla Tovar, Nkeiruka Aziekwu, Dr. Bidisha Sengupta

9am **#072-U Mechanistic Insights into Transition-Metal Binding to HSA Using Dual-Probe UV–Vis and Site-Specific Tryptophan Fluorescence Spectroscopy**

» Tess Corbett, Dr. Bidisha Sengupta

9:15am **#073-U Structure-Based Identification of Inhibitors Targeting Staphylococcus aureus D-Alanine:D-Alanine Ligase Using Virtual Screening**

» Mahdia Rahman, Makynzie Kitzmann, Manal Saad, Dr. Josh Beckham

9:30am **#074-U Occurrence and Quantitation of Microplastic Contamination of Wastewater Treatment Plants in Deep East Texas**

» Jacob Swallow, Dr. Kefa Onchoke, Dr. Robert Friedfeld

9:45am **#075-U Camille: Automated Drug Screening at Scale**

» Michael Gillman, Dr. Josh Beckham

10am **#076-U Coumarin-enamine Derivatized Cascade Fluorescent Sensor for Multianalytes**

» Marlene Zepeta-Rodriguez, Prof. Rashid Mia, Jack Weeks

Continued from **Saturday, 28 February**

10:15am **#077-G Synthesis and Characterization of Thiazole-Based Cryptand-like Tricyclic Fluorescent Macrocyclic Cages for Aromatic Hydrocarbons**

» Jack Weeks, Prof. Rashid Mia

10:30am **#078-N Occurrence and Quantitation of PFAS in biosolids collected form WWTPs in Deep East Texas**

» Dr. Kefa Onchoke, Dr. Michael Janusa, Dr. Jamie Humphries, Kendal Fiffick, Anthony Broom, Thanh Tien Dao

10:45am **#079-N Mitochondrial membrane potential and mitophagy as modulators of light therapy**

» Dr. Violet Bumah

11am **#080-N Selective Recognition of G-Quadruplex and i-Motif DNA by Curcumin and Kaempferol: A Spectroscopic and Computational Study**

» Dr. Bidisha Sengupta

8:30am **Anthropology (8:30am-9:15am) & Section Meeting (9:15am-9:30am)**

COB 214

Chaired by: Ms. Stephanie Baker

8:30am **#081-G A Deep Learning Approach for Postmortem Interval Estimation**

» Stephanie Baker

8:45am **#082-G Investigating how heat, humidity, and solar radiation affect postmortem dental crack volume changes in human dentition**

» Bec Krolczyk, Dr. Daniel Wescott, Dr. Elaine Chu, Dr. Nicholas Herrmann

9am **#083-G Investigating Pelvic Sexual Dimorphism in Japanese, American Hispanic, and American White Samples**

» Madison Glenwinkel, Dr. Elaine Chu

8:30am **Freshwater Science (8:30am-10am) & Section Meeting (10am-10:15am)**

COB 212

Chaired by: Dr. Mary Kay Johnston

8:30am **#084-U Sticky Situation: Investigating eDNA and Microplastic Interactions**

» Jordan Emerson, Heaven Eskandar, Emma Flores, Dr. Romi Burks, Dr. Matthew Barnes, Andre Felton

8:45am **#085-U Bobbing for apple snails: Detecting Pomacea maculata in San Antonio waterways using environmental DNA**

» Heaven Eskandar, Emma Flores, Jordan Emerson, Dr. Romi Burks, Dr. Matthew Barnes, Adrian Reyna

9am **#086-N Status and Distribution of Freshwater Mussels in the Tensas River and Bayou Bartholomew of Louisiana**

» David Ford, Dr. Neil Ford, Dr. Lance Williams

9:15am **#087-N On the observed inverse relationship between rainfall amount and dissolved mineral content**

» Dr. John Stout

9:30am **Coffee Break**

COB

10am **Geosciences (10am-11:15am) & Section Meeting (11:15am-11:30am)**

COB 214

Chaired by: Dr. Michael Read

10am **#088-U Evaluating the viability of Pennsylvanian conodont and brachiopod 87Sr/86Sr values from the Santa Fe Mountains, New Mexico**

» Natalya Plourde, Dr. Michael Read

Continued from **Saturday, 28 February**

10:15am	**#089-U A Re-evaluation of Morphological Characters Used to Identify Fossil Viperid Snakes in Neogene and Quaternary Deposits of the United States.** » Theodore Ransom, Christopher Bell
10:30am	**#090-N Mid-Artinskian (Early Permian) conodonts and fusulinids from the "Wolfcamp B"-"Wolfcamp A" transition of the southern Midland Basin, West Texas** » Dr. Michael Read
10:45am	**#091-N Stratigraphic Analysis of the conglomeratic sandstone of Knight Canyon (Paleocene?), Grant County, New Mexico** » Dr. R. LaRell Nielson
11am	**#092-G Cultivating Mars: Testing Crop and Microbial Growth in Optimized Regolith Aboard the ISS** » Harrison Coker, Caleb Shackelford, Dr. Julie Howe
10:30am	**Biomedical Sciences II (10:30am-11:45am) & Section Meeting (11:45-noon)** *COB 212* Chaired by: Dr. Joni Ylostalo
10:30am	**#093-U Discovering Novel Inhibitors of Yersinia pestis 3-Oxoacyl-[Acyl-Carrier-Protein] Reductase (YpFabG) Using Comprehensive Virtual Screening** » Saumya Seth, Dr. Josh Beckham
10:45am	**#094-G Investigation of the Pathogenesis of Bourbon virus at the Tick-Host-Virus Interface** » Megan Burch, Dr. Catherine Olal, Agnes Udoh, Dr. Dennis Bente
11am	**#095-G Crimean-Congo Hemorrhagic Fever Virus Infection in Human and Animal Cell Lines: A Pathway to Understanding Species-Specific Pathogenesis** » Kiyah Costin, Dr. Catherine Olal, Dr. Anastasia Accoti, Megan Burch, Dr. Maria Cajimat, Dr. Dennis Bente
11:15am	**#096-N Targeting aurora kinase, A and BRD4 as a translational therapeutic strategy for cutaneous T-cell lymphoma** » Dr. Mamta Gupta
11:30am	**#097-N Rapid recovery of peripheral oxygen saturation and hypoxic COVID-19 patients with ivermectin-based multidrug therapy** » Dr. Eleftherios Gkioulekas, Dr. Peter McCullough, Prof. Colleen Aldous
10:30am	**Terrestrial Ecology & Management (10:30am-11am) & Section Meeting (11am-11:15am)** *COB 203* Chaired by: Eli Hartung
10:30am	**#098-U Vocalization Signatures of Frog Species: A Study of Call Patterns for Species Identification and Biodiversity Monitoring in a Temperate Wetland Ecosystem** » Sunshyne Parrish, Dr. Joel Brant, Dr. T.J. Boyle
10:45am	**#099-U Environmental impacts: how humidity and temperature affect the growth of Ophidiomyces isolates** » Emilee Minor, Alan Lizarraga
12pm	**Boxed Lunch** *COB 112*
1pm	**Graduate Student Oral Presentation Competition** *Robert R. Muntz Library (401)* Chaired by: Dr. Travis LaDuc
1pm	**#001-GC Comprehensive insights into mosquito species diversity and habitat-specific host selection patterns in Cameron Park Zoo, Waco, Texas.** » Dhivya Rajamanickam, Dr. Jason Pitts

Continued from **Saturday, 28 February**

1:15pm	**#002-GC Potential Disruptors of the Acoustic Habitat of the Carolina Wren and the Implications for Reproductive Isolation** » Zachary Seidel, Dr. Diane Neudorf
1:30pm	**#003-GC The impact of nutrition on insecticide resistance and gene expression in Aedes aegypti** » Esmeralda Rosas, Sarah Maestas, Jason Tidwell, Dr. Christopher Vitek
1:45pm	**#004-GC Influence of Mint and Basil Phytochemicals against Bacterial Biofilm Formation** » Cephus Bess-Grunewald, Dr. Bidisha Sengupta
2:30pm	**Post-Section Chairs' Meeting** *COB 307*
4pm	**Commute to Holiday Inn Conference Center for Awards Banquet**
4:30pm	**Outstanding Texas Educator - Mrs. Jamie Flint** *Constellation Ballroom, Holiday Inn Conference Center*
5:15pm	**Distinguished Texas Scientist - Dr. Rusty Towell** *Constellation Ballroom, Holiday Inn Conference Center*
6pm	**Awards Banquet** *Constellation Ballroom, Holiday Inn Conference Center*


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Abstracts

#001-U Mirtron-5010 Enhances Stemness and Iron Accumulation in Aggressive Breast Cancer Cells

Noah Padilla [1], Reagan Farrell [1], Maya Vaela [1], Alejandro Ruiz [1], Trevor Jones [1], Kuan-Hui Ethan Chen [1] (1. Texas Tech University)

Invasive breast cancer affects approximately one in eight American women over the course of their lifetime. Despite advances in treatment, current therapeutics often lack precise molecular targets that modulate cancer cell behavior, particularly in aggressive breast cancer subtypes. Mirtron-5010, a novel class of non-canonical, intron-derived microRNA, remains an underexplored regulatory molecule with emerging potential roles in tumor progression and invasion. This study aims to investigate how Mirtrons influence cancer cell stemness and contribute to the accumulation of the essential element iron. To assess stemness, we evaluated classical markers such as SOX2, OCT4, NANOG, and KLF4. We observed across bulk and stem cell populations utilizing Immunohistochemistry and quantitative PCR methodologies. Our data shows that MDA-MB-231 breast cancer stem cells upregulate Mirtron-5010, further enhancing elevated SOX2 expression, suggesting an enhancement of stem-like properties. Furthermore, expression of SOX2 and NANOG are increased in comparison across MDA-MB-231 bulk cells, suggesting induction of other stem cells to indicate mirtron-5010 expression assists in tumor stem cell transformation to stem-like properties. Our previous work identified that iron re-distribution into tumor cells in the tumor microenvironment impairs tumor immunity. Consistent to this, Mirtron-5010 overexpressing cells increase intracellular iron accumulation, illustrated by an increase of FerroOrange labile iron fluorescence of MDA-MB-231 mirtron upregulation as compared to control. Taken together, our results identify mirtron-5010 as a promising molecular target in breast cancer, particularly within highly invasive subtypes. Future studies will assess their impact on cellular proliferation and viability, as well as their roles across additional breast cancer cell lines.

#002-U Screening Compounds for Their Anti-Cell Proliferation Properties

Tina Prajapati [1], Vaishali Chaubal [1], Rachna Sadana [1] (1. University of Houston-Downtown)

Cancer encompasses a diverse range of diseases characterized by abnormal cell proliferation and the evasion of apoptosis, a programmed cell death process, due to disruptions in regulatory signaling pathways. Ongoing mutations in cancer cells often lead to resistance against current therapies, necessitating the discovery of novel anticancer drugs. In our laboratory, we focus on evaluating the effects of novel synthetic compounds, designed to have enhanced efficacy and reduced toxicity. In this study, we evaluated 17 compounds of a series coded as TZ. The compounds are functional groups. Using a colorimetric MTT Cell-Proliferation Assay, we initially assessed these compounds at 20μM final concentration against MOLT 4 (leukemia), A549 (lung cancer), BXPC3 (pancreatic cancer), and MCF7 (breast cancer) cell lines for cell survival. The TZ series demonstrated promising results, with compounds TZ5, TZ62, TZ68, TZ70, and TZ71 reducing cell survival by over 50%. Further analysis revealed that TZ62, TZ70, and TZ71 induces apoptosis in cancer cells as measured by enhanced caspase 3/7 activity, significantly implying these compounds induce apoptosis by cleaving protein substrates. Future research will focus on figuring out if TZ62, TZ70, and TZ71 compounds can prevent metastasis of cancer cells using the cell migration invasion assay, where initial testing of the wound closure assay shows some promising results.

#003-U Histological Characterization of Cardiovascular Malformations in a Chick Model of Maternal Phenylketonuria

Desarey Reyna Gaytan Robles [1], Danny Gutierrez [1], Nikki J. Seagraves [2], Adriana P. Visbal, PhD [1] (1. University of Houston-Downtown, 2. Oklahoma City University)

Phenylketonuria (PKU) is an autosomal recessive disorder caused by deficiency of phenylalanine hydroxylase, leading to toxic accumulation of phenylalanine (PHE). In pregnancy, elevated maternal PHE results in fetal exposure and Maternal Phenylketonuria (MPKU), a condition associated with growth restriction, neurodevelopmental impairment, and a high incidence of congenital cardiovascular malformations (CVMs). Although these clinical outcomes are well documented, the developmental mechanisms driving MPKU-associated heart defects remain poorly understood. To investigate how excess PHE affects cardiac morphogenesis, our collaborator developed a reproducible chick embryo model in which embryos are microinjected with 2.5 mM PHE at Hamburger-Hamilton stage 6 (HH6). Hearts were collected at HH34, a stage when the chambers, valves, and major outflow structures are fully formed. Our goal was to generate preliminary histological evidence, both qualitative and quantitative, characterizing structural abnormalities in MPKU-exposed hearts. Here we show that sectioned, paraffin-embedded tissues stained with hematoxylin and eosin exhibit deviations in myocardial wall thickness, chamber morphology, and outflow tract organization compared to untreated controls. Using Masson's Trichrome, we further observed differences in collagen distribution and extracellular matrix remodeling. Quantitative analyses of chamber area, vessel diameter, collagen localization, and matrix density were performed using Nikon image analysis software, with statistical comparisons conducted using Student's t-test. These findings identify measurable structural consequences of elevated embryonic PHE and demonstrate that systematic histological staining and methods will strengthen future mechanistic investigations and advance our understanding of how elevated PHE disrupts embryonic heart formation.

#004-U The Skin Microbiome & Acne: How Common Skincare Ingredients Affect Bacteria and Inflammation *Alanis Cotto [1], Irene Perry [1] (1. University of Texas Permian Basin)* This research project aims to examine how commonly used skincare ingredients influence the growth of *Cutibacterium* acnes (formerly known as *Propionibacterium* acnes), an important bacterium involved in the development of acne. Acne affects millions of people globally, yet most still do not fully understand how the products many of us use day and night might help or worsen our condition. With ingredients like niacinamide and hyaluronic acid becoming increasingly popular, it is important to look at how they actually interact with the skin's microbiome. To do this, *C.* acnes will be grown in a lab and exposed to different concentrations of selected skincare ingredients. By observing how the bacteria react, this study aims to find out whether these ingredients slow down bacterial growth, encourage it, or have no noticeable effect at all. Understanding these interactions can help us learn more about how skincare products may influence inflammation, breakouts, and overall skin health. The goal of this research is to make the connection between skincare and the skin microbiome clearer. By highlighting how everyday ingredients might affect acne-related bacteria, findings can help guide the development of safer, more effective products for people with acne-prone skin, and help consumers make informed choices.

#005-U Cytotoxicity of Freebase Nicotine and Its Analogs Using Cellular and Statistical Methods *Kiera Griffin [1], Taylor Jefferis [1], Dominic Pruss [1], Mohana Sengupta [2], Rodney Sturdivant [1], Amanda Charlton-Sevcik [1], Robert Strongin [2], Christie Sayes [1] (1. Baylor University, 2. Portland State University)* (*S*)-nicotine has been used for decades in traditional cigarettes and, more recently, in modern e-cigarettes. However, (*S*)-nicotine induces adverse health effects, particularly in the lungs. Analogs of (*S*)-nicotine, such as (*R,S*)-nicotine, 6-methyl nicotine, nicotinamide, nicotine lactate, and nicotine benzoate, are growing in popularity as (*S*)-nicotine replacements. These analogs are marketed as 'safer alternatives,' yet little information is available on their induced health effects or toxicological properties. In this study, we systematically investigated methods for predicting the lethal concentration (LC) values of (*S*)-nicotine and five of its analogs using cell cultures and statistics. Human bronchiolar epithelial lung cells (BEAS-2B) were exposed to five nicotine analogs over a 24-hour exposure period. Cellular metabolism and cellular membrane integrity were measured and subsequently modeled using a four-parameter dose-

of potency. Out of the 5 analogs of interest, 6-methyl nicotine had the most adverse effects on cell health according to the overall ranking. However, all the analogs showed differential responses depending on which endpoint was being analyzed. The methods used in the study establish a framework for comparing toxicological evaluations and provide important insights into the lethality of emerging nicotine analogs.

#006-G Production of 3-cyanopyridine upon vaping nicotinamide and evaluating the toxicological effects of individual and combined exposures via isobologram-based analysis
Taylor Jefferis [1], Mohana Sengupta [2], Kiera Griffin [1], Robert Strongin [2], Christie Sayes [1] (1. Baylor University, 2. Portland State University) Nicotine has been used in e-cigarettes for many years; however, recently, nicotine analogs have risen in popularity. E-cigarettes containing nicotine analogs are currently marketed as safer alternatives to nicotine-containing products, without proper research to support this claim. Our work investigates the nicotine analogs, along with their major degradant, which is produced when vaped. First, mass spectrometry analysis verifies that upon heating and aerosolization, both chemicals are present. Dose-response curves are created for relative concentrations of each chemical, and an isobologram is formed to investigate their mixture effects. The first study examined the nicotine analog nicotinamide (NA) and its major degradant, 3-cyanopyridine (3CP). Results showed that NA is toxic at concentrations greater than 2637 ppm; however, 3CP is harmful in concentrations as low as 0.0001 ppm. The most significant finding is that the isobologram indicates synergistic mixture effects, with a decrease in viability observed at minimal doses of 3CP (i.e., 1 ppt) and 1350 ppm NA. The interaction index was calculated for each point, and all values were less than 1, indicating a statistically synergistic biological response. The study highlights how low levels of 3CP can induce toxic responses to a presumed safe chemical. These results suggest that chemical and biochemical reactions, as well as interactions between e-cigarette aerosol components, including nicotine analogs, warrant further investigation. Future work will continue to investigate these same types of relationships with other common active ingredients in e-cigarettes: (*S*)-nicotine and its degradant myosmine, as well as 6MN and its degradant 6-methyl myosmine.

#007-U Boron Is Special: Unique Role of Boron in C-B Bond Forming Reactions *Avree Fields [1], John Gary [1] (1. Stephen F. Austin State University)* Formation of carbon-boron bonds are highly desirable given the large body of synthetic organic chemistry with boronic acids and esters. Thus, understanding the processes which lead to these bond formations are of profound importance. Typically, processes at platinum group metals. These processes often follow typical periodic trends of ionization energies along with simple nucleophile and electrophile arguments to rationalize reactivity rates. Boron is a unique heteroatom in these bond forming reactions because it has stable a configuration with an empty p-orbital. This talk will examine the unique role boron plays in oxidative addition and reductive elimination processes in comparison to more common X-type ligands (such as Cl, OR, or NR2). The extreme pi-acceptor character of the boron ligand will be used to explain the unique reactivity pattern observed with platinum complexes using computational chemistry.

#008-U No Ring Required: Constraints for Organic Components in Redox Cooperativity *Emma Patton [1], John Gary [1] (1. Stephen F Austin State University)* Cooperativity between multiple redox sites is common in enzyme systems. This cooperativity allows enzymes to use multiple cheap Earth-abundant metals, which typically undergo one-electron redox processes, to perform multi-electron chemistry. Previously, our group has highlighted the interplay between cobalt and a pyridine-di-immine (PDI) ligand system by a unique electronic configuration. This system allows cooperation between a cobalt and reduced pyridine anion to perform 2-electron chemistry. We have studied this system and observed that the dihedral angle of the Co-N bond is important to orbital overlap and communication. This talk will examine what are the key features of the organic unit in communication. Specifically, this talk will establish if an aromatic ring is required or just a simple pi-system, the effect of the atom connector (N, P, As, O, S, Se), and the effect of the bond angle at the connecting atom. These results will highlight that the flexibility of organic groups in electronic communication and cooperativity is much larger than currently employed in experimental systems.

#009-U Battle of the Geometries: Square Planar Versus Tetrahedral Geometry for Electronic Communication

Aiyana Gonzalez [1], John Gary [1] (1. Stephen F Austin State University) Multiple electron redox events are fundamental to chemical reactions. Most chemical processes are two-electron processes (organic arrow pushing mechanisms, resonance, and oxidative addition/reductive elimination in organometallic chemistry). Due to the frequency of this two-electron process, platinum group metals are often used in catalysis due to their ability to perform two-electron redox events. In nature, enzymes often pair Earth-abundant metals which undergo one-electron (radical) redox events to perform multi-electron chemistry. While prevalent in enzymes, the energetic, proximity, and geometric orientation requirements to allow this cooperativity are not well understood. Previously, our group has

configuration. Traditionally, we have focused on square planar complexes with eight d-orbital electrons. This talk will highlight how moving from square planar to tetrahedral metal complexes change the electronic and geometric requirements for electronic communication. These insights increase the possibilities in the design of new redox non-innocent systems in the future.

#010-U The Great Shape Debate: How Geometry and Electron Count Affect Electronic Communication *Sophia Myers [1], John Gary [1] (1. Stephen F Austin State University)* Cooperativity between multiple redox sites is ubiquitous in enzyme systems. This cooperativity allows for the use of multiple cheap Earth-abundant metals, which typically undergo one-electron redox processes, to perform multi-electron chemistry. The key design features which allow for redox cooperativity are not well understood. In an effort to design new experimental model systems, computational chemistry is employed to understand the key design features. Previously, our group has highlighted the interplay between cobalt and a pyridine-di-immine (PDI) ligand system by a unique electronic configuration. Traditionally, we have focused on square planar complexes with eight d-orbital electrons. This talk will highlight how different metal electron counts and octahedral complexes are also capable of redox communication, expanding the possibilities for new redox non-innocent systems in the future.

#011-U The Crystal Clear Truth About Salts: A Dive into Characterization of Global Salt Samples *Katelyn Jones [1], Alyx Frantzen [1], Julie Bloxson [1] (1. Stephen F. Austin State University)* Salt formations are a unique geological feature that represent a time of basin restriction and arid conditions, allowing for precipitation of minerals from saturation waters. They will also play a key role in energy transition, such as storage of hydrogen, CO2, and natural gas liquids. Salt domes can also aid in geothermal exploration by acting as conduits for heat transfer to shallower depths. However, salt is often a collective term for evaporite minerals. Often salt domes or formations are comprised of halite (NaCl), calcite (CaCO3), anhydrite (CaSO4), and bittern salts (e.g. carnallite, sylvite, epsomite), which could affect their capacity for storage or heat transfer. "Salt" samples from across geologic time and around the globe are being characterized to better understand the composition. Due to their composition, salts are incredibly difficult to analyze, therefore require several techniques to properly characterize. Samples are analyzed using ICP-MS, IC, TGA, and XRD.

#012-U In Situ Characterization of HIMARS Launch Sites: A Proof of Concept for Portable XRF Screening *Aaron Beavers [1], Kiley Miller [1] (1. Schreiner University)* Military training with High Mobility Artillery Rocket assessment tools. This study serves as a proof of concept for the efficacy of handheld X-ray fluorescence (XRF) in detecting soil contamination at active firing points. Using a Thermo Scientific Niton XL2 analyzer, we surveyed surface soils (0–5 cm) at Fort Sill, Oklahoma, to establish a baseline for contaminant distribution. The in situ analysis successfully quantified distinct "hotspots" of potentially toxic elements, revealing barium (74–341 ppm), chromium (up to 76.91 ppm), and lead (up to 22.46 ppm) significantly above background levels. Field data was corroborated by geotechnical observations of soil compaction and acidification (pH <6.0), which suggest conditions favorable for contaminant mobility. These findings validate portable XRF as a viable primary screening tool for military ranges. The next phase of research will correlate XRF data with ICP-MS laboratory validation and initiate spatial modeling to map contamination flow and migration pathways into the local environment.

#013-U IMAC protein purification via Ni(II)-NTA and histidine tags: A computational approach of incremental binding energies
Kaci Thomson [1], Brian Barngrover [1] (1. Stephen F. Austin State University) The binding energies between nickel-nitrilotriacetic acid (Ni-NTA), specifically Ni^{2+}, and histidine (His) residues in immobilized metal affinity chromatography, or IMAC, were examined. IMAC is a purification process for proteins that uses metal affinity to separate desired proteins from other proteins. Utilizing density functional theory (DFT) via Amsterdam density functional (ADF) software package, the bonding energies between the Ni^{2+}-NTA complex and incremental histidine residue chains ranging from one to six were calculated. Chains one through six were chosen because in published literature any chain above six histidine residues were found to be unnecessary, as the binding energy would be the same. In performing the DFT calculations, the binding between the Ni^{2+}-NTA and the pentahistidine residue chain was more favored with a value of -0.1191 eV when compared to the published values. In literature, the hexahistidine residue was the most favorable binding to Ni^{2+}-NTA. To simulate the removal of the target protein, further DFT calculations were run on the same software to determine the elution energies to remove the His chains and replace them with an imidazole. It is found that the imidazole was more favored than any of the incremental His residue chains, allowing for the residues to be removed easily.

#014-U Growth of Bismuth Nanoparticles from BiCl Salts Using DFT *Barbie Adams [1] (1. Stephen F. Austin State University)* Density functional theory (DFT) calculations were carried out to investigate the nucleation and growth of bismuth nanoparticles derived from BiCl salts. The reduction of $BiCl_3$ with hydride donors was

formation. The initial reduction step produces $BiCl_2^-$, which serves as a key intermediate in the assembly of larger clusters. Subsequent reactions generate small bismuth chloride species such as $Bi_2Cl_5^-$, $Bi_2Cl_4^-$, Bi_4Cl_{10}, and $Bi_4Cl_8^-$, each stabilized by residual chloride ligands. These clusters exhibit structural motifs consistent with early nanoparticle cores and provide the foundation for further growth. The simulations highlight how chloride ligands influence both the geometry and stability of intermediate clusters, allowing them to persist long enough to undergo coalescence and surface atom migration. These processes enable the gradual transformation of BiCl salts into extended bismuth frameworks. Charge redistribution within the clusters was observed to play a central role in maintaining structural integrity, while ligand desorption facilitates the exposure of reactive sites necessary for continued growth. Overall, the study demonstrates that hydride-mediated reduction of BiCl salts provides a viable pathway for nanoparticle nucleation. The identified intermediates establish a mechanistic link between precursor chemistry and nanoparticle architecture, showing how discrete molecular species evolve into larger nanostructures. These findings underscore the utility of DFT in revealing atomistic processes that govern nanoparticle formation and highlight the predictive value of computational approaches for guiding experimental synthesis of bismuth nanomaterials

#015-N The chemistry of the Si-Ge bond, 2 *Keith Pannell [1] (1. The University of Texas at El Paso)* The syntheses and photochemistry of organometallic compounds containing a direct silicon-germanium bond and a transition metal substituent will be presented. The compounds studied are of two general forms, LM-Si-Ge (**Ia**) and the isomeric LM-Ge-Si (**Ib**), where LM is (cyclopentadienyl)Fe(CO)$_2$
and the same grouping separated from the metalloid element by a CH_2 group, LM-CH_2-Si-Ge (**IIa**) and LM-CH_2-Ge-Si (**IIb**). The photochemistry of the materials illustrate the formation of silenes, germenes, silylenes and germylenes *via* a series of 1,2 and 1,3 shifts of substituents to favour the germylene formation at the expenses of silylene formation.

#016-N Designing Strategies of H-Bonded Chemosensors for Molecular Recognition *Rashid Mia [1] (1. Stephen F. Austin State University)* Non-covalent interaction, especially hydrogen bonding, is an attractive approach to design molecular sensors by introducing various fluorescence mechanisms. We have designed variety of molecular probes by incorporating hydrogen bonding, synthesized, and deployed to selectively bind with various analytes such as metals (Zn^{2+}, Cd^{2+}, Cu^{2+}, Ni^{2+}, Hg^{2+}, Co^{2+}, Pb^{2+}), and anions (CN^-, CH_3COO^-, F^-, PO_4^{3-}), and organophosphorus compounds. Hydrogen such a way so that enamine-NH moiety is adjacent to coumarin keto (C=O) group (or imine moiety is adjacent to phenolic hydroxyl group) that allows to form a new six-membered ring system through resonance-assisted hydrogen bonding (RAHB) which is typically stronger bond and give rise to optical properties of the sensor due to the extended conjugation. Upon the addition of target analytes, RAHB perturbed which produced unique optical responses because of sensor-analyte interactions both in UV-Vis and fluorescence spectroscopy. Furthermore, we designed another coumarin-quinidine molecular probes having no RAHB, we found that this sensor can bind to metal cations (Cd^{2+} and Zn^{2+}) with high affinity *via* an excimer formation (*π-π interaction*) due to the quinaldine moiety adopting a *syn* arrangement when coordinated to the metal Zn^{2+} ions.

#017-U Wanted Dead, Not Alive: Using eRNA:eDNA ratios to assess viability of invasive apple snail (Pomacea maculata)
Kylie Allemeier [1], Katelin Pilarski [1], Romi Burks [1], Matthew Barnes [2] (1. Southwestern University, 2. Texas Tech University) Native to South America, but highly invasive across Texas and the southeastern United States, the apple snail, *Pomacea maculata,* poses considerable ecological and economic threats to freshwaters. Given its cryptic nature, uncertainty remains regarding apple snail persistence even after populations appear locally eradicated through targeted removals. Environmental DNA (eDNA) analysis exhibits widespread use as a valuable molecular tool for detecting species presence and distribution by examining trace genetic material shed into aquatic environments. Using eDNA enables sensitive, non-invasive detection of non-native populations, facilitating early intervention. Yet, persistence of eDNA after organismal death limits its ability to reflect real-time viability. In contrast, environmental RNA (eRNA), owing to its less stable structure and rapid degradation, may serve as a more transient biomarker of recent biological activity. Therefore, eRNA analysis may help confirm successful management efforts. To quantify eRNA persistence, we conducted a short-term examination of eRNA and eDNA net accumulation in active live snails, snails with decreased activity, and dead snails alongside no-snail controls (N=5). We collected water samples (250-mL) after 24-hrs of initial buildup of genetic material (all snails alive) then again after 4 and 8 hrs of treatments. Successful extraction of eRNA (kit) and eDNA (bulk chloroform) will provide the first evaluation of extra-organismal eRNA released by *P. maculata* under controlled conditions and assess whether eRNA:eDNA ratios provide reliable indicators of organism viability and metabolic activity. Our findings aim to refine molecular monitoring approaches for invasive species by integrating eRNA dynamics with traditional eDNA detection.

#018-U Examining angiosperm conservation methods through the diet of Bombus pensylvanicus *Gabriel Ramos [1], Christopher Randle [1], Justin Williams [1] (1. Sam Houston State University)*
Bombus pensylvanicus, better known as the American bumblebee, is a species of bumblebee within the insect family Apidae and insect order Hymenoptera. Individuals are generally characterized as having black heads, yellow coloration on the upper half of their thorax, and black coloration on the remainder. These eusocial organisms are generalist foragers in that they do not have specific preferences when choosing flowers to forage from. Unfortunately, B. pensylvanicus is among the 11 bumblebee species that are at risk of becoming endangered within the state of Texas due to destruction of overwintering sites and flowing plant species. Unidentified pollen samples were collected by our collaborators from the hind legs of our species of interest and sent to us for identification. Scanning electron microscopy, SEM, was used to capture high magnification images that allowed for species identification. The species observed were classified as either native or non-native, and the native species were cross-referenced with the Texas Parks and Wildlife endangered species database to observe any species that may be at-risk. Once the data was compiled, conservation methods were developed with respect to the plant species' home ranges within Texas with the goal of increasing population numbers of both *B.* pensylvanicus and its associated plant species simultaneously.

#019-U Where Could This Moth Go? Predicting Future Distribution Using SDMs *Zyra Johnson [1], Christopher Randle [1] (1. Sam Houston State University)*
Thaumetopoea is a processionary moth that is native to Europe. It produces one generation per year. The larvae are polyphagous, with the main hosts being pine and cedar. The moth has a cyclical outbreak every 7-8 years, which causes severe defoliation in trees, resulting in stunted growth and tree death. Eggs, larvae, and adults occur above ground while pupation takes place below ground. Adults emerge from June to August. Females lay 70–300 cylindrical eggs. The larvae hatch after 25–40 days and aggressively feed on pine needles from autumn to early spring. The larvae undergo five instars. Pupation occurs at a depth of approximately 10 cm. Pupae remain underground from 4 to 5 months until the summertime. Species distribution modeling was used to predict the likely range of suitable habitat in the contiguous United States. We trained three models including Generalized Additive Models, Maximum Entropy Models, and Boosted Regression Trees, and summarized the results in the form of weighted average ensembles predictions. The ensemble prediction showed high predictive accuracy (AUC = 0.921) and was well-calibrated (Boyce index = 0.806). Models predict suitable habitat for *Thaumetopoea* pityocampa in the Pacific Northwest, the Coastal Range of California, and parts of the Sierra Nevada.

#020-U Effects of Invasive Chinaberry Tree Fruits on Invasive Asian Clams Amy Lowe [1], *Chris Distel [1] (1. Schreiner University)*
Corbicula fluminea is an invasive clam found in many freshwater ecosystems around the world and has an incredible ability to reproduce and consume resources. These clams are often used to test for chemical toxins such as heavy metals, but there is minimal research on how they filter and survive against natural toxins, such as those produced by chinaberry trees (*Melia azedarach*). Chinaberries are also known to severely deplete dissolved oxygen in water soon after exposure and decrease the survivability of crayfish and tadpoles. We performed an ecotoxicology experiment using clams from the Guadalupe River, we examined the clams' ability to survive in the presence of toxins from environmentally realistic whole chinaberry fruits and assessed how exposure to the toxins affected their growth and reproduction. Throughout the trial, clams were fed the same amount of cultured phytoplankton twice a day. Dissolved oxygen, pH, and total dissolved solids were recorded once a day for the first week and then every couple of days for the rest of the trial. Clam survival and oxygen levels did not change much over the course of the 6 week trial. The dissolved oxygen of the treatment tanks was similar to that of the control. To assess whether or not the clams successfully reproduced, we dissected them under a microscope and examined whether or not eggs were present, leading to unpredicted results. These results justify further study on toxins from invasive plants, and support this invasive clam as a useful animal model.

#021-G Comparing the efficacy of three crayfish sampling methods on two Texas SGCN Procambarus species during different seasons *Matthew Blow [1], McKenzie Adkins [1], Jared Dickson [1], Katrin Kellner [1], Archis Grubh [2], Matt Greenwold [1] (1. University of Texas at Tyler, 2. Texas Parks and Wildlife)* Two endemic Texas crayfish species (*Procambarus nigrocinctus* and *Procambarus nechesae*) were recently listed as Species of Greatest Conservation Need (SGCN) by the Texas Parks and Wildlife Department. There is little known about their life history and current distribution as they have only been sampled twice since their description in 1990. In conjunction with a life history project, this study will develop an environmental DNA (eDNA) assay for both target species. There are many aspects of eDNA sampling that have not been standardized due to it being a relatively new tool in conservation biology. Crayfish, in particular, have proven notoriously difficult to track using standard eDNA methods. Therefore, in addition to creating eDNA assays, this project aims to compare the efficacy of water and sediment eDNA techniques to live capture sampling throughout one year. Sampling may be affected by seasonality due to changes in abiotic and biotic factors related to life history characteristics. We hope to add to the understanding of the effects of seasonality on crayfish eDNA quantities and to establish if there are differences among water, sediment, or live capture sampling methods. Monthly sampling began in January 2025 and will conclude in December 2025. We expect to present on the development of species-specific molecular probe assays for droplet digital PCR (ddPCR) and the results of twelve months of sampling. Overall, this project will provide a greater understanding of the target species' life history, the effects of seasonality on sampling, and best practices for crayfish eDNA sampling techniques.

#022-G Comparative physiology and thermal biology of sympatric toad species *Peter J. Babcock [1], William I. Lutterschmidt [1] (1. Sam Houston State University)*
Physiological adaptations to environmental conditions play an important role in mediating species distributions and ecological resource requirements. Amphibians are ectothermic and sensitive to desiccation. Therefore, they must possess adaptations allowing them to tolerate extreme temperatures and water loss or invest energy in behavioral avoidance of such environmental extremes. Adaptations vary among species, and species with more similar physiologies generally experience greater niche overlap and increased competition for resources. To understand differences in spatial distributions and potential habitat partitioning, we compared the physiology and thermal preferences of three sympatric toad species, including the Houston Toad (*Anaxyrus houstonensis*). We investigated potential differences in evaporative water loss, metabolic rate, thermal preference, and thermal tolerance. Overlap in physiological performance of sympatric species may indicate direct competition for resources. Additionally, species less tolerant of increased temperature and/or desiccation may be more sensitive to the effects of climate change. Ultimately, the ability to explain geographic distributions and patterns of microhabitat use, as influenced by physiological tolerance of environmental conditions, may inform conservation efforts for vulnerable species such as the Houston Toad.

#023-G Monitoring the effects of environmental variations on nesting success of Eastern Bluebirds (Sialia sialis) on a university campus*Gwendolyn Nichols [1], Jessica Coleman [1], Matt Greenwold [1] (1. The University of Texas at Tyler)* Climate change is altering environmental conditions across ecosystems, with potential consequences for the reproductive success of secondary cavity-nesting birds. Prior studies indicate that high temperatures can reduce embryo viability, especially later in the breeding season, yet the combined influence of environmental variation, habitat, and clutch timing remains insufficiently understood for secondary cavity-nesting birds. To address this, we analyzed four years of microclimate, developmental, and nest-survival data collected from twenty Eastern Bluebird (Sialia sialis) nest boxes across four habitat types at the University of Texas at Tyler. Internal and external temperatures during the

2025 breading season (late February to August) were collected using Kestrel data loggers, and embryo viability was measured using a Buddy Digital Egg Monitor. Weather and climate trends from the past four years were compiled from local meteorological records. Using these data, we quantified how clutch order, habitat, and temperature influences daily nest survival rate. RMark analyses indicate that nest survival was best explained by an interaction between the habitat type, year, and differing temperatures, suggesting that reproductive success is shaped by multiple interacting variables. A Welch's ANOVA comparing temperatures (internal and external) of the second and third clutch of the season revealed a significant difference ($F_{1,16} = 7.95$; $p<0.05$). Overall, these results help to further our understanding of how microclimate and habitat interact to shape avian reproductive ecology and suggest that nestbox monitoring programs can provide early indicators of climate-driven changes in local population stability.

#024-G Environmental influences of eDNA detection and persistence inform sampling protocol *William I. Lutterschmidt* [1], *Kyra S. Woytek* [1] *(1. Sam Houston State University)* Environmental DNA (eDNA) sampling is a relatively new methodology for indirect detection of organisms and is often used in conservation research of rare or endangered species. Past studies have shown environmental variables of current velocity, pH, and water temperature to influence both the rate at which organisms shed eDNA into the environment, and how long eDNA molecules persist before becoming undetectable. Here, we summarize results of past field research on the spatio-temporal patterns of eDNA detectability for the alligator snapping turtle (*Macrochelys temminckii*). We also report on more recent results from the use of controlled mesocosm and laboratory experiments examining eDNA persistence, suggesting high stability of eDNA molecules with short-term exposure to pH and temperature extremes with relation to typical field observations of these abiotic factors. We discuss these results and provide recommendations that may be most informative within the context of field collection and transport of eDNA samples.

#025-U Comparative Analysis of Anti-Hemolytic Properties in Ilex Species: A Study of Plant Extracts against Streptococcus and Enterococcus Bacteria *Atlanta Williams* [1], *Hanna Erfanian* [1] *(1. University of Texas Permian Basin)* Hemolysis, the accelerated breakdown of red blood cells can result from infections, inflammation, or bacterial toxins, leading to anemia, fatigue, and physiological stress. Last year's research identified Ilex vomitoria as a promising native West Texas plant capable of protecting red blood cells from hemolysis caused by Streptococcus species. Building on these findings, this project focuses on studying the natural defense chemicals found in three species of Ilex: *Ilex vomitoria*, *Ilex decidua*, and *Ilex paraguariensis* (yerba mate). These plants may contain compounds that help protect against bacteria that break down red blood cells. Only leaves and berries from each species will be collected to determine which tissue produces the strongest protective extract. Organic solvent extraction will be used to isolate potential bioactive compounds. These extracts will then be tested against hemolytic bacteria, including *Streptococcus sanguis*, *Streptococcus pyogenes*, and *Enterococcus faecalis*. Blood agar plates will be used to observe reductions in hemolysis, while liquid blood cultures will assess whether the extracts limit bacterial growth or toxin-induced red blood cell damage. Because many hemolytic bacteria are developing increasing levels of antibiotic resistance, identifying effective plant-based alternatives is essential. The goal of this study is to see which Ilex species and which plant parts show the strongest anti-hemolytic effects. Learning more about how these plants fight off harmful bacteria may help us understand their natural defense strategies and could support future research on plant-based remedies or natural anti-inflammatory properties.

#026-U Diquat Herbicide-Induced Effects on Cherry Tomatoes
Yamilex Hernandez [1], *Honey Golden* [1] *(1. Temple College)* Many commercial herbicides are associated with long-term health implications in children and agricultural communities. Specifically, diquat dibromide is used as a non-selective contact herbicide applied to control vegetation in agricultural settings for pre-plant burn-down, crop desiccation, and weed control in landscape beds, ponds, lakes, and canals. Diquat dibromide has recently been shown to cause severe human poisoning characterized by cytotoxicity and extensive multi-organ damage through dysregulation of various intracellular signaling cascades, including mitogen-activated protein kinase (MAPK) signaling. Although MAPK signaling mechanisms are known to play an important role in mitigating plant abiotic stress, the specific effects of diquat dibromide on plant MAPK signaling remains unknown. In addition, we sought to understand whether inoculation with arbuscular mycorrhizal (AM) fungi would counteract the effects of the herbicide on MAPK activation and plant growth. Here we show the effects of spraying a diquat dibromide Roundup formulation on soil to treat weeds prior to transplanting gold nugget cherry tomatoes (*Solanum lycopersicon*). Our investigation assesses the effects of diquat dibromide on plant health and MAPK signaling in the presence and absence of AM fungi inoculation. Our results demonstrate that cherry tomatoes are significantly impacted by the diquat dibromide herbicide, even in the presence of AM fungi symbiosis, with varying MAPK activation. We anticipate that these results will help elucidate the effects of commercial herbicides, and warrant further caution in their use and application.

#027-U Gene flow between ‘races’ of the annual wildflower Mentzelia pectinata (Loasaceae) based on multiple microsatellite loci

Gisela Guerrero [1], Ana Rodriguez [1], Hannah Anthony [1], Amy Osborn [1], Joshua Brokaw [1] (1. Abilene Christian University)

Mentzelia pectinata is an annual wildflower native to southern California that was recently split into two varieties, M. pectinata var. chrysopetala (Obispo blazingstar) and M. pectinata var. pectinata (San Joaquin blazingstar). The former is typically yellow in appearance, and the latter is generally orange. To investigate whether flower color is a good predictor of genetic subdivision, we developed several trinucleotide microsatellite markers to determine if populations of the respective varieties experience gene flow consistent with levels observed in other infra-specific taxonomic groups. We genotyped a total of 87 individuals across 4 populations of Mentzelia pectinata var. chrysopetala and 146 individuals from 8 populations of M. pectinata var. pectinata. The greatest Fst value (0.75) was between populations with different flower colors, and the smallest Fst (0.00) was between two orange populations. However, there were also populations with mismatching colors that had low Fst (0.17) and populations with matching colors that had high Fst (0.69), creating an inconsistent relationship between flower color and genetic subdivision. Instead, Fst was more consistently correlated with geographic distances between populations, and a Mantel test showed that 25% of the variation in Fst could be explained as isolation by geographic distance, whereas flower color explained less than 1% of the genetic subdivision of populations. These results suggest that flower color may not be a sufficient indicator of subspecific divergence within M. pectinata.

#028-U Microhabitat variation influences streambed plant diversity at the Independence Creek Preserve

Edmundo Avalos [1], Olivia Fischer [1], Matthew Allen [1] (1. Wayland Baptist University) The Nature Conservancy’s Independence Creek Preserve (ICP) is located within the lower Pecos River basin where it greatly enhances both water volume and quality within the watershed and serves as a hotspot of biodiversity within the Chihuahuan desert ecosystem. Despite its ecological significance, limited data exists on the floristic structure and community composition of the preserve’s plant communities. This study aimed to describe the abundance and diversity of streambed plant communities within the Independence Creek streambed. Twelve transects, each 40 meters in length and spaced approximately 20 meters apart, were established perpendicular to the creek channel. Every 2m along the transects we recorded plant coverage, habitat type, water depth, and relative elevation in 1m2 plots. A total of 29 plant species were identified across 240 plots, with an average of 1.14 species per plot. Glides and runs were the most common habitats, but the least likely to contain plants. Gravel bars and silt beds tended to host more plant species and have more plant coverage. Overall, habitat type appeared to explain most of the variation in species richness. As water depth increased, plant richness decreased, though weakly. These results suggest that habitat heterogeneity supports modest but structured plant diversity within the streambed. These findings contribute to a growing understanding of how microhabitat variation and hydrological conditions shape riparian plant communities within semi-arid freshwater systems.

#029-U Development of new microsatellite loci to study geneflow in the annual wildflower Mentzelia pectinata (Loasaceae).

Ana Rodriguez [1], Hannah Anthony [1], Gisela Guerrero [1], Joshua Brokaw [1] (1. Abilene Christian University)

Understanding patterns of gene flow is critical for the conservation and management of rare plant species. Mentzelia pectinata, an annual wildflower native to southwestern California, has limited population connectivity, yet little is known about its genetic structure. To address this, we developed novel microsatellite markers using Illumina whole-genome sequence reads. Candidate loci were identified through in silico screening for short tandem dinucleotide and trinucleotide repeats, and primers were designed for PCR amplification. We optimized amplification by performing a PCR gradient analysis across annealing temperatures and validated loci with Sanger sequencing. We then sampled multiple individuals within and across populations to confirm allelic variation and heterozygosity. These loci provide sufficient resolution to detect population differentiation, estimate gene flow, and assess genetic diversity within and among populations. The availability of these markers establishes a molecular toolkit for future studies investigating reproductive biology, dispersal mechanisms, and landscape connectivity in M. pectinata. Additionally, this project demonstrates an integrative approach for undergraduate researchers, combining next-generation sequencing, bioinformatics, and classical molecular techniques. By linking molecular marker development to ecological and evolutionary questions, this work contributes both to the conservation of a native plant species and to the training of students in modern plant genetics research.

#030-G Shedding Light on Plant and Soil Sciences with Synchrotron-Based Spectroscopy

Caleb Shackelford [1] (1. Texas A&M University; Invited Speaker) Understanding how elements associate and transform in plants and soils requires tools capable of probing elemental interactions at molecular and micro-scale levels. Synchrotron spectroscopy provides such capabilities, using high-intensity, tunable X-ray radiation to reveal elemental speciation, oxidation states, coordination environments, and spatial distributions in complex biological and environmental systems. Techniques including X-ray absorption spectroscopy (XANES and EXAFS), micro–X-ray fluorescence (µXRF), and X-ray micro-tomography (µCT) have expanded the ability to investigate processes that are otherwise inaccessible with conventional methods. In plants, these approaches have illuminated elemental uptake, transport, and compartmentalization, as well as redox-driven biochemical responses to environmental stress. In soils, synchrotron methods have revealed the dynamics of mineral weathering, nutrient cycling, and the formation and persistence of contaminants on soil colloids, providing insight into reactive mineral phases and micro-scale chemical heterogeneity. In the rhizosphere, the interface between plants and soils, synchrotron spectroscopy has provided insight into processes that are otherwise difficult to study. These techniques enable direct characterization of chemical gradients, mineral–organic interactions, and transformations driven by plant and microbial activity. This presentation will highlight the development and capabilities of synchrotron techniques and illustrate their applications in plant biology, soil science, and the plant–soil interface. These advances provide new insights into biogeochemical processes and are enhancing our understanding of terrestrial ecosystems.

#031-N Microbial Strategies to Promote Legume Tolerance to Soil Alkalinity Ahmad Kabir [1] *(1. Lamar University)* Soil alkalinity severely limits legume growth. Effective pH management in agricultural soils remains challenging, but microbial interventions may offer a promising solution to overcome this issue. In this study, we investigated whether and how *Bacillus subtilis* promotes alkaline stress tolerance in garden pea. We found that diverse garden pea genotypes inoculated with *B. subtilis* under soil alkalinity exhibited improvements in morphological traits in a host-specific manner. Mechanistic analyses focused on the Sugar Snap genotype revealed significant improvements in root nodulation, tissue mineral status, and photosystem efficiency when inoculated with *B. subtilis* under alkaline stress. The split-root assay demonstrated that *B. subtilis* inoculation induces systemic signaling, which underlies alkaline tolerance in pea. Furthermore, co-culture experiments showed increased growth of both *Rhizobium leguminosarum* and *B. subtilis*, pointing to their complementary interactions that promote mutual fitness under alkaline stress. RNA-seq analysis identified 958 and 1134 differentially expressed genes upregulated and downregulated, respectively, in the roots inoculated with *B. subtilis* under alkaline conditions. The upregulated genes were mostly involved in the sugar-mediated symbiotic association (*SWEET*, *GLUT*), pH homeostasis (*cation/H+ exchanger*, *ATPase*), and nutrient assimilation (*Ammonium transporter*, *Zn/Fe permease*). Amplicon sequencing revealed lower richness and diversity of rhizosphere bacterial and fungal communities under alkaline stress. However, *B. subtilis* inoculation enriched beneficial taxa such as *Pseudomonas*, *Pseudorhizobium*, *Pseudallescheria*, and *Chaetomium* that may act as helper microbes to enhance pea survival under alkalinity. In summary, microbial interventions such as *B. subtilis* offer an effective strategy to boost legume tolerance to alkaline soils.

#032-N Preserving the Biodiversity of the UT Permian Basin Kurtz Herbarium by Inclusion in the Texas Oklahoma Regional Consortium of Herbaria (TORCH) Irene Perry [1] *(1. University of Texas Permian Basin)* An herbarium is a collection of preserved plant specimens that can last for centuries when pressed, processed, and stored properly. These collections represent a wealth of information about plant biodiversity and their ecosystems. Making high-resolution digital images publicly available has been an international herbaria trend. The herbarium at the University of Texas Permian Basin (UTPB) was started with the 1973 school founding. Specimens are added annually from the Botany students and faculty. In August 2022, UTPB received federal grant funding to support undergraduate research and skill development in STEM fields. In turn, the Biology department received funds to purchase supplies for an imaging station and student salaries for the herbarium digitization. The first year the basic setup of camera, lightbox and computer was completed. During the second year, the high-resolution photographing of historical herbarium specimen started. The third year marked the completion of the existing herbarium specimen and image file processing was begun. In the fourth year, uploading the image files to the Texas Advanced Computer Center and inclusion in TORCH is anticipated. Since the start of the project in 2022, ten undergraduate students have received training and experience in some aspect of the project: camera lightbox set up, image capture and processing software, proper preparation and handling of delicate specimen, maintenance of the database. Annually, student local and state level research presentations (oral and poster) have been given.

#033-N Expert in a Dying Field? Botany's Decline in Tuition-Dependent Colleges and Universities Joshua Brokaw [1] *(1. Abilene Christian University)* Across the United States, undergraduate plant biology and organismal natural-history training have experienced a decades-long decline, reflecting broader cultural and institutional shifts that increasingly prioritize biomedical and molecular life-science fields. While this trend is evident across many types of institutions, it is especially acute at tuition-dependent private colleges and smaller universities. These campuses face stronger enrollment pressures, more limited staffing flexibility, and greater dependence on market-driven degree programs, making botany, field biology, and taxonomy particularly vulnerable when faculty retire or student interest appears uncertain. At the same time, nationwide reductions in botanical research positions, herbarium funding, field-station support, and public engagement have compounded

the erosion of expertise in plant identification, systematics, and ecological literacy.
I argue that small private institutions represent a “weakest link” in the national botanical capacity chain: they educate large numbers of first-generation and pre-professional students, serve regions without major public universities, and often supply future teachers, land managers, and conservation practitioners. Preserving—and rebuilding—botanical education at these colleges will require targeted interventions. These include dedicated scholarships for organismal and field-based study; donor and foundation support for faculty lines and field courses; partnerships with museums, government agencies, and conservation nonprofits; and clearer pathways from undergraduate botany into conservation, horticulture, biotechnology, and environmental-industry careers.

#034-N Navigating Human Values and Motives in STEM Education: Insights from the Preteen Years *Sajid Bashir[1], Jingbo Liu[1] (1. Texas A&M University-Kingsville)* This study presents a decade-long investigation into student perceptions of performance in general chemistry education, framed by an operational model that connects perception with relevance. The goal was to generate evidence-based practices for identifying at-risk students and linking their outcomes to measures of emotional intelligence, defined here as human values, autonomy, and motives (VAM). Data were collected through course scores, tailored questionnaires, and classroom observations of student–instructor interactions. Instructional approaches were compared across acid–base theory and equilibrium topics, using traditional lectures, video kiosks (VK), on-site mentoring (MeriT), and off-site tutoring through the Pathways Academic Assistance Center (PACT). Collectively termed VKaoT, these interventions were designed to reinforce student engagement and provide flexible access to support. A unified lesson plan was implemented by two faculty members, supplemented with always-available tailored videos. Students were incentivized to participate in tutoring, and their performance was correlated with self-declared perceptions of relevance (VAM). Key indicators—including course scores, attendance, classroom engagement, and emotional intelligence ratings—showed positive correlations between reinforced perceptions of chemistry’s relevance and improved learner outcomes. Students with higher emotional intelligence demonstrated stronger connections between logical content mastery and psychological readiness to seek help, requiring less instructor intervention and reporting greater enjoyment of chemistry.The findings highlight the importance of aligning instructional delivery with student perceptions and career aspirations. By reinforcing VAM through accessible mentoring and tutoring, this framework supports knowledge retention, critical thinking, and workforce readiness, offering a scalable model for STEM education improvement.

#035-N The successful application of WOKE funding to STEM progress *Keith Pannell[1] (1. The University of Texas at El Paso)*
In today's world the definition of WOKE is apparently a matter of choice. This is, of course, unacceptable. The author uses of the Oxford English Dictionary, the most comprehensive record of the language, as the starting point to present, and discuss, the incredibly positive impact of WOKE funding upon the development of STEM education and research excellence at the University of Texas at El Paso. From a research deficient institution in the early 70's to a Tier One Research University today, the transition could not have occurred without the WOKE seed money that catalyzed the transformation.

#036-N A Pedagogical Experiment: Repackaging Introductory Biology Labs and Research Classes Into Professional Skills Courses *Chris Distel[1] (1. Schreiner University)* Traditional introductory sequences in biology include discrete topical labs, and possibly some research focused courses. This arrangement severely limits continuity because topics and research projects change substantially from one course to the next. Additionally, while active learning in introductory labs has increased appreciably over the past two decades, it’s usually within the context of an isolated project or themed course rather than an overarching pedagogical model across courses. To improve continuity and retention, Schreiner University repackaged two introductory labs and three research courses into four new professional skills courses. Beginning in 2021, all biology majors took two, 2-credit courses in the first year and two, 1-credit courses in the second year that balanced three boad professional skills in biology: experimental design, scientific communication, and manual skills. We used the Small World Initiative CURE as the research model for all courses. In this way, students have iterative experiences with experimental design, proposal preparation, literature review, journal clubs, oral presentation, group work, microscopes, metric system, biodiversity identification, evolution, pipetting, solutions, and biochemistry. Preliminarily results showed great promise among students after the first two professional skills courses in genetics. However, the approach proved not to satisfy our goals.

#037-U A Novel Multiphysics Simulation Engine for Modelling High-Enthalpy Plasma-Surface Interactions in Hypersonic Flight Regimes *John-Ryan Lawrence[1], Sajid Liu[1], Jingbo Liu[1] (1. Texas A&M University-Kingsville)* Hypersonic flight in high-enthalpy environments induces complex plasma-surface interactions that challenge traditional single-physics modeling approaches. Accurate prediction of thermal loading, surface chemistry, and material response requires the integration of ionized flow dynamics, heat transfer, and surface reaction mechanisms within a unified computational framework. This work presents the development of a modular multiphysics simulation platform designed to explore plasma-surface interactions relevant to reusable hypersonic vehicles and advanced thermal protection materials. The framework couples high-temperature gas dynamics with surface energy balance and species transport models, enabling investigation of plasma-driven heating and material response under representative hypersonic conditions. Preliminary simulations demonstrate the capability of the platform to capture key trends in thermal flux and surface interaction behavior. This tool provides a foundation for future parametric studies and experimental validation in high-enthalpy wind tunnel environments

#038-G Benchmarking Transformer Models for the Classification of Gravitational-Wave Detector Glitches

Rudhresh Manoharan [1], Brian Phillips [1], Tanish Chettiar [2], Gerald Cleaver [1] (1. Baylor University, 2. Yale University) Gravitational-wave observatories such as LIGO routinely detect short-duration non-astrophysical noise transients, commonly known as *glitches*, which can limit the sensitivity of searches for astrophysical signals. Accurate classification of these glitches is therefore essential for detector characterization and data quality assessment in gravitational-wave astronomy. In this work, we present a systematic benchmarking study of modern transformer-based deep-learning models for the classification of gravitational-wave detector glitches using time–frequency representations of detector data. We evaluate a range of state-of-the-art transformer architectures, including Vision Transformers (ViT), Swin Transformers, and Data-efficient Image Transformers (DeiT), and compare their performance against established convolutional and traditional machine-learning baselines.

Model performance is assessed using standard classification metrics with particular emphasis on macro-averaged F1 score to account for class imbalance across glitch categories. In addition to classification accuracy, we examine training stability, inference efficiency, and model robustness, providing a comprehensive comparison of transformer-based approaches in a scientific data-analysis context.

Our results demonstrate that transformer architectures offer competitive and, in several cases, improved performance relative to conventional methods, highlighting their potential for automated glitch classification in current and future gravitational-wave detectors. This study provides practical guidance for selecting machine-learning models for detector characterization and illustrates the growing role of transformer-based methods in gravitational-wave data analysis.

#039-N From Discovery to Application: Engineering Atomic-Ternary Semiconductors into TRL-4 Resilient Power Modules

Jingbo Liu [1], Sajid Bashir [1] (1. Texas A&M University-Kingsville) This presentation introduces a reproducible pathway for advancing atomically engineered ternary semiconductors from materials to device demonstrators. These boride–carbide–chalcogenide composites are designed to meet the demands of next-generation microwave-absorbing systems operating under extreme thermal, electrical, and mechanical stress. Microwave-absorbing devices (MADs) are critical for wireless networks, radar, aerospace, and defense electronics, yet conventional systems face persistent limitations in impedance matching, thermal tolerance, and bandwidth coverage. A series of novel TiB_2–TiC–SiC composites were synthesized using molten salt-assisted carbothermal reduction. The lamellar structure and engineered nano-interfaces enhanced electromagnetic absorption and thermal resilience, delivering broadband performance across 2–18 GHz with a minimum reflection loss of –47.8 dB at 6.0 GHz and bandwidth ≥3 GHz at ≤–10 dB reflection loss. Devices validated across multiple trials achieved this performance at a lightweight thickness of 2.4 mm. Green chemistry methods enabled stoichiometry control, conformal coating, and interface tuning. In situ analytics and SPC-gated workflows ensured traceability and reproducibility, with version-controlled datasets aligned to CHIPS standards. Compared to incumbent semiconductors (Si, SiC, and GaN), which suffer from thermal bottlenecks and dielectric fatigue, the engineered ternary composites delivered 20–30% performance gains in conductivity, dielectric strength, and mechanical endurance. This effort bridges materials innovation and device-level integration, demonstrating reproducible TRL-4 readiness. Applications span grid converters, EV inverters, aerospace RF systems, and industrial electronics. By integrating atomic-level design, scalable synthesis, and audit-ready workflows, this work establishes a resilient semiconductor platform aligned with U.S. supply chain priorities and the Texas Academy of Science's mission to advance innovation with societal impact.

#040-U Impact of Topology on Coral Larvae Settlement on Concrete Matrices

Jennifer Hunt [1], Matthew Barnes [2], Brian Flowers [1], Thomas Ready [3] (1. University of Texas Permian Basin, 2. Texas Tech University, 3. The Glass Sponge Foundation) Coral reefs are essential ecosystems, supporting biodiversity and protecting coastlines from storms. However, global threats, including climate change and pollution, have led to significant coral bleaching and mortality. To combat these declines, artificial reefs have been created to facilitate coral recovery. However, these artificial structures often fail to attract sufficient coral larvae for long-term settlement and growth. By investigating how the topology of concrete surfaces impacts coral larvae settlement, this research seeks to improve artificial reef designs and make coral restoration efforts more effective. This project used different topological features on 3D-printed concrete matrices to influence the settlement of coral larvae. By understanding how these features affect coral settlement, we aim to enhance artificial reef designs to promote coral growth, supporting coral restoration efforts in degraded marine ecosystems. Concrete "cupcakes" with four channel spacings (smooth, 1.27 mm, 2.54 mm, and 5.07 mm) were 3D-printed to mimic reef structures. The cupcakes were then deployed around several dive sites in Tela Bay, Honduras, and left for different periods of time to observe marine organism settlement patterns. Initial findings suggest that small and medium channels exhibit higher rates of living organisms, particularly tubeworms. In contrast, smooth and large channels show a greater prevalence of algal coverage. DNA extraction was done at Texas Tech University. Current analysis of the whole genome is pending.

#041-U The Role of Symbiotic Status of Exaiptasia diaphana in Serratia marcescens Pathogenesis *Amy Joffrion [1], Tanya Brown [1] (1. University of Texas at Tyler)* Symbiosis does not just shape how reef organisms live; it may also shape how they die. As a model for coral-algal symbiosis, *Exaiptasia diaphana* offers a window into how mutualism can influence disease proliferation. *Serratia marcescens* is a bacterium that functions as an opportunistic pathogen in cnidarians. It is also proven to cause mortality in sea anemone *E. diaphana*. Under stressful conditions *E. diaphana* can lose their Symbiodinium which leads to decreased photosynthetic energy, slowed growth, and limited reproduction. We investigated whether symbiotic state impacts lethality of *S. marcescens* infections. We conducted 10-day bacterial challenges at 30°C to assess mortality at three concentrations (10^6, 10^7, 10^8 CFU/mL) for symbiotic and aposymbiotic *E. diaphana*. A significant difference in mortality (p=0.006) was observed at with 10^8CFU/mL *S. marcescens* showing 100% mortality by day four in symbiotic anemones while complete mortality was achieved by day three in aposymbiotic anemones. Lower bacterial concentrations of *S. marcescens* showed no mortality over the 10-day microbial challenge. Symbiotic state may play an important role in *S. marcescens* lethality with aposymbiotic anemones dying earlier than symbiotic *E. diaphana*. Symbiodinium not only provides important nutritional support for symbiotic cnidarians but also aid in defending against pathogens.

#042-U Abundance and Disease Status of Starlet Corals in Roatán, Honduras *Gloria Dominguez [1], Ashley Tejada [1], Kaylee Aguilar [1], Xaile Garza [1], Ana Quintanilla [1], Leon Rosales [1], Annie Mowry [1], Ashlyn Kennedy [1], Matthew Hicks [1], Racheal Gomez [1], Traesha Robertson [2], Stephanie Lockwood [3], Jacqueline Dove [1], Stephanie Randell [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University)* Climate change-precipitated rising temperatures threaten coral reefs, which host 25% of all marine life. Increasing water temperature and decreasing water quality has led to coral bleaching and disease. This study aimed to assess the abundance and health status of starlet corals *Siderastrea siderea, Siderastrea radians,* and *Stephanocoenia intersepta* located on the Mesoamerican Barrier Reef in Roatán, Honduras. Research focused specifically on Dark Spot Syndrome (DSS) and Stony Coral Tissue Loss Disease (SCTLD). Divers utilized the Randell-Robertson Marine Survey Technique, starting at a depth of 18 meters, at five dive sites. For *S. siderea* (n=128), 4.69% were healthy, 91.41% were damaged, 17.97% were bleached, 21.09% were diseased, and 2.34% were dead. Of the 37 that were diseased, 78.38% had DSS and 29.73% had SCTLD. For *S. radians* (n=71), 9.86% were healthy, 84.51% were damaged, 63.38% were bleached, 8.45% were diseased, and 2.82% were dead. Of the 6 identified as diseased, all had DSS and none had SCTLD. For *S. intersepta* (n=28), 21.43% were healthy, 71.43% were damaged, 21.43% were bleached, 7.14% were diseased, and none were dead. Of the 2 diseased, both had DSS and none had SCTLD. For all identified starlet corals (n=227), 18.06% had DSS and 4.85% had SCTLD. These findings suggest that very little starlet corals are healthy, however, damage is more prevalent than disease. These findings also suggest that DSS, a non-lethal disease is more prevalent than SCTLD, which is fatal.

#043-U The Diversity of West Caribbean Octocorals in Roatán, Honduras *Harrison Wolf [1], Christopher Allovio [1], Hannah Dawson [1], Zoe Hilliard [1], Traesha Robertson [2], Annie Mowry [1], Ashlyn Kennedy [1], Jacqueline Dove [1], Stephanie Lockwood [3], Stephanie Randell [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University)* Sea fans, rods, and whips, known as octocorals, serve vital functions in tropical marine ecosystems, providing habitats and supporting biodiversity. Current research regarding Caribbean octocorals is limited as research in the tropics has primarily focused on the threatened scleractinian coral populations. Renewed interest in octocorals has been stimulated by anthopogenic needs as Octocorallia exhibits promising results for new natural marine products. Ecological surveys suggest octocorals provide necessary insight into the health of the reefs in response to environmental disruptions from climate change, industry, and disease. This study was conducted to assess the diversity and health of octocoral communities in Western Caribbean shallow reefs in Roatán, Honduras. Divers conducted belt transects at 4 sites along the Mesoamerican Barrier Reef and enumerated specimens by species. At each site: species were evaluated for density per meter squared and sites analyzed through Simpson’s Diversity Indices, and Simpson’s Evenness. This present study identified 19 species across 9 genera: *Antillogorgia*, *Briareum*, *Eunicea*, *Gorgonia*, *Muricea*, *Muriceopsis*, *Plexaura*, *Plexaurella*, *Pseudoplexaura*, and *Pterogorgia.* Researchers noted differential community compositions between spur and groove formations and patch reef formations, but Chi-Square Test revealed no statistical significances between site richness, diversity, evenness, or density. Low disease incidence along transects prevented any analyses regarding health. Continued monitoring, expanded surveys, and genetic studies are recommended.

#044-U A Longitudinal Study of Macroorganism Associations and Health Status of Demospongiae Species in Roatán, Honduras

Cambria Blanton [1], Caden Helona [1], Ashlyn Kennedy [1], Anne Mowry [1], Traesha Robertson [2], Jacqueline Dove [1], Stephanie Lockwood [3], Naomi Hammond [1], Stephanie Randell [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University)

Sponges are some of the most prevalent and vital members within coral reefs. Some poriferan species possess a spongocoel and large protuberances, which provide refuge for marine organisms. Species such as Niphates digitalis, Callyspongia plicifera, and Xestospongia muta are notable for these features. Associations between sponges and macroorganisms are generally incidental or opportunistic. However, interactions between brittle stars and poriferans can be mutualistic to parasitic. The association between macroorganisms and sponges and sponge health is unknown. This study examined microorganism associations and health status for Demospongiae species in Roatán, Honduras between May 2024 and 2025. In 2024, X. muta displayed noteworthy macroorganism diversity, with one individual harboring ~130 fish (92.9%). Of note were seven juvenile threespot damselfish (Stegastes planifrons), a species typically associated with staghorn corals. Over 60% were algae fouled or diseased. N. digitalis were predominantly healthy (75%), but brittle star presence correlated with lesions in 61.9% of hosts. All C. plicifera were found healthy andunassociated with macroorganisms. In 2025, X. muta health status increased, with 51.8% being healthy. N. digitalis was consistent in health (90%), while C. plicifera showed increased stress with only 50% being healthy. Across both years, X. muta exhibited the greatest number of macroorganism associations (311 fish, 8 crustaceans). Five juvenile threespot damselfish were observed with X. muta in 2025. N. digitalis primarily hosted brittle stars (60%) and crustaceans (7%), and C. plicifera had minimal associations. This research serves as a foundation for future studies on sponge health and macroorganism associations.

#045-U Rope Sponge Diversity and Health Status in Roatán, Honduras

Yuto Goto [1], Nicholas Mischtian [1], Tafadzwa Duri [1], Juliusz Bachleda-Curus [1], Traesha Robertson [2], Annie Mowry [1], Ashlyn Kennedy [1], Jacqueline Dove [1], Stephanie Lockwood [3], Stephanie Randell [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University) Sponges play essential roles in Caribbean reefs through filtration, nutrient cycling, and habitat formation, and their abundance has increased where coral cover has declined. Rope sponges such as *Aplysina cauliformis* and *Aplysina fulva* are common in this region, and emerging diseases—*Aplysina* Red Band Syndrome (ARBS) in *Aplysina* spp. and Sponge White Patch Disease (SWPD) in *Amphimedon compressa*—have been reported. A paucity of data on rope sponge populations and disease status in Roatán limits the ability to detect future outbreaks. This study was conducted to assess rope sponge diversity and disease prevalence in Roatán, Honduras. Data were collected from 27 to 30 May 2025 at four reef sites, using belt transects (BT) and the Randell–Robertson Marine Survey Technique (RRMST). A total of 220 rope sponges were recorded. The most abundant species were *A. cauliformis* (n = 78), *A. fulva* (n = 48), *Niphates amorpha* (n = 37), *Niphates erecta* (n = 30), and *Amphimedon compressa* (n = 24). Most sponges were healthy (85.9%), but ARBS (3.6%), SWPD (1.8%), physical damage (3.2%), and unknown disease (5.5%) were present. Lesion material from ARBS was visually identified as filamentous cyanobacteria (*Lyngbya sordida*) and red algae. Chi-square tests showed that species composition differed significantly among sites for both BT and RRMST. Disease patterns were species-specific: ARBS affected *A. cauliformis* and *A. fulva* (6.3%), whereas SWPD occurred only in *Amphimedon compressa* (16.7%). These findings confirm the presence of sponge disease in Roatán and provide baseline data for monitoring and reef management in Caribbean reefs.

#046-G From Anemone to Coral: Establishing Nematostella vectensis as a Translational Model for Coral Disease Research

James Campbell [1], Tanya Brown [1] (1. University of Texas at Tyler) In recent years, there have been consistently increasing environmental stressors that have applied pressure upon the world's coral reefs. Because of this, these ecosystems that provide a wealth of biodiversity and ecosystem services have reached a tipping point. Along with forecasted decline of reefs, it is expected that there will be a loss of biodiversity, economic benefits, and coastal protection. With current models predicting an increase in disease outbreaks, it is imperative that a foundational understanding of disease response be established. Unfortunately, the life history of most coral models does not lend themselves to conducting rapid molecular research. To accelerate immunological research, several translational models have been proposed, including *Nematostella vectensis*. Current work utilizes *N. vectensis* in microbiome-host interactions studies, but immunological studies have been impeded by the lack of a known bacterial challenge. To identify a potential microbial challenge, *N. vectensis* larvae were treated with three different lipopolysaccharides (LPS). The sources of the LPS was selected based on previous use in immune studies or the known ability to elicit disease in corals. Following treatment, the larvae were observed for mortality and developmental progression. Overall, LPS appears to inhibit the survival of larvae over the course of 14 days, however LPS derived from *Serratia marcescens* was noted to have a significantly greater effect on mortality within the first week. While further work will need to confirm the response is immune in nature, these results demonstrate the promise of *S. marcescens* as a potential bacterial challenge for cnidarian disease research.

#047-N Effects of Transcranial Photobiomodulation on Cognitive Processes, Anxiety Symptoms, and Brain Hemodynamics

Adrian Nguyen [1], Laura Gamboa [1], Isabelle Rose [1], Jordan Schwartz [1], Nicole J. Moore [1], Douglas Barrett [1], F. Gonzalez-Lima [1] (1. The University of Texas at Austin) Transcranial infrared laser stimulation (TILS) is a novel, non-invasive form of photobiomodulation that uses near-infrared light to stimulate bioenergetic and neurophysiological processes in the brain. By enhancing mitochondrial respiration and cerebral oxygen metabolism, TILS offers a promising approach to improve cognition and emotion through prefrontal cortical modulation. Prior studies have shown that TILS enhances attention, working memory, and mood in both healthy and clinical populations. Meta-analyses of transcranial photobiomodulation (tPBM) indicate consistent cognitive and affective improvements. While the mechanisms underlying its effects on anxiety are unclear, its potential as an adjunctive neuroenhancer remains promising. Attention Bias Modification, a behavioral therapy that targets attentional bias to threat, has shown mixed efficacy, suggesting that neuromodulation may enhance its impact. This study addresses these gaps by examining whether TILS to the right dorsolateral prefrontal cortex reduces attention bias to threat and anxiety in adults with elevated but subclinical anxiety. Here we show that two 8-minute sessions of right-prefrontal TILS decrease attentional bias to threat and self-reported anxiety relative to sham stimulation, as measured across three laboratory visits using behavioral tasks. Prefrontal cortex activity was assessed during the sessions using functional near-infrared spectroscopy. These findings indicate that TILS modulates prefrontal functional connectivity, mediating improvements in attentional control and emotional regulation. Compared with prior behavioral interventions, TILS provides a neurophysiological mechanism for enhancing anxiety-related cognitive processing. This work supports TILS as a safe, rapid, and non-invasive neuromodulatory intervention for improving emotion regulation and anxiety-related cognition. Supported by the Oskar Fischer Project and Elhapa Foundation.

#048-U Gene Currents: Understanding Genetic Diversity of Apple Snails in Northern and Southern Belizean Watersheds

Johun Reyes [1], Gage Mallo [1], Romi Burks [1] (1. Southwestern University) Apple snails (genus *Pomacea*), which possess both a gill and a lung, provide an invertebrate model for studying amphibiousness as floodwaters often transport them or they bury to survive drought periods. Apple snails play key roles as aquatic consumers and prey and their morphological diversity makes them interesting candidates to examine cryptic diversity. Crooked Tree Wildlife Sanctuary, in the north-central part of biodiverse Belize, hosts the only documented population of the native apple snail known as *Pomacea flagellata.* This dynamic area connects the Belize River and the New River watersheds hydrologically in times of flooding. No other records exist for apple snails outside Crooked Tree, although these snails may help us understand landscape-level gene flow because they inhabit transitional areas. Our work sought to document population-level differences by conducting a haplotype analysis (cytochrome oxidase c I gene) of the 105 apple snails we collected from 12 sites in north and south-central Belize that spanned six major water bodies. We identified all of our snails as the same species, although ongoing analysis suggests that it might differ from what we currently know as *P. flagellata*. Preliminary analysis of 95 sequences (590 bp) indicates at least 27 haplotypes between the sites across Belize, indicating a large amount of intraspecific variation. Approximately ⅓ belonged to a single haplotype occurring in 3 of 6 water bodies. Additional haplotypes occurred in multiple sites as well. These patterns highlight how the environment shapes gene flow and helps identify cryptic diversity.

#049-U Opercularis Muscle in Facultatively Metamorphic Eurycea sp. A Comparison between Paedomorphs and Metamorphs

Kelsey M. Malousek [1], Joseph Humphrey [1], Ruben U. Tovar [2], Thomas J. Devitt [3], David M. Hillis [3], Dana M. Garcia [1] (1. Texas State University, 2. St. Mary's University, 3. University of Texas at Austin) The opercularis system is a part of the extratympanic auditory system in metamorphosed anurans and some salamanders, which is proposed to aid hearing by transmitting vibrations from the environment via the opercularis muscle to the inner ear. The morphology of this system varies between taxa and comparative analyses are lacking. This system is a sensory adaptation present in terrestrial metamorphs and is absent in aquatic paedomorphs. An undescribed species of *Eurycea* is a facultatively metamorphic species of salamanders with some individuals retaining their juvenile features throughout their lives and others undergoing metamorphosis, raising the question of whether metamorphs are likely to develop an opercularis muscle. Here we show morphological differences in the opercularis system between paedomorphic and metamorphic *E. sp*. Dice-CT scanned images of two paedomorphic and two metamorphic specimens revealed the two metamorphs had paired opercularis muscles; in one adult paedomorph, the opercularis muscles were not detected while in the other a single opercularis muscle was found. In the paedomorphic adult with the muscles, other juvenile features, including gills, were evident, making the appearance of the opercularis surprising. Seeing a feature associated with metamorphosis in an individual that has not completed metamorphosis highlights the need to undertake further developmental studies to elucidate the sequence of events leading to full metamorphosis; perhaps this individual was in the process of undergoing transition. Future segmentation of a developmental series of facultatively metamorphic *Eurycea* may expand upon these observations.

#050-G Comparative morphology of the American and Houston Toad *Lauren N. Scherrer[1], Juan D. Daza[1], William I. Lutterschmidt[1] (1. Sam Houston State University)* The American and Houston toads are sister species with similar morphological characters and genetics. While classical taxonomy has used external characters and behavior to distinguish these species, we investigated potential differences in osteology and present diagnosable differences in skull shape. We used High-Resolution Computed Tomographies of American (n =28) and Houston (n =18) toads showing different post-metamorphose stages. Morphological landmarks (n = 33) of skull shape will be analyzed using geometric morphometrics in 3D. These data will allow us to quantify morphological variation across developmental stages and to compare the skull anatomy between species. We also used 3D surface scanning to obtain high resolution images of dorsal surfaces to investigate potential differences in the number of warts per area of skin between species. We expect these morphological analyses combined with newly obtained genomic data to help better define the taxonomic relationship between these sister species.

#051-G Diversity and Mitogenomics of Archinominae Species (Annelida: Amphinomidae) From Marine Biodiversity Hotspots
Bernard Mbithi[1], Fernando Calderón-Gutiérrez[2], Utpal Smart[1], Beatriz Yáñez Rivera[3], Elizabeth Borda[1] (1. Texas A&M University-San Antonio, 2. Stephen F. Austin State University, 3. Instituto de Ciencias del Mar y Limnología, Unidad Académica Mazatlan)
Fireworm species of the genera *Chloeia* and *Notopygos* (Amphinomidae) are essential components of benthic marine ecosystems, yet their taxonomy and deeper evolutionary relationships remain unclear due to limited genomic and morphological resources. To address these gaps, this study integrates morphological assessment, mitochondrial genome reconstruction, and phylogenetic/genomic inference to evaluate evolutionary patterns across marine biodiversity hotspots. We analyzed seventeen specimens collected from 50–1050 m across benthic habitats in the Mozambique Channel, Bismarck Sea, Solomon Sea, Coral Sea, and Melanesia, together with publicly available Amphinomidae sequences. Here we show that low-pass whole-genome sequencing (~3 Gb per specimen) enables successful assembly of complete mitogenomes. All mitogenomes contained the standard set of 13 protein-coding genes, 2 rRNAs, and 22 tRNAs. Phylogenetic analyses conducted in IQ-TREE recovered two well-supported *Chloeia* and *Notopygos* clades with clear depth-associated lineage structuring. Phylogenies inferred from complete mitochondrial datasets yielded a robust, well-supported topology. Gene-order comparisons revealed largely conserved mitochondrial architecture, with subtle rearrangements in deep-sea lineages, including shifts in the control region. These findings demonstrate that mitogenomic data substantially enhances the resolution of Archinominae diversity and uncovers cryptic or previously unrecognized lineages that require further evaluation. By integrating genomic, ecological, and morphological evidence, this study refines Archinominae systematics and provides a foundation for understanding depth-driven evolutionary divergence in marine fireworms.

#052-G Adaptation to Acidic Environments Potentiates Pathogenicity of Bacteria *Kingsley Amoateng[1], Wei-Chin Ho[1] (1. The University of Texas at Tyler)* Microbes frequently adapt to altering environmental stress with novel molecular substitutions and phenotypic changes favored by natural selection. For example, acidic stress appears in various natural and anthropogenic contexts, from living within animal guts to food being acidified in factories. However, the rate, trade-offs, and genetic mechanisms of adaptation under persistent acidic stress remains poorly understood. More importantly, whether the adaptive results can also alter the opportunity of host infection or difficulty of host treatment remains largely unexplored. To address these questions, we experimentally evolved Escherichia coli to acidic stress as a model system. Specifically, we propagated 12 replicate populations of E. coli for ~1,900 generations in Luria-Bertani media with two pH values (acidic: 4.5; neutral: ~7.0) with daily transfers, and shaking at 37°C. Despite diminishing return, the evolved populations in the acidic environment adapted rapidly, sustaining a significant increase in carrying capacity by (136 ± 7.3 x 106 CFU/mL), which is higher than those in the neutral environment (60 ± 9.8 x 106 CFU/mL). Similarly, the competitive fitness of evolved populations in the acidic environment increases significantly by 55.8 ± 7.3 %, while no significant difference was found in the neutral environment (-0.9 ± 1.5 %). Strikingly, adaptation in the acidic environment uniquely resulted in the emergence of population-level biofilm formation and collateral resistance to the aminoglycoside class of antibiotics. Together, our results demonstrate that environments can strongly shape the speed of microbial adaptation and reveal how pathogenicity can evolve as a byproduct of new adaptation to stressful environments.

#053-GMorphological variation in the molar dentition of a population of Neotoma micropus from Chaparral Wildlife Management Area, La Salle County, Texas

Stacie Skwarcan [1], *Christopher Bell [1] (1. The University of Texas at Austin)*Understanding morphological variation in extant organisms is essential for interpreting the preserved remains of organisms in the fossil record. The morphological variation observed within a single population provides important baseline data for the minimum amount of variation that exists within a species. We sought to establish such a baseline as part of a larger project investigating variation within the 27 nominal species of extant woodrats (*Neotoma*). We studied a sample of 44 individuals of the southern Plains woodrat (*Neotoma micropus*) in the collections at the Natural Science Research Laboratory at the Museum of Texas Tech University. That sample was collected on 8, 9, and 10 October 2004 from the portion of Chaparral Wildlife Management Area (CWMA) in La Salle County, Texas, and comprises 22 males and 22 females that range in age from juvenile to senescent adult. The upper and lower dentition of each individual was photographed in occlusal and right lateral views. We reviewed the literature for instances in which authors discussed variation in the molar dentition of *Neotoma micropus* and the dental features used to refer material to that species. We discretized each of those dental features into states and independently evaluated them on the photographs of the dentition of the 44 individuals of *Neotoma micropus* from CWMA to document the morphological variation present within the population. We found that most features were polymorphic within the population of *Neotoma micropus* from CWMA and showed more variation (often linked to wear, or ontogeny) than was previously appreciated.

#054-U Standardizing Academic Syllabi Using Artificial Intelligence

Daniel Antonio [1], *Dipak Singh [1] (1. Stephen F. Austin State University)* In higher education, students are required to manage large amounts of academic information distributed across multiple course syllabi. These syllabi vary widely in structure and file formats, making automated processes difficult. Recent advances in Artificial Intelligence (AI) and it's subsets natural language processing (NLP) and large language models (LLMs) have enabled more effective extraction of information from unstructured text. However, the lack of standardized syllabus formatting remains a major barrier to reliable academic data automation. The problem addressed in this study is the inability of existing systems to consistently extract and organize key academic information from syllabus documents. Here we show that a modular AI-driven processing pipeline can convert unstructured syllabi from multiple file types into a standardized, machine-readable academic format. Our pipeline integrates document parsing, language model analysis, and schema-based validation to extract critical elements such as grading policies, assignment weights, and calendar events. Compared to traditional manual entry and rigid rule-based systems, this approach adapts to diverse syllabus structures while maintaining consistency in data output. This model enables integration of academic information into calendar and productivity tools, improving accessibility for students. More broadly, this research demonstrates how artificial intelligence can support the formalization of unstructured academic data and enhance digital educational infrastructure.

#055-U In Silico Design of Peptides to Prevent Insulin Aggregation

Thanh Tien Dao [1], *Bidisha Sengupta [1] (1. Stephen F. Austin State University)* Diabetes is a growing health concern for individuals across the globe. A large population used insulin protein injections to control blood sugars, which sometimes led to a higher chance of aggregation, forming toxic products. Designing a protein with therapeutic effect proved to be an expensive task with a cosmic searching space, with 20 common amino acids making up human proteins and hundreds in nature. By generating varied protein sequences randomly, the screening campaign aims to establish potential frameworks for creating potential therapeutic peptides. Autodock Crankpep (ADCP), AlphaFold2 (AF2), and Molecular Dynamics (MD) are utilized in this study. The screened peptides interacting with the insulin peptide residuals (B11−B17) LVEALYL, an important segment in self-aggregation. The docking result of combining AF2, MD, and ADCP on promising peptides from screening campaign are also compared with AlphaFold 3 and Boltz 2 on complexes prediction to cross-validate. The binding affinity will be experimentally measured for chosen candidates. We also applied machine learning to predict the binding affinity of sequences trained on docking results, by using pre-trained protein language model ESM-2, ESM-1b and ProteinBERT to investigate the potential of deep learning on target-specific task. Our approach in utilizing state-of-the-art tools and Machine Learning to generate de novo peptide sequences can be extended to design therapeutic peptides that interact with other proteins, such as beta-amyloid or essential biomolecules. With the advancement of machine learning, increasing experimental results, and growing computing power, our approach, if successful, can contribute to existing drug discovery pipeline for therapeutic peptides.

#056-N Reasoning from the Code Image of a Graph

Paul Feit [1] *(1. University of Texas Permian Basin)* The speaker found a problem in graph theory which may be accessible through computer programming. This lecture describes the context and the specific challenge. Let G be a connected graph and let ρ be its metric. Let $\mathbf{e}_1,\ldots,\mathbf{e}_r$ be a list of vertices. Define a function on vertices by $x \rightarrow (\rho(\mathbf{e}_1,x),\ldots,\rho(\mathbf{e}_r,x))$. If this is injective, we call it a code map of rank r. We call its image a *code image*. The original question on code maps was: Given a graph, can one find the shortest list of vertices which support a code map? The speaker reversed the issue. What can be deduced from a code image about the original *G*? A single code may be shared by many graphs. The revised study is to determine when one can select a graph from all those with a specified code image which has certain properties. One questions is: Given a code image from a list of specified length r with n vertices, can one find an upper bound for the number of edges for at least one graph with these parameters? When r/2, it is known that the there is a graph whose number of edges is <10/7. The proof reduced to study to a short list of subgraphs. Conceivably, the case for other r may be reduced to a finite study.

#057-N Category Theory or How to Talk Easily about Hard Things *Paul Feit [1] (1. University of Texas Permian Basin)* This talk is a brief introduction to Category Theory. Mathematicians refer to Category Theory as ``abstract nonsense". This characterization is recognized as slightly unfair. The theory is closer to a *grammar* which can be shared across disciplines. All homology theories can be defined broadly, with huge impact in specific contexts. (Theories of homotopy can be presented as tweaks on the same work.) The power of Category Theory arises from the fact that many constructions in many subfields are driven by a simple purpose. Technical objects may require elaborate manipulations, yet the *reason for the details* is elementary from a shrewd perspective. This lecture illustrates with differentiable manifolds and algebraic varieties. In each case, the *intuition* of the thing studied predated a satisfactory definition. In particular, the definition of algebraic varieties struggled for a standard over decades, even as powerful theorems about them developed.

#058-U Finding Novel Inhibitors of Francisella tularensis Enoyl-ACP reductase FabI (FtFabI) in Francisella tularensis
Yiming Chen [1], Josh Beckham [1] (1. University of Texas at Austin) Growing concerns over antibiotic resistance and biodefense preparedness drive the search for new drug targets. Francisella tularensis, a Category A bioterrorism agent that is highly infectious due to its ability to transmit through aerosols, is dependent on the protein Francisella tularensis Enoyl-ACP reductase FabI (FtFabI). F. tularensis is the bacterium that causes Tularemia, or rabbit fever. Right now, Tularemia can be treated using antibiotics such as doxycycline, which is a bacteriostatic agent, meaning that it stops bacterial growth but does not kill it. Due to limitations like this, FtFabI has become an important target because it is an essential enzyme for the type II fatty acid synthesis (FAS-II) pathway of F. tularensis, which is necessary for membrane formation and bacterial viability. The PDB crystal structure of FtFabI (2JJY) was used to virtually screen numerous compounds using ICM (Molsoft) and GOLD (CCDC) software. Compounds that scored the highest and fit Lipinski's Rule of Five were further analyzed during wet lab using binding studies of FtFabI with differential scanning fluorimetry (DSF). This protein has been expressed using autoinduction in BL21(DE3) E. coli and purified using Nickel-NTA chromatography, which led to pure, high-yield protein. This was further confirmed through SDS-PAGE analysis, when the presence of a strong band appeared at ~29 kDa, matching the expected molecular weight of FtFabI. By integrating computational modeling with experimental assays, this methodology facilitates rapid discovery of promising inhibitors for FtFabI to address the global health crisis of antibiotic resistance and the risks of bioterrorism.

#059-U Cancer Stem Cells as Mitochondrial Donors: Implications for Macrophage Polarization and Tumor Immune Evasion *Nicholas Pascuzzi [1], Luke Peck [1], Chris Uliberri [1], Diya Shah [1], Kuan-Hui Ethan Chen [1] (1. Texas Tech University)*
Mitochondria play a role in cancer biology far beyond energy production. Recent studies have shown that mitochondria can move between cancer cells through mechanisms such as tunneling nanotubes, extractor vesicles, and membrane fusion. Macrophages are highly plastic immune cells that can shift between anti-tumorigenic (M1) and pro-tumorigenic (M2) states, a process referred to as macrophage polarization. Yet it is currently unknown if cancer cells transfer mitochondria to macrophages. This knowledge gap limits our current understanding about how cancer cells manipulate immune cells in the tumor microenvironment. In the study, we tracked mitochondrial transfer using co-cultures with bulk tumor cells, cancer stem cells (CSC), and macrophages. We found that macrophages uptake mitochondria from both bulk tumor cells and CSC. CSC co-cultures often produce stronger transfer patterns, suggesting they serve as a prominent source of mitochondrial exchange. Moving forward, we plan to address how cancer cell mitochondria exchange affects macrophage metabolism and polarization state. Future possibilities for manipulating or preventing mitochondrial transfer may improve or restore macrophage immune responses to cancer.

#060-U Investigating The Formation and Biological Impact of Oxysterol-RNA Adducts in Drosophila Melanogaster
Tyson Easterling [1], Miriam Andersen [1], Zoey Storch [1], Godwin Ifere [1] (1. Hardin-Simmons University) RNA is increasingly recognized as a direct target of chemical modifications induced by endogenous metabolites and environmental stressors. Among these, oxysterols—oxidized derivatives of cholesterol and other sterols—have emerged as biologically active molecules implicated in signaling, lipid metabolism, and oxidative stress. Elevated oxysterol levels are associated with proliferation, and some cause tumor formation in mammalian systems. Recent studies suggest that oxysterols are reactive and may form covalent adducts with nucleic acids, potentially altering RNA stability, folding, translation efficiency, and regulatory function.

While DNA-oxysterol adducts have been reported, the landscape of RNA-oxysterol adduct formation remains unexplored. The fruit fly, *Drosophila melanogaster*, is an ideal model for this investigation due to its: a). Conserved sterol and lipid metabolism pathways, b). Genetic tools for manipulating oxidative stress, sterol levels, and RNA repair enzymes. Understanding oxysterol-RNA adduct formation in *Drosophila* could provide insights into how lipid metabolism and oxidative stress affect RNA biology, with implications for human diseases. Hypothesis: Oxysterols formed during oxidative stress in *Drosophila melanogaster* covalently modify RNA, generating oxysterol-RNA adducts that influence RNA stability and gene expression. Detection and Characterization: To detect and chemically characterize oxysterol-RNA adducts in *Drosophila melanogaster* under normal and oxidative stress conditions. Experimental Conditions: Control diet vs. high-cholesterol/oxidative stress-inducing diets (e.g., paraquat exposure). Outcomes: Using (LC-MS/MS), we identified novel oxysterol-RNA adducts in *Drosophila.* Significance: This first systematic investigation of oxysterol-RNA adducts in a living organism revealed a novel mechanism connecting lipid metabolism, oxidative stress, and RNA biology.

#061-U Screening TZ62, TZ70, TZ71 and DKNR8, DKNR10, DKNR13 for Induction of Apoptosis and Inhibition of Metastasis

Maximiliano Perez [1], Tina Prajapati [1], Vaishali Chaubal [1], Rachna Sadana [1] (1. University of Houston-Downtown)

Cancer cells have a distinct trait known as metastasis, which is an intricate process in which cells from a primary tumor site can detach, enter the bloodstream, infiltrate other organs, and proliferate, thereby spreading cancer. Previous results within our lab established 3 promising compounds, TZ62, TZ70, and TZ71, from a set of 17 compounds (coded as TZ), as well as 3 promising compounds from our DKNR series, which are DKNR8, DKNR10, and DKNR13, that induced apoptosis in A549 and Molt-4 cancer cells when tested using the Caspase 3/7 Activation assay. To establish the effectiveness of the compounds in reducing metastasis, our lab utilized a Wound Healing Assay on the A549 cell line, an adherent lung cancer cell line, and the MDA-MB-231 cell line, which is a triple-negative breast cancer cell line, to see if compounds that inhibit cell survival can also inhibit metastasis. Cells were incubated in a 12-well plate for 24 hours. A streak was made within each well, and cells were treated with 20 μM of final concentration with the respective compound. PBS and Doxorubicin were used as the negative and positive controls, respectively. Images were taken over a period of 48 hours, and the change in area was measured. Our preliminary results indicate that effective Tz70 has the potential to inhibit metastasis. Additionally, our lab has begun conducting RT-PCR analysis to look into the genetic expression of pro-apoptotic and anti-apoptotic genetic markers.

#062-G Exploring the Role of Lung cancer-associated Variants and Genes in DNA Damage Promotion

Maryam Vaziripour [1], Daniel Snyder [2], Christopher Amos [3], Yanhong Liu [4], Jun Xia [1] (1. Texas A&M University, 2. Creighton University School of Medicine, 3. University of New Mexico, 4. Baylor College of Medicine)

Lung cancer is the leading cause of cancer death, and up to 25% of cases occur in never-smokers. Many GWAS-identified risk loci lack defined functional drivers. We previously identified and characterized 25-40% of the rare and common lung cancer risk variant and genes that promote endogenous DNA damage and genomic instability, a hallmark of cancer. We collaborated with the Genetic Epidemiology of Lung Cancer Consortium (GELCC) and utilized their findings of lung cancer rare variants from whole genome sequencing. Variant frequencies were compared between familial lung cancer cases and cancer-free controls to evaluate their potential association with cancer risk. We previously tested 19 variants, and we expanded our cell-based assays to screen additional 17 variants, many with odds ratio greater than 10-fold, aiming to elucidate their mechanistic role in lung cancer susceptibility. Our analysis revealed a significant enrichment of 5 out of 36 rare variants in genes involved in endogenous DNA damage promotion. Notably, Far Upstream Binding Protein 1 (FUBP1) caused high gH2AX when overproduced. Secondly, DNA binding domains are sufficient for the high damage. In addition, single-cell RNA-seq revealed ferroptosis and lipid metabolism related pathways alterations in FUBP1 overproduced cells. Lastly, FUBP1 Cleavage Under Targets and Tagmentation (CUT&Tag) uncovers a binding motif like AP1 transcription factors. These findings suggest that individuals harboring lung cancer risks may have increased DNA damage levels, leading to increased genomic instability and a heightened risk of developing lung cancer, offering opportunies for better immunotherapy and potential synthetic lethal strategies such as PARP inhibition.

#063-G Fibroblast Lineage Remodeling in Uterine Blood Reveals a Conserved Protumorigenic Trajectory in Endometrial Cancer

Bingru Feng [1], Jun Xia [1], Yusi Fu [1] (1. Texas A&M University)

Cancer-associated fibroblasts (CAFs) are key components of the tumor microenvironment, yet how they emerge during early endometrial carcinogenesis and whether these states can be detected noninvasively remain unclear. Here, we introduce a sampling strategy that analyzes uterine blood collected directly from the uterine cavity, which contains endometrial epithelial and immune cells shed from the local tumor microenvironment. This method captures cellular dynamics without invasive tissue biopsies, enabling sensitive assessment of microenvironmental changes across disease stages. Using single-cell RNA sequencing and RNA velocity analysis of uterine blood from women spanning benign endometrium, endometrial intraepithelial neoplasia (EIN), invasive transition, and endometrial cancer (EC), we described a unidirectional fibroblast trajectory from control through EIN and transition toward EC. Along this path, fibroblasts progressively upregulate a conserved protumorigenic program marked by INHBA, ITGA1, CNTN1, and the RNA-binding protein RBMS3. And late-stage cells were identified to have enhanced matrix engagement, tissue remodeling, and immunoregulatory potential. Velocity and gene set based analyses reveal coordinated enrichment of extracellular-matrix organization, motility, and host-defense response pathways in EC-stage fibroblasts, whereas control fibroblasts retain junction-maintaining, quiescent stromal signatures. Comparable INHBA- and integrin-high CAF subsets reported in pancreas, breast, and colorectal cancers suggest that this fibroblast lineage remodeling represents a conserved, tumor-type-agnostic trajectory. Notably, these dynamic CAF signatures are readily captured in uterine blood, demonstrating that local liquid biopsy can also resolve stromal lineage progression in parallel with epithelial and immune reprogramming. Our findings position uterine blood-derived fibroblast states as accessible biomarkers and its potential as noninvasive diagnostic tools for EC.

#064-G PAX6 in Mechanosensory Neuromasts of Salamanders and Zebrafish: A Molecular, Microscopic, and Computational Investigation *Nisa Sindhi [1], Nikhil Pawar [2], Ruben U. Tovar [3], Thomas J. Devitt [2], David M. Hillis [2], Dana M. Garcia [1] (1. Texas State University, 2. University of Texas at Austin, 3. St. Mary's University)* The transcription factor PAX6 is a master regulator of developmental processes and sensory organ formation. Recent findings from our lab reveal unexpected PAX6 localization within the apical stereociliary bundles of salamander neuromast hair cells, structures enriched in F-actin and responsible for detecting water movement. This localization suggests a noncanonical, cytoskeletal-associated function for PAX6, potentially influencing hair-cell structure and regenerative capacity. Using immunohistochemistry and confocal microscopy, we observed distinct colocalization of polyclonal anti-rabbit PAX6 and phalloidin-labeled F-actin within stereociliary bundles, supported by specificity controls confirming authenticity of the signal. Ongoing transmission electron microscopy (TEM) studies aim to define the precise ultrastructural positioning of PAX6 in relation to actin filaments. To complement experimental observations, we developed a deep-learning-based protein - protein interaction prediction pipeline integrating 1D convolutional neural network embeddings and a random forest classifier approach. Computational predictions highlight potential PAX6 interactors, including actin. Future co-immunoprecipitation experiments will test PAX6 and F-actin interactions biochemically. To enable other corroborative assays interrogating PAX6's role at a noncanonical neuromast site, we next asked whether PAX6 is present in a more experimentally tractable species, namely zebrafish (*Danio rerio*). Interestingly, whole-mount immunohistochemistry of zebrafish larvae (5 days post-fertilization) localized PAX6 to neuromast mantle cells. We aim to perform immunohistochemistry with zebrafish-targeted anti-PAX6 antibodies to corroborate these results. Based on these results, we aim to perform CRISPR-based experiments to assess PAX6's influence in neuromast organ. Together, our integrative approach bridges neurodevelopmental biology and AI-driven bioinformatics, advancing understanding of PAX6's putative, unconventional role in sensory system development and evolution.

#065-G Expression and Functional Analysis of Profilin Genes (pfn1, pfn2a, pfn2b) During Early Embryonic Development in Zebrafish *Samira Alam [1], Andre Gil [1], Alicia Mendoza [1], Sharmin Hasan [1] (1. Sam Houston State University)* Profilins are conserved actin-binding proteins essential for actin polymerization and cytoskeletal regulation in eukaryotes. Disruption of profilin function is linked to developmental abnormalities and several human pathologies. Zebrafish possess four profilin paralogs (*pfn1*, *pfn2a*, *pfn2b*, *pfn4*), but their developmental roles remain incompletely understood. This study examines the expression and function of *pfn1*, *pfn2a*, and *pfn2b* during zebrafish embryogenesis. RT-PCR analysis confirmed that all three isoforms are expressed during early developmental stages. Whole-mount *in situ* hybridization revealed that *pfn2a* and *pfn2b* exhibit enriched expression in the developing brain. Functional perturbation using mRNA overexpression, morpholino-mediated knockdown, and CRISPR-Cas9 based gene disruption of *pfn1* and *pfn2a* did not produce overt morphological phenotypes in F0 embryos. These results suggest potential buffering mechanisms, including redundancy among profilin isoforms and contributions from maternally supplied transcripts or proteins. Future studies using stable double and triple knockout lines will help clarify isoform-specific roles and the extent of functional compensation within the profilin gene family.

#066-N Three left standing: Population wide investigation of histone missense mutation landscape reveals novel constraint pattern *Tiffany Bastos [1], Dustin Fetch [1], Wan Song [1], Natalie Redding [1], Marzieh Rouzbehani [1], Ava George [1], Ksenia Dydo [1], Juliannah Rua-Avendano [1], Gauri Raje [1], Alexey Soshnev [1] (1. University of Texas San Antonio)* The fundamental repeating unit of chromatin is the nucleosome; an octamer complex comprised of the four core histones, H2A, H2B, H3, and H4, along with associated DNA. Although recurrent histone mutations are implicated in developmental disorders and cancers, the functional significance of most individual residues remains unclear, in part because each histone is encoded by numerous paralogues, obscuring the interpretation of pathogenic variants. To identify residues essential for histone function, we analyzed missense variation in the Genome Aggregation Database (gnomAD v4.1), comprising approximately one million exomes from healthy individuals. We reasoned that functionally indispensable amino acids would exhibit extreme constraint in healthy populations, while missense variation would be prevalent in dispensable residues. Supporting this idea, all known disease-associated "oncohistone'' mutations—dominant inhibitors of SET methyltransferases and known drivers of malignancy—were entirely absent from gnomAD.Despite the profound evolutionary conservation of histones, only three residues were completely constrained in healthy populations. Structural analyses suggest that two of these—H4 K91 and H4 Y98—engage the Mrc1/Claspin chaperone during DNA replication. We propose that the interaction between Mrc1 and H4 K91/Y98 is required for nucleosome recycling at the replication fork and that disruptions of this interaction compromise epigenetic inheritance. Our studies provide a starting point for defining critical histone residues of unknown function and for uncovering mechanisms that link nucleosome dynamics to epigenetic homeostasis, ultimately refining an as-yet-unknown facet of the Histone Code.

#067-N Androgen regulation of the reproductive cycle in male-pregnant pipefishes *Sunny K. Scobell [1] (1. Southwestern University)*
Throughout the animal kingdom, pregnancy is a phenomenon that happens in females. A notable exception is the fish Family Syngnathidae: seahorses, pipefishes, and seadragons are unique in that they all reproduce via male pregnancy. Females place their eggs into the male brood pouch wherein he fertilizes them and broods them until birth. In most vertebrates, hormones regulate reproductive cycles. Is male pregnancy hormonally regulated in a manner similar to females, or can male-typical hormones evolve to regulate pregnancy, too? I measured plasma androgen levels in two species of pipefishes, the Gulf pipefish, *Syngnathus scovelli,* and the Northern pipefish, *S. fuscus*, across the reproductive cycle. Despite the sex-role reversal exhibited in these species, androgen levels showed a sex-typical pattern. In males, androgen levels varied across the pregnancy in a manner that suggests males regulate their sex steroids to protect offspring from exposure to high steroid levels. Although a growing body of evidence suggests that androgens mediate brood pouch development in juvenile syngnathids, my results suggest that adult males do not use androgens to regulate the brood pouch during pregnancy, but rather to promote spermatogenesis in the testes during the reproductive cycle.

#068-U Ripe for Discussion: The Curious Case of Fungus on Wine Grapes and What It Means for Our Palates *Zachary Dennison [1], Alyx Frantzen [1] (1. Stephen F. Austin State University)*
The Texas wine industry generates close to $20.35 billion in total economic activity to the state of Texas. To maintain this impact, it is important for all wineries to create a high quality, consistent product. The ability to test during all stages of the wine-making process provides that product. The process starts with testing grapes throughout the growing season for key ripeness indicators such as; sugar content, titratable acidity, and pH. In addition to testing for desirable traits, other undesirable traits can also be analyzed. Fungicides are beneficial to the wine industry, keeping the plants healthy and increasing the yield of fruit, but they can also lead to problems. Fungicides can negatively affect the yeast that is used in the fermentation process, causing fermentation to take longer and changing the composition of the wine. This change would affect the taste and overall sensory experience of the wine and result in an undesirable product.

#069-U Redox Cooperativity Analysis with Computational Chemistry: Role of 3d Versus 4d/5d Metals *Hadley Watts [1], John Gary [1] (1. Stephen F Austin State University)* Enzymes commonly use multiple redox sites in conjunction to perform multi-electron processes with Earth-abundant metals. These metals, which typically undergo one-electron redox processes, can work cooperatively to perform multi-electron chemistry. The key design features which allow for redox cooperativity are not well understood. In an effort to design new experimental model systems, computational chemistry is employed to gain insights into the role of energy matching, distance dependence, and geometric orientation for redox communication. Previously, our group has highlighted the interplay between cobalt and a pyridine-di-immine (PDI) ligand system by a unique electronic configuration. Commonly used 4d/5d metals often perform clean two-electron redox processes. This talk will focus on what changes in redox cooperativity when moving from 3d to 4d/5d metal complexes. These changes provide design principles for developing new catalyst systems with 3d metals.

#070-U The Grapes of Wrath: How to Store Wine Without Letting It Go Bad (and Other Oenological Adventures) *Ev Crowe [1], Alyx Frantzen [1] (1. Stephen F. Austin State University)* Oxygen plays an essential role in several stages of winemaking, but excess exposure during storage can lead to undesirable oxidation. Oxidation degrades key compounds responsible for a wine's aroma, flavor, and color, and can also promote the breakdown of ethanol, reducing alcohol content. Numerous commercial and at-home storage technologies, ranging from traditional corks to modern gas-based preservation systems, aim to limit oxygen exposure. Six different storage methods were tested on Franzia Cabernet

Sauvignon and Franzia Crisp White box wines; synthetic and real corks, silicone bottle stoppers, Repour Wine Savers, the Coravin Pivot+ system, VacuVin wine savers, and the original bags. The effectiveness of these common, at-home wine preservation methods at minimizing oxidation was evaluated by measuring; the dissolved oxygen content, the absorbance, ethanol percentage, density, specific gravity, and the pH of the wine every two weeks. The final results will identify the most effective system enhancing the storage of opened containers of wine.

#071-U Protective Effects of Mint Extracts Against Oxidative Stress in Human Serum Albumin Protein

Perla Tovar [1], Nkeiruka Aziekwu [1], Bidisha Sengupta [1] (1. Stephen F. Austin State University)

The buildup of oxidative stress in the body can contribute to the progression of many diseases. Therefore, it is important to study the effects of oxidative stress on target molecules and natural remedies to help reduce or prevent it. Human serum albumin (HSA) protein is the most abundant protein in the blood plasma and is responsible for carrying out crucial functions in the body. In the presence of oxidative stress, its structure and function can be perturbed. Antioxidants can stabilize free radicals, reducing the damage caused by oxidative stress. This study investigates the effects of phytochemicals found in *Mentha piperita* and *Mentha spicata* on native HSA and oxidized HSA to study their antioxidant potential. The protein structural changes that occur upon oxidation with the hydroxyl radicals formed with the Fenton reaction have been studied with optical spectroscopic techniques (UV-Vis, fluorescence, circular dichroism), SDS polyacrylamide gel electrophoresis, high-performance liquid chromatography (HPLC), and bicinchoninic acid protein assay. From the optical spectroscopic techniques, particularly with circular dichroism, it was observed that the alpha-helix structure of the HSA protein was maintained to a larger extent with the mint extracts than without them. With the SDS-PAGE, the band intensity of the protein reduced less in the presence of the mint extracts, indicating less structural changes. From the gathered data, the mint extracts have shown antioxidant potential in helping maintain the protein's conformation even in the presence of oxidative stress, giving promise as a natural remedy in the fight against oxidative stress and its adverse effects.

#072-U Mechanistic Insights into Transition-Metal Binding to HSA Using Dual-Probe UV–Vis and Site-Specific Tryptophan Fluorescence Spectroscopy

Tess Corbett [1], Bidisha Sengupta [1] (1. Stephen F. Austin State University)

Human Serum Albumin (HSA) is the most abundant protein in plasma and a key transporter of essential and non-essential metal ions. Because HSA contains several partially selective metal-binding sites, characterizing how transition metals interact with the protein is important for understanding their biological roles and potential therapeutic relevance. In this study, we examined the binding behavior of Mn^{2+} and Co^{2+} with HSA using both UV–Vis absorbance and fluorescence spectroscopy to monitor metal–protein interactions across a concentration range of 50–200 µM, introduced in 50 µM increments. UV–Vis measurements showed a steady increase in absorbance at 280 nm upon addition of Mn^{2+} or Co^{2+}, consistent with progressive interaction between the ions and HSA. A pronounced decrease at higher concentrations (150–200 µM) suggests saturation of high-affinity binding sites and possible partial recovery of native protein structure. Fluorescence spectroscopy provided complementary insight into the local environment around Trp-214, the primary intrinsic fluorophore of HSA. By selectively exciting Trp-214 at 295 nm, we observed quenching behavior that reflects changes in the microenvironment of this residue upon metal binding. Excitation spectra collected while monitoring emission at 340 nm further confirmed alterations in the fluorophore's environment as metal concentration increased. Together, these spectroscopic results highlight the dynamic, concentration-dependent nature of Mn^{2+} and Co^{2+} coordination to HSA. Future work will examine thermodynamic parameters and structural effects to better understand how transition-metal binding influences HSA's conformational landscape and transport function.

#073-U Structure-Based Identification of Inhibitors Targeting Staphylococcus aureus D-Alanine:D-Alanine Ligase Using Virtual Screening

Mahdia Rahman [1], Makynzie Kitzmann [1], Manal Saad [1], Josh Beckham [1] (1. University of Texas at Austin)

Staphylococcus aureus is a major cause of skin, soft-tissue, and invasive infections, and its increasing antibiotic resistance underscores the need for new therapeutic strategies. Because resistance often arises from mutations in penicillin-binding proteins, targeting alternative essential enzymes is critical for treatment options. This project focuses on D-alanine:D-alanine ligase (SaDdl), an ATP-dependent enzyme required for producing the D-Ala-D-Ala dipeptide essential for peptidoglycan assembly and cell-wall stability. In designing the docking approach for virtual screening, the strategy focused on the active site where two D-alanine molecules react with ATP, with the goal of identifying compounds that can compete with D-alanine and prevent this reaction. The crystal structure of SaDdl (PDB 7U9K) was used for structure-based virtual screening of over 150,000 compounds from the Maybridge and ZINC libraries. Docking was performed using GOLD after benchmarking against ICM to ensure accurate reproduction of the native D-alanine pose. The original D-alanyl-D-alanine ligand produced a corrected GOLD score of 0.357, which was used as a reference for hit evaluation. For experimental validation, SaDdl was expressed via autoinduction in *E. coli* BL21(DE3), purified by Ni-NTA chromatography, and confirmed by

SDS-PAGE. Differential scanning fluorimetry established an apo-enzyme melting temperature of 44 °C, and DSF screening of predicted ligands is underway prior to spectrophotometric enzyme assays. Ultimately, this work combines computational docking with biochemical characterization to advance discovery of new chemical scaffolds for this target and support development of improved therapeutic options for *S. aureus* infections.

#074-U Occurrence and Quantitation of Microplastic Contamination of Wastewater Treatment Plants in Deep East Texas

Jacob Swallow [1], Kefa Onchoke [1], Robert Friedfeld [1] (1. Stephen F. Austin State University)

MPs are ubiquitous plastic polymers classified in the size range of 5 mm to 1 µm. MPs are emerging pollutants that cause health hazards to humans and the environment. Wastewater treatment plants (WWTPs) are secondary sources of MP contamination in the aquatic and terrestrial environments. The physical and chemical characteristics of MPs from four Deep East Texas WWTPs were investigated using brightfield microscopy, scanning electron microscopy/energy dispersive X-ray spectroscopy (SEM/EDX), and Fourier transform infrared spectroscopy (FTIR). The most common shapes of MPs were found in the order: fragments (49%) > filaments (25%) > beads (10%) > fibers (9%) > rods (7%). MPs were quantified in size ranges of < 150 µm, 150 – 850 µm, 850 µm – 1.70 mm, 1.70 mm – 2.36 mm, and > 2.36 mm. Most MPs were sized <150 µm (36%) and 150-850 µm (24%). MPs were most abundant in samples from San Augustine (38%), followed by Jasper (32%) WWTPs. FTIR spectra indicates the presence of nylon, polyethylene, polytetrafluoroethylene, and polyethylene terephthalate. A spectral database (Open Specy) identified the presence of polytetrafluoroethylene, polyvinyl acetate, polystyrene, polypropylene, and polyethylene. High concentrations of elements, such as carbon, oxygen, and chlorine in SEM/EDX spectra are indicative of the presence of MPs. Many WWTPs discharge treated water into nearby creeks and biosolids are incorporated into soil. Thus, WWTPs directly contribute to environmental MP contamination. The ubiquity of MPs in the environment poses risks towards plants, animals, and humans leading to an urgent public health concern.

#075-U Camille: Automated Drug Screening at Scale

Michael Gillman [1], Josh Beckham [1] (1. University of Texas at Austin)

Current drug discovery pipelines are sequential and expert-driven, and protein preparation requires intervention before high-throughput screening. Most workflows are bespoke, poorly scalable, and focused on few targets. Systematic exploration of the drug–protein interaction landscape remains rare, and polypharmacology, which leverages multi-target drug interactions, remains underutilized. Atlas addresses these limitations through a fully automated, end-to-end protein–ligand screening and design platform. Starting from raw DNA sequence, AlphaFold-based structure prediction enables screening from genomic data, making it possible to move directly from DNA to inhibitor candidates. Atlas orchestrates the workflow, from structure prediction and protein preparation (ligand removal, altLoc resolution, MODELLER-based loop reconstruction, Phenix cleaning, Reduce protonation) to active-site detection via P2Rank, multi-stage docking with dynamic box sizing, and ligand preparation with filtering. Multiple fail-safes, including fallback pocket recentering, surface-atom-aware pose validation, and multi-pose scoring, maximize docking success rates, even for challenging targets. Designed for scalability, Atlas' focus is proteome-scale screening. In polypharmacology mode, Atlas applies tiered scoring to generate drug–protein interaction heatmaps, supporting drug repurposing, predicting side effects, and revealing therapeutic opportunities. Beyond large-scale screening, Atlas supports precision medicine by docking against patient-specific mutant proteins, enabling clinicians to test drug efficacy before treatment. Systematic off-target mapping could elucidate the basis of side effects. By reducing the time and expertise barriers to proteome-wide docking and integrating generative design, Atlas lays the groundwork for a reproducible, automated drug discovery engine, capable of mapping all known drugs against the human proteome, customizing predictions for patient-specific genomes, and accelerating translation from computational prediction to clinical application.

#076-U Coumarin-enamine Derivatized Cascade Fluorescent Sensor for Multianalytes

Marlene Zepeta-Rodriguez [1], Rashid Mia [1], Jack Weeks [1] (1. Stephen F. Austin State University)

A urea-bis(7-DEA-coumarin-enamine) molecular probe has been synthesized to show relay recognition of anion and cation via optical spectroscopy. Incorporating enamine-moiety into hydroxycoumarin allows it to form a two-new six-membered ring system through Resonance-assisted-hydrogen-bonding (RAHB) that extends conjugation hence fluorescence intensity. Photophysical properties have been studied in different solvent systems. In DMSO, the solution produced a pale greenish color with two broad absorption bands at 388nm and 475nm and emission at 550nm. Upon adding various anions, only CH_3COO^-, F^-, CN^-, and PO_4^{3-} anions perturbed the new ring system (RAHB) and generated optical response both in UV-vis and fluorescence. Cyanide ions produced distinct absorption and emission bands due to Michael-addition to enamine moiety whereas CH_3COO^-, F^-, PO_4^{3-} abstract proton from RAHB and form a tetradentate ligand cage. Upon the addition of various metals, only Cu^{2+} and Cu^+ ions show optical response, absorption spectra shift bathochromically from 361nm to 370nm, and emission spectra at 451nm quenched which means fluorescence turned 'OFF' via chelation quenched fluorescence (CHQF) mechanism. Furthermore, based on

Hard-soft acid-base (HSAB) theory Cu^{2+} and Cu^{+} ions are hard acids and the tetradentate ligand is a combination of hard bases, thus due to hard-hard interaction they form a strong coordination bond. The size of the Cu^{2+} and Cu^{+} ions is also compatible as Ni^{2+} and Zn^{2+} ions show weak interactions (copper ions size is between nickel and zinc).

#077-G Synthesis and Characterization of Thiazole-Based Cryptand-like Tricyclic Fluorescent Macrocyclic Cages for Aromatic Hydrocarbons *Jack Weeks* [1], *Rashid Mia* [1] *(1. Stephen F. Austin State University)* Fluorescent macrocyclic cages that selectively recognize neutral aromatic hydrocarbons are attractive tools as a smart sensing device for petroleum derived hydrocarbons in environmental analysis but remain limited in number. We are designing a modular library of cryptand-like, thiazole-based tricyclic macrocyclic cages to address this need. Each cage is assembled in a [2+3] macrocyclic cage system from two cap linkers and three ligands bearing chromophore and fluorophore units, creating an internal cavity whose size and shape can be tunned through linker and ligand substitution. A synthetic route based on Schiff-base condensation has been developed and at least one prototype cage has been successfully synthesized and isolated, indicating promise in the modular design. We have synthesized our first macrocyclic [2+3] cage **1** by coupling the previously synthesized precursor ligand (meta-phenylenebis(2-aminothiazole)) and the cap tFPA (Tris(4-formylphenyl) amine). Macrocyclic cage 1 is characterized by NMR and photophysical is underway. Computational studies also are being carried out to optimize the geometry, cavity size of the cage, and to assess the interaction between host cage and guest PAHs. The spatial arrangement of donor-acceptor units within this framework is intended to support fluorescence resonance energy transfer (FRET), enabling host-guest interactions with polycyclic aromatic hydrocarbons (PAHs) to be monitored via changes in emission profiles. n. Current efforts are directed toward expanding the cage library and initiating photophysical and inclusion studies with PAHs commonly found in petroleum, with the goal of establishing host guest relationships relevant to real time monitoring applications.

#078-N Occurrence and Quantitation of PFAS in biosolids collected form WWTPs in Deep East Texas *Kefa Onchoke* [1], *Michael Janusa* [1], *Jamie Humphries* [1], *Kendal Fiffick* [1], *Anthony Broom* [1], *Thanh Tien Dao* [1] *(1. Stephen F. Austin State University)*

Per- and polyfluoroalkyl substances (PFAS) are synthetic chemicals ubiquitous in the environment, exhibit extreme persistence, and are resistant to degradation. PFAS pose environmental and human health concerns and contribute to disease and disability across the lifespan. Via Ultra Performance Liquid Chromatography-tandem mass spectrometry (UPLC/MS/MS) concentrations of eleven PFAS were quantified in three wastewater biosolids (NWWTP, LWWTP and STC) in Deep East Texas (USA). PFAS were detected in all biosolids in samples with following concentration ranges: PFPeA (0 - 0.58 ng/L), PFHxA (3.26 – 26.45) ng/L, PFHpA (0.675 - 13.985 ng/L), PFOA (14.17 - 123.00 ng/L), PFNA (0.81 - 8.86 ng/L), PFDA (7.91 - 1303.15 ng/L), PFOS (8.81 - 1013.84 ng/L), PFTrDA (0.116 - 10.39 ng/L), PFDS (0.931 - 6.017 ng/L), PFUdA (0.097 - 5.913 ng/L), PFDoA (2.19 - 11.17 ng/L). PFDA, PFOA and PFOS were the predominant species while PFHxA, PFDS and PFDoA were predominant in samples from STC. Principal component analysis showed very strong correlations (> 0.99) between PFUdA - PFHxA, PFUdA – PFNA, PFDS- PFOA, PFDS- PFTrDA, PFNA- PFHxA, PFDoA- PFOA, PFDoA- PFDS. Establishment of further extensive studies is essential to PFAS concentration amounts from WWTPs over long periods. To the best of our knowledge this study demonstrates ill health potential on exposure to PFAS and implications for regulatory agencies. This information is useful for predicting cycling and bioavailability of PFAS of < 12 carbons in biosolids produced from WWTPs, for public health concerns and possible interventions for enactment of necessary policies to reduce exposure to PFAS.

#079-N Mitochondrial membrane potential and mitophagy as modulators of light therapy *Violet Bumah* [1] *(1. Stephen F. Austin State University)* A growing acceptance of the benefits of light-based therapies on human performance has enabled the use of photobiomodulation (PBM), a non-invasive modality that uses specific wavelengths of light to stimulate cellular processes for healing. While clinical studies continue, knowledge of cellular and physiological mechanisms of PBM therapy (PBMT) is lacking. One underlying hypothesis is that mitochondria are centrally involved. Light has been shown to interact with mitochondrial components like cytochrome c oxidase, influencing the electron transport chain and impacting mitochondrial membrane potential. Therefore, the overall objective of this study was to investigate the effects of laser exposure in the range from 400 nm – 1100 nm, on membrane potential (MMP) and mitophagy, with the goal of identifying dosimetry markers that produce optimal mitochondrial metabolic gains. Human telomerase reverse transcriptase transformed retinal pigment epithelium (hTERT-RPE) cells, were cultured and MMP investigated using JC-1 dye and confocal microscopy, while fluorescence imaging – mitophagy and lyso dye were used to visualize mitophagy. The data showed that MMP was increased in 808 nm irradiated cells compared to non-irradiated controls, while mitophagy increased in both 405 nm and 808 nm treated cells. 405 nm light has high photon energy with the potential to adversely affect the mitochondria and increase mitophagy. Increased mitophagy in 808 nm treated cells, could be as a result of high irradiance used or may be indicative of an increased membrane potential. This study has advanced our understanding of the mechanisms involved in PBMT as it relates to MMP and mitophagy.

#080-N Selective Recognition of G-Quadruplex and i-Motif DNA by Curcumin and Kaempferol: A Spectroscopic and Computational Study Bidisha Sengupta [1] *(1. Stephen F. Austin State University)* Curcumin (CUR) and Kaempferol (KMP) are two plant-based molecules widely recognized for their therapeutic potential in treating inflammation, cardiovascular disease, and cancer. In parallel, interest has grown around unusual DNA structures such as G-quadruplexes (G_4) and C-tetraplexes (C_4, or i-motifs). Unlike the classic double helix, these noncanonical forms appear in biologically important genomic regions such as telomeres, where they can act as structural switches that influence gene expression and cellular stability. Because many flavonoids interact directly with DNA, we aimed to explore how CUR and KMP engage with these unique DNA architectures. Using circular dichroism, differential absorption, and steady-state fluorescence spectroscopy, we detected clear and distinct binding events between these compounds and the DNA motifs. Our experiments revealed a striking selectivity: KMP showed a strong preference for the acidic C_4/i-motif structures, whereas CUR displayed greater affinity for G_4 DNA. These findings highlight that even small natural molecules can recognize and discriminate between complex DNA folds. To gain deeper insight into these interactions, we used molecular docking and molecular dynamics simulations to visualize the likely binding sites and investigate the structural behavior of each ligand–DNA complex over time. These computational results supported our spectroscopic observations and provided an atomistic explanation for the contrasting binding preferences. Overall, this study demonstrates how CUR and KMP selectively stabilize different noncanonical DNA structures. By integrating spectroscopy and computational modeling, we present a powerful framework for examining drug–DNA interactions and offer a foundation for developing targeted therapeutic strategies involving G_4 and C_4 motifs.

#081-G A Deep Learning Approach for Postmortem Interval Estimation Stephanie Baker [1] *(1. Texas State University)* Estimating the postmortem interval (PMI), or the time that has elapsed since the death of an individual, remains a challenge in forensic anthropology due to the absence of standardized protocols and the variable nature of human decomposition across biological and environmental contexts. Traditional methods often rely on subjective assessments or ordinal scales that fail to capture the nonlinear, multivariate relationships influencing decomposition. This project refines PMI estimation using a deep learning (DL) framework trained on standardized longitudinal human decomposition data collected at body donation facilities. To standardize data collection, all donors will have a known time of death, be free of trauma and unautopsied, and be placed in protective surface cages to decompose in situ for at least one year. High resolution cameras mounted to each cage will capture full body color photographs at 30 minute intervals, generating continuous 24hour image series across the entire decomposition trajectory. Each image will be integrated with corresponding donor demographic (age, sex, body mass) and environmental (temperature, humidity, rainfall) metadata that will be used to train, validate, and test the model's ability to estimate PMI from gross morphological change. Ultimately, the utilization of a DL algorithm offers a data-driven approach that has the potential to mitigate human bias and enhance the objectivity of PMI assessments. By leveraging advanced computational techniques, the algorithm will establish reproducible research standards to facilitate comparative analyses across forensic investigations.

#082-G Investigating how heat, humidity, and solar radiation affect postmortem dental crack volume changes in human dentition Bec Krolczyk [1], *Daniel Wescott [1], Elaine Chu [1], Nicholas Herrmann [1] (1. Texas State University)* Using human dentition for anthropological analyses is advantageous when faced with poor preservation since their mineral composition allows for better preservation in comparison to other skeletal elements. However, no study to date has utilized human dentition to understand how environmental factors affect postmortem dental crack propagation and prevent anthropological analyses of the dental structures. To investigate this problem, this study recorded the changes in crack propagation volume during outdoor surface decomposition for 10 central maxillary incisors from individuals who donated their bodies to the Forensic Anthropology Center at Texas State (FACTS). This sample consists of 7 female and 3 male individuals, and the whole sample has an average age-at-death of 70 years. These donors were placed at the Forensic Anthropology Research Facility from June to August 2025 to obtain varying durations of environmental exposure. Hourly measures of heat, humidity, and solar radiation were then collected from a remote weather station on Freeman Ranch. Recording changes in crack propagation volume with FACTS's NSI X5000 micro-CT system and Dragonfly's deep learning segmentation tool allowed for analysis using correlation and Kruskal-Wallis tests in RStudio. Overall, the tests concerning the effects of heat, humidity, solar radiation found no significant differences between the measures of these environmental factors and the changes in crack propagation volume ($p > .05$). While this project's sample size was small due to the variation in placement durations, these results illustrate that further investigation with larger samples could better describe the patterns of postmortem crack propagation in human dentition.

#083-G Investigating Pelvic Sexual Dimorphism in Japanese, American Hispanic, and American White Samples Madison Glenwinkel [1], *Elaine Chu [1] (1. Texas State University)* While the pelvis is regarded as the truest indicator of sex, sex estimation methods in forensic anthropology have lower accuracy and higher bias when applied to Hispanic and Asian individuals due to reduced dimorphism in size and shape. Statistical shape analysis (SSA) of the left os coxa (5000 points) and 19 traditional measurements of the pelvic girdle were used to investigate population-specific patterns of sexual dimorphism in modern Japanese (F=50, M=50), American White (F=53, M=52), and American Hispanic (F=48, M=48) samples. Japanese samples were obtained from postmortem computed tomography (PMCT) scans from Chiba University, while American White and American Hispanic samples were obtained from the New Mexico Decedent Image Database. Principal Components Analysis (PCA) was used to reduce the number of dimensions, keeping SSA and metrics separate. Kruskal-Wallis and post-hoc Dunn's tests found statistically significant ($p<0.05$) relationships between male groups across populations for SSA PCs 1, 3, 4, and 5 (capturing 44.23% of total variation), highlighting shape variation in key pelvic regions, including the iliac fossa and the anterior superior iliac spine. Measurement PCs revealed broad morphological differences ($p<0.05$), with PC1 (35.8% variance) reflecting canal pelvis dimensions and PC2 (21.93% variance) capturing overall pelvic width and height. This research identifies population-specific patterns of sexual dimorphism in the os coxa and the full pelvic girdle, providing insight into anatomical regions that should be prioritized in developing more globally accurate sex estimation methods.

#084-U Sticky Situation: Investigating eDNA and Microplastic Interactions Jordan Emerson [1], *Heaven Eskandar [1], Emma Flores [1], Romi Burks [1], Matthew Barnes [2], Andre Felton [3] (1. Southwestern University, 2. Texas Tech University, 3. University of Texas San Antonio)* Organisms release genetic material called environmental DNA (eDNA) into aquatic environments. Gaining popularity, eDNA analysis serves as a non-invasive species detection tool for monitoring biodiversity. In aquatic environments, polar properties of eDNA may interact with sediments or other materials in the environment. Microplastics (MP), degraded pieces of plastic 1µm-5mm in size, occur abundantly in surface waters, causing possible adhesion to eDNA. We aimed to understand potential interactions between MPs and eDNA, as implications exist that MPs possibly influence eDNA analysis as a species detection method. We conducted a pilot study (N=3-6) with Pomacea maculata (apple snail) eDNA and standard microfiber concentrations in buckets with 5L of water. Our study included four treatments: a control (no snails, no MPs), snails alone (no MPs), and snails with low (0.05 g) or high MPs (0.25 g). During four sampling periods (1 hr, 4 hr, 7 hr, 10hr), we took 250mL of water from each bucket, removing the snails at 8 hrs to allow for immediate eDNA degradation. After collection, we filtered water samples on Millipore 0.45 micron membrane filters, extracted eDNA using CTAB-chloroform, and then analyzed quantity and detection with quantitative PCR (qPCR) using species-specific primers and a standard curve. Our preliminary 1 hr and 4 hr results indicate that eDNA does attach to microplastics, and ongoing work will continue to examine this trend with increased time. This work represents the first step to determining if MPs' interactions with eDNA increase or diminish our ability to detect invasive species.

#085-U Bobbing for apple snails: Detecting Pomacea maculata in San Antonio waterways using environmental DNA Heaven Eskandar [1], *Emma Flores [1], Jordan Emerson [1], Romi Burks [1], Matthew Barnes [2], Adrian Reyna [3] (1. Southwestern University, 2. Texas Tech University, 3. San Antonio River Authority)* Environmental sampling plays an essential role in monitoring ecosystem health and detecting invasive species. While traditional methods require extensive time and labor, potential collection and identification of genetic material (i.e., environmental DNA/eDNA) in aquatic environments makes ecological monitoring more efficient. South American apple snails (*Pomacea maculata*) have occurred in Texas since the early 2000s, and they have maintained reproductively viable populations in San Antonio since 2019, despite intensive removal efforts. The City recently made substantial investments in San Antonio River restoration beyond snail-colonized areas (i.e. San Pedro Creek). In collaboration with San Antonio River Authority (SARA), we sampled eDNA to investigate suspected waterways that may house invasive apple snails. We collected water from 7 sites (N=6), two of which we visually confirmed had apple snails and the other five that SARA suspected might contain snails, due to hydrologic connectivity. We filtered all samples (1.2 µm), performed bulk extraction, and ran qPCR using species-specific primers. Initial analysis in June 2025 identified eDNA in San Pedro Creek, which warranted re-sampling in August. Results from August supported our original findings of eDNA in the recently restored San Pedro Creek, with eDNA detected in 100% of all sites (2.2x10^{-5}ng/µL-3.0x10^{-3}ng/µL). Detection in the remaining sites suggests possible new or low-density populations due to the lack of visual confirmation. Speculation remains about whether apple snail detection reflects interconnected waterways or genuine invasion. Continued future collaboration will help guard against unwanted expansion of this highly invasive species.

#086-N Status and Distribution of Freshwater Mussels in the Tensas River and Bayou Bartholomew of Louisiana David Ford [1], *Neil Ford [2], Lance Williams [2] (1. Edge Engineering and Science, 2. University of Texas at Tyler)* Freshwater mussels are among the most imperiled faunal groups in North American, with many species declining in diversity and abundance. Louisiana has implemented multiple efforts to document and protect remaining mussel resources, yet numerous species continue to exhibit reduced ranges and uncertain conservation status. We assessed mussel distributions and abundances in the Tensas River and Bayou Bartholomew, both key components of the mussel diversity of Louisiana. Surveys were conducted at 36 sites to characterize assemblage structure, and shell lengths were measured to evaluate population viability across our study sites. We also compared our findings to historical data to assess long-term trends. We recorded 8,841 live individuals representing 28 species in the Tensas River and 5,960 individuals of 28 species in Bayou Bartholomew. Length-frequency distributions indicated ongoing annual recruitment for multiple species, and juveniles of several rare taxa, including the federally listed *Theliderma cylindrica*, were located. Comparisons with previous studies showed no evidence of major declines in overall species occurrences or distributions in either system. We attribute the apparent stability in the mussel assemblage to the lack of major anthropogenic alterations. Both systems will likely continue to be hotspots of regional mussel diversity if large-scale anthropogenic alterations do not occur and management actions are taken to protect and allow for the persistence of suitable habitats.

#087-N On the observed inverse relationship between rainfall amount and dissolved mineral content John Stout [1] *(1. USDA-Agricultural Research Service)* As the Ogallala Aquifer is gradually depleted, many farms on the Texas High Plains will be forced to shift from irrigated to rain-fed agriculture. As the region's economy becomes increasingly dependent on rainfall, knowledge of various aspects of precipitation becomes increasingly important. Agricultural producers will need to know more about the quantity of rain, the timing and distribution of rain events, and possible variations of rainfall chemistry. To study rainfall chemistry, the author has collected intermittent rainfall samples since June of 2012. The analysis of over one thousand rainfall samples suggests a very weak correlation between rainfall chemistry and atmospheric factors, such as wind speed and direction. Further analysis of these samples revealed a significant inverse relationship between the concentration of total dissolved solids (TDS) and the volume of rainfall collected in the rain gauge. The reason for this inverse relationship is not intuitively obvious but results clearly suggest that brief low-magnitude rainfall samples of less than 1 mm typically contain a higher concentration of dissolved solids compared to larger rain events of many millimeters. A theory was proposed that explains why the concentration of dissolved solids in a collected rainfall sample tends to be inversely proportional to the amount of rainfall.

#088-U Evaluating the viability of Pennsylvanian conodont and brachiopod 87Sr/86Sr values from the Santa Fe Mountains, New Mexico *Natalya Plourde [1], Michael Read [1] (1. Stephen F. Austin State University)* The present study aims to assess the viability of conodont elements (tooth-like microfossils of jawless chordates) and brachiopod shell samples for use in strontium (Sr) geochemical analysis. The ^{87}Sr/^{86}Sr system is often used by stratigraphers as an isotopic age control supplement to the relative age constraint provided by index fossils. In Paleozoic rocks, conodont elements and brachiopod shells are the premiere fossil indices for recording paleoceanographic strontium signatures, as they yield more homogeneous values than bulk calcium carbonate samples. However, diagenetic (i.e., post-burial) alteration of conodont elements (composed of calcium phosphate) and brachiopod shells (composed of low-Mg calcite) can lead to pervasive recrystallization of fossil material and the loss of original seawater ^{87}Sr/^{86}Sr values. Thus, both conodont elements and brachiopod shells must be carefully examined for signs of alteration prior to preparation and mass spectrometry. The present preassessment involved the use of polished thin sections from potentially unaltered brachiopod specimens and the chemical extraction of conodont elements from limestone host rock. As both specimens were preserved within the same matrix, brachiopods were removed first with a trim saw before the remaining material was subjected to formic acid digestion to begin the process of collecting conodont elements. The remaining insoluble residues were then picked by hand under a stereomicroscope. Once specimens were isolated, we evaluated the completed thin sections of brachiopod samples with a petrographic microscope utilizing cathodoluminescence and obtained scanning electron photomicrographs of the conodont element's external and internal textures.

#089-U A Re-evaluation of Morphological Characters Used to Identify Fossil Viperid Snakes in Neogene and Quaternary Deposits of the United States. *Theodore Ransom [1], Christopher Bell [1] (1. University of Texas at Austin)* The snake family Viperidae is represented in the United States by *Agkistrodon, Crotalus, and Sistrurus*. Fossils of those taxa are reported from across the country but are mostly represented by isolated vertebrae. Few authors stated the characteristics used to identify specimens, but often used modern geographic ranges to limit the pool of species with which comparisons were made. That approach predetermines taxonomic and geographic stability through time. We assessed published morphological characters independent of geographic considerations. We found only seven discreet characters are typically used to identify viperids. Using 41 specimens of *Agkistrodon*, 201 of *Crotalus,* and 15 of *Sistrurus* from collections at UT Austin we found that two characters are plesiomorphic: a straight hypapophysis and a pit on either side of the cotyle. Other characters vary too much to be useful for generic or species identification; e.g., the number of foramina adjacent to the cotyle. The only character that shows some promise for refined taxonomic identification is the presence of a small spine anterior to the neural spine in *Sistrurus.* However, it is only present in some vertebrae of some specimens of *Sistrurus*. These data indicate that a limited number of characteristics are used to identify fossils in North America and those characteristics have limited utility for taxonomic discrimination. Based on morphological characters alone we are unable to discriminate between *Crotalus* and *Agkistrodon,* and only some vertebrae of *Sistrurus* are identifiable at the generic level. We found no morphological justification for identification of species and of the genera.

#090-N Mid-Artinskian (Early Permian) conodonts and fusulinids from the "Wolfcamp B"-"Wolfcamp A" transition of the southern Midland Basin, West Texas Michael Read [1] *(1. Stephen F. Austin State University)* Early Permian conodonts and fusulinids recovered from core samples of the Simpson Canyon 4045 Unit #1 well, Crockett County, TX, provide biostratigraphic zonation for a previously unconstrained subsurface succession of the so-called "Wolfcamp Shale" in the southernmost Midland Basin, West Texas. The Simpson Canyon 4045 Unit #1 well penetrates the entirety of the "Wolfcamp A" unit and the total depth of 6300' likely places the bottom of the well in the lower portion of "Wolfcamp B." The cored interval (5996.6'-5876') consists of hemipelagic siliciclastic sediments, argillaceous limestone, and allochthonous carbonate material transported downslope from the Central Basin Platform margin by submarine gravity flows. Digested samples produced sparse conodont elements of *Sweetognathus* ex gr. *clarki*, *Mesogondolella bisselli*, and an irregular sweetognathid specimen that might be a transitional morphotype in the lineage from *Sweetognathus clarki* to *Neostreptognathodus pequopensis*. The occurrence of conodonts belonging to the *Sweetognathus clarki* group at a depth of 5911' indicates this interval is mid- to upper Artinskian (mid-Lower Permian), which is correlative with the lower part of the North American Leonardian Stage. Fusulinid species recovered from the Simpson Canyon 4045 Unit #1 well include *Schwagerina hawkinsi* (5922'), *Schwagerina hessensis* (5922'), *Skinnerella schucherti* (5922'), *Skinnerella biconica* (5911'), and *Parafusulina allisonensis* (5894'). All five fusulinid taxa are known to occur in lower Leonardian carbonate platform successions of the greater Permian Basin. Combining these occurrences of conodont and fusulinid index taxa with well log data enables multifarious correlation with several other biostratigraphically constrained reference wells from across the Midland Basin.

#091-N Stratigraphic Analysis of the conglomeratic sandstone of Knight Canyon (Paleocene?), Grant County, New Mexico

R. LaRell Nielson [1] *(1. Stephen F. Austin State University)* Excellent exposures of lithic conglomerate to feldspathic wacke (sandstone) are present near the mouth of Knight Canyon. Hedlund (1980) used the term conglomeratic sandstone of Knight Canyon for these outcrops. Stratigraphic analysis of these conglomerates and feldspathic sandstones indicates that three distinct stratigraphic units are present in the Knight Canyon area. The lowest unit in the southern part of the area consists of lenses of cobble and pebble conglomerate to coarse-grained cross-laminated sandstone with beds 30 to 80 centimeters thick. The second and largest unit contains 20 to 50 centimeter thick cross-laminated, lens-shaped beds of conglomerate and feldspathic wacke. This unit extends the length of the study area. The third unit consists of 30 to 90 centimeters of cross-laminated lens-shaped beds of coarse-grain sandstone to cobble conglomerate. Channels in the conglomeratic sandstone of the Knights Canyon area range between 1 and 4 meters in length and are between 10 and 50 centimeters in thickness. At the base of these channels are cobble and pebble-size clasts that fine upward and represent channel lag. The conglomeratic sandstone of Knights Canyon is exposed in a 2-kilometer belt south of Knights Peak. They come to a depositional edge north and south of Knights Peak and are not seen in other parts of the Knight Canyon area. The lens-shaped geometry, the upward-fining sequences in the channels, and the presence of channel lag deposits in the conglomerate and sandstone bodies suggest deposition in local braided fluvial channels.

#092-G Cultivating Mars: Testing Crop and Microbial Growth in Optimized Regolith Aboard the ISS

Harrison Coker [1], *Caleb Shackelford [2], Julie Howe [2] (1. Texas A&M University; Invited Speaker, 2. Texas A&M University)* Regolith-based agriculture is the most sustainable management option for large-scale plant cultivation on Mars. However, Martian regolith has numerous issues that must be overcome before it can sustain plants. It lacks beneficial microorganisms, requires nutrients, needs improved soil structure, and contains toxic components. A study was designed to evaluate the effect of spaceflight (e.g., reduced gravity and radiation) on plant and microbial growth in organic-amended Martian regolith. Specifically, barley was grown in Martian simulant (JSC- Mars-1) amended with brewer's spent grain (BSG) as a barley-based food waste added to improve regolith and provide a carbon source for consortia of beneficial soil microorganisms (Pseudomonas fluorescens, Azospirilium brasilense, Azotobacter chroococum, Saccromyces cerevisiae). The fluid processing apparatus (FPA) was optimized for barely growth with a substrate matrix containing 2.25 g of JSC-Mars-1 amended with 0.25% BSG, 20 µL of each microbial inoculant broth and hydrated to 29%

gravimetric water content. The final configuration of the FPA's led to an experiment containing three treatments: sterile substrate (control), inoculated substrate (microbe), and inoculated substrate with germinating barley seed (microbe & plant). The treatments were prepared at NASA's Kennedy Space Center and travelled to the International Space Station (ISS) for approximately one week. The design and optimization of the FPA's ensures that key parameters of plant productivity can be measured including plant nutrition, greenhouse gas production, and activity of rhizosphere microbial communities.

#093-U Discovering Novel Inhibitors of Yersinia pestis 3-Oxoacyl-[Acyl-Carrier-Protein] Reductase (YpFabG) Using Comprehensive Virtual Screening

Saumya Seth[1], Josh Beckham[1] (1. University of Texas at Austin) Rising antibiotic resistance highlights the need for new therapeutic targets beyond traditional target pathways. Yersinia pestis, a Category A bioterrorism agent with its high lethality and aerosol risk, is dependent on the enzyme 3-oxoacyl-[acyl-carrier-protein] reductase (YpFabG), which catalyzes an essential step in fatty acid biosynthesis (FAS II pathway) in membrane lipid synthesis, making this protein an attractive target for small molecule drug discovery. This project focuses on identifying and characterizing novel small-molecule binders of YpFabG, theoretically blocking enzyme activity, ultimately leading to bacterial death. Using a crystallographic structure of YpFabG from the RCSB Protein Data Bank (5CDY), over 100,000 compounds were screened through structural and forcefield-based molecular docking with ICM (Molsoft) and GOLD (CCDC). Compounds with the highest ICM and/or GOLD docking scores, while also meeting Lipinski's Rules, were prioritized for wet lab testing using binding studies of YpFabG with differential scanning fluorimetry (DSF). This protein has been expressed using autoinduction in BL21(DE3) E. coli, and purified using Nickel-NTA chromatography, which led to pure, high-yield protein, with a melting temperature of 56 degrees Celsius. Three top compounds have been tested in DSF, leading to a promising candidate, which led to a 4-6 degrees Celsius decrease in the melting temperature of YpFabG, demonstrating a possible allosteric mechanism. By integrating computational modeling with experimental assays, this methodology facilitates the more rapid discovery of promising inhibitors for YpFabG to address the global health crisis of antibiotic resistance and the risks of bioterrorism.

#094-G Investigation of the Pathogenesis of Bourbon virus at the Tick-Host-Virus Interface

Megan Burch[1], Catherine Olal[1], Agnes Udoh[1], Dennis Bente[1] (1. University of Texas Medical Branch)

Bourbon virus (BRBV) is an emerging tick-borne virus in the Midwest and southern United States, with five confirmed human cases and two fatalities. The vector for BRBV, *Amblyomma americanum,* also known as the lone star tick, is rapidly expanding geographically, increasing the risk of BRBV spreading further in the US. Currently, the pathogenesis of BRBV, including early cellular targets, remains poorly understood. Our goal is to define the kinetics of infection and identify cellular targets at the tick-host-virus interface. Here, we have developed an *ex vivo* skin model that can be used to investigate BRBV tropism in the skin. Human skin discarded from abdominoplasty surgery was used to generate human skin explants for infection via intradermal injection or abrasion with topical application. Explants were assessed for infection and viral shedding with plaque assays, pathogenic changes in the skin structure with H&E staining, and infected cell types with immunohistochemistry. Initial results indicate that BRBV infects and replicates in the *ex vivo* model, resulting in pathological changes within the skin. Future studies will focus on the influence of tick saliva on BRBV pathogenesis, in-depth characterization of infected cell types, and the assessment of their contribution to the local response to infection. This project will contribute to a better understanding of the early pathogenesis of BRBV in the skin and will inform future vaccine and therapeutic design and development aimed at counteracting this emerging tick-borne virus.

#095-G Crimean-Congo Hemorrhagic Fever Virus Infection in Human and Animal Cell Lines: A Pathway to Understanding Species-Specific Pathogenesis

Kiyah Costin[1], Catherine Olal[1], Anastasia Accoti[1], Megan Burch[1], Maria Cajimat[1], Dennis Bente[1] (1. University of Texas Medical Branch) Crimean-Congo hemorrhagic fever virus (CCHFV) is a zoonotic, tick-borne virus of the *Nairoviridae* family that causes severe hemorrhagic fever in humans. In contrast, infected amplifying hosts such as ruminants and small mammals typically remain disease-free. Currently the immunological mechanisms that drive this species-specific pathogenesis remain unknown. We hypothesize that bovine and rabbit cell lines will exhibit reduced viral infectivity compared to human cell lines, potentially due to unidentified host-specific antiviral factors. We are utilizing immunofluorescence (IFA) and plaque assays using SW-13 (human), MDBK (bovine), and RK13 (rabbit) cell lines, with Hazara virus (HAZV) serving as a BSL-2 surrogate for CCHFV, to investigate differences in viral infectivity between human and animal hosts. Preliminary data indicates that animal cell lines have lower infection rates compared to the human cell line. Future studies will focus on characterizing HAZV and CCHFV infection in primary human and animal immune cells obtained from whole blood. Findings from this research will aid in identifying species-specific factors that contribute to viral control in animals, informing strategies that reduce disease prevalence of CCHFV, and protecting agricultural workers in endemic regions.

#096-N Targeting aurora kinase, A and BRD4 as a translational therapeutic strategy for cutaneous T-cell lymphoma Mamta Gupta [1] *(1. Stephen F Austin State University)* Cutaneous T-cell lymphoma (CTCL) is a rare type of skin cancer that often develops resistance to available therapies, creating an urgent need for new molecularly targeted treatment strategies. Aurora kinase A (AURKA) is over-expressed in CTCL, yet the therapeutic relevance of its biological functions remains unexplored. In this study, we investigated the translational potential of AURKA inhibition alone and in combination with BRD4 blockade or ionizing radiation (IR). Pharmacologic or siRNA-mediated inhibition of AURKA significantly increased phosphorylation of histone H2A.X, with γ-H2AX formation and comet assays confirming pronounced DNA damage. This effect translated into markedly reduced proliferation and colony formation. AURKA inhibition also selectively enhanced acetylation of histone H4 at lysine 12, promoting BRD4 recruitment and DNA repair complex formation, suggesting a compensatory chromatin-mediated repair response. Dual inhibition of AURKA and BRD4 suppressed this repair pathway, resulting in amplified DNA damage, reduced BRD4 chromatin binding, and a synergistic decrease in cellular growth and clonogenic potential. In vivo, AURKA inhibition produced significant antitumor activity in a HUT-78 xenograft model ($p < 0.001$), demonstrating its therapeutic promise. Additionally, IR increased AURKA expression, and co-treatment with IR plus AURKA and BRD4 inhibitors generated a potent synthetic effect on DNA damage and growth suppression. Collectively, these findings reveal AURKA as a regulator of DNA damage responses in CTCL and provide strong preclinical justification for translational development of combined AURKA and BRD4 inhibition alone or with radiation as a targeted therapeutic strategy for patients with CTCL.

#097-N Rapid recovery of peripheral oxygen saturation and hypoxic COVID-19 patients with ivermectin-based multidrug therapy Eleftherios Gkioulekas [1], *Peter McCullough [2], Colleen Aldous [3] (1. University of Texas Rio Grande Valley, 2. McCullough Foundation, 3. University of KwaZulu-Natal)* Several combination therapies for the early outpatient treatment of COVID-19 were proposed by independent research groups at the onset of the pandemic during 2020 and 2021. Of particular interest is the proposal by Borody and colleagues, of a 10-day triple drug therapy consisting of ivermectin, doxycycline, and zinc, with adjunct vitamin C and D supplementation, which was widely adopted and further refined in Zimbabwe and South Africa. A key characteristic of the refined protocol was the dynamic adjustment of ivermectin dosage to patient severity and response to treatment. However, despite the successful use of this protocol, the use of ivermectin in the treatment of COVID-19 has remained controversial. Here, we review 3 case series of 119 patients treated in the United States, Zimbabwe, and Nigeria with similar ivermectin-based protocols based on Borody's proposed therapy, of whom 61 presented with less than 90% oxygen saturation on room air. The patients were successfully treated with no deaths. Rapid recovery of oxygen saturation levels was observed within 24 hours from the onset of treatment, with response rate dependent on the intensity of treatment. Statistical comparison with external controls supports mortality rate reduction by the preponderance of the evidence. Furthermore, a detailed narrative review supports the efficacy of the most aggressive protocols, used in 2 of the 3 case series, by the Bradford Hill criteria for temporality, strength of association, biological gradient, biological plausibility, coherence, consistency, and analogy.

#098-U Vocalization Signatures of Frog Species: A Study of Call Patterns for Species Identification and Biodiversity Monitoring in a Temperate Wetland Ecosystem Sunshyne Parrish [1], *Joel Brant [2], T.J. Boyle [1] (1. McMurry University, 2. Midwestern University)*
Frog vocalizations are used for species identification,communication, and mate selection, providing a valuable tool for ecological studies and biodiversity assessments. This study investigates the use of frog vocalization, specifically calling patterns, to distinguish between frog species within a shared habitat. We recorded the calls of multiple frog species from different genera in a temperate wetland ecosystem in three different locations over several months using the Song Meter Mini (Wildlife Acoustics). Calls were analyzed for key acoustic features, including frequency, duration, and call structure in the Kaleidoscope Pro software. Results revealed significant interspecies variation in call characteristics, with each species displaying unique call signatures. Our findings demonstrate that specific acoustic parameters, such as pulse rate and dominant frequency, can reliably differentiate between species even in the presence of overlapping ecological niches. These results suggest that acoustic monitoring can be a non-invasive, efficient tool for species identification, monitoring population dynamics, and conserving amphibian biodiversity. Further research will focus on refining these techniques for use in automated bioacoustics monitoring systems in their native habitats.

#099-U Environmental impacts: how humidity and temperature affect the growth of Ophidiomyces isolates Emilee Minor [1], *Alan Lizarraga [1] (1. The University of Texas at Tyler)*
Snake Fungal Disease (SFD), or *Ophidiomyces ophidiicola*, is now a widespread threat to wild snakes. Its adaptability to increasingly warm and humid climates, particularly in the context of global climate change, underscores the urgency of understanding its growth dynamics. In this experiment, we investigated the effects of temperature and humidity on the growth rates of *O. ophidiicola* using two isolates from Texas and one from

Florida. Given Florida's higher average humidity and comparable temperature profile, we hypothesized that the difference in growth under varying conditions might emerge.

POSTERS

P1-U Evaluating bone strength in press-fit versus cement-fit arthroplasty via micro-CT *Theresa de Cree [1], James Myrick [1], Daniel Wescott [1] (1. Texas State University)* Due to the increase in arthroplasty rates, it is imperative to understand the impact that arthroplasty fixation has on the skeleton. For an implant to succeed clinically a stable bone to implant interface is necessary. The two types of fixation are press-fit and cement-fit. Distribution of biomechanical forces is dependent on implant fit. Therefore, proper integration encourages appropriate bone mass and minimal bone loss during remodeling. Medical literature has found that press-fit fixations are more likely to result in clinical failure or a decrease in bone integrity. The use of micro-CT in forensic studies on deceased individuals can yield higher resolutions when compared to medical CT studies on the living. This study included micro-CT scans of femoral shafts for 15 individuals from the two donated skeletal collections in Texas. Slices at the mid-shaft were analyzed for cross-sectional area (CSA) and pore surface area (PSA) in the programs ImageJ and Dragonfly. Unpaired t tests were utilized to analyze the resultant values. Results indicated that CSA was trending towards significance with a p value 0.0607 with cemented implants having a higher CSA, meaning higher bone mass. Contrastingly, the ratio of PSA to CSA did not show a difference between the fixation groups with a p value of 0.9249. The micro-CT data from this study is trending in support of the medical literature's conclusion that cement-fit implants have a higher success rate in arthroplasties. Further research is currently underway to determine if these trends are significant in a larger sample.

P2-G Can low-resolution imaging be used to assess living activity level in skeletal remains? A comparison of imaging modalities using the Texas State Donated Skeletal Collection (TXSTDSC)
ChristiAna Dunham [1], Elaine Chu [1] (1. Texas State University)
Anthropologists and exercise scientists have used various imaging modalities to visualize and measure bone structural properties, which can inform on an individual's activity level. High-resolution x-ray computed tomography (HRCT) and peripheral quantitative computed tomography (pQCT) are commonly used to assess these properties in living and deceased individuals; however, these systems are not readily available and are often cost-prohibitive. This project examines the correlation between bone structural properties gathered with more accessible low-resolution imaging systems, such as medical computed tomography (med-CT), and HRCT. Eighty (40 females, 40 males) left femora were sampled from individuals within the TXSTDSC and scanned using med-CT at John's Hopkins University School of Medicine and HRCT at Texas State University. Cortical, cross-sectional geometric, and trabecular bone properties were collected from both scans using the BoneJ plugin within ImageJ, Avizo, and Python and compared using Kendall's Tau Rank Correlation. Cortical and cross-sectional geometric properties were statistically significantly correlated ($p < 0.001$) between med-CT and HRCT, while trabecular properties were not statistically significantly correlated ($p > 0.05$). These results indicate that low-resolution imaging is sufficient for collecting accurate cortical bone and cross-sectional geometric property data, but moderate-to-high resolution is required to obtain accurate trabecular property data. Because cortical and cross-sectional geometric properties can inform on body mass and childhood activity, the results of this project suggest that more accessible low-resolution imaging can be used to assess these individualizing characteristics in skeletal remains.

P3-U Evaluation Of Sunscreen Properties Of Ancient Maya Body Paints *Jessi Loyd [1] (1. Howard Payne University)* Using materials derived from plants and clay, including annatto (*Bixa orellana*), indigo (*Indigofera suffruticosa*), copal resin, and palygorskite clay, the ancient Maya made vibrant, nature-based pigments for art, rituals, and body paint. Of these pigments, Maya blue is formed by combining palygorskite clay and indigo, making a stable compound. The red and black pigments were formed by mixing copal resin with annatto and charcoal respectively. While these pigments are known for their cultural significance, their potential role in skin protection remains largely unexplored. As the plant-based pigments contain carotenoids, flavonoids, and anthocyanins known to absorb ultraviolet (UV), each plant has been explored individually for its ability to absorb UV radiation. This project aims to evaluate the UV-absorbing and photostability properties of synthesized Maya pigments and compare them with modern sunscreens, including zinc oxide and titanium dioxide-based sunscreens, organic/botanical sunscreens, and chemical-based sunscreens. UV-Vis absorbance spectra for each pigment and its components will be measured and used to calculate in-vitro SPF values. Followed by this, the pigments will be tested under controlled light and heat exposure to find the photostability of each extract. Microbial UV protection assays will be conducted to test biological efficacy on *E. coli* and compared to a control without pigment extracts. By combining this historical insight with modern dermatological testing, the results will advance the understanding of the protective properties of Maya body paints, aid in the development of natural sunscreens, and highlight the relevance of ancient biotechnological knowledge to advance dermatological applications today.

P4-U The importance of projectile trauma analysis training for undergraduate students Javier Garcia [1], *Theresa de Cree [1] (1. Texas State University)* Hands-on learning is essential in forensic anthropology because it connects theoretical knowledge with real-world application. Being involved with lab work, mock scenes, and field projects helps students gain practical skills, think critically, and gain professional confidence that lectures alone cannot provide. These experiences prepare future practitioners to apply scientific methods in investigative settings. To exemplify the impact that hands-on learning has on undergraduate students, this project, the result of experience-focused pedagogy, reviews current literature on projectile skeletal trauma and the analysis of a case study from the Texas State Donated Skeletal Collection. Projectile trauma displays consistent features that reveal both the mechanics of injury and projectile behavior. The diagnostic traits include entrance and exit wound morphology, beveling, fracture systems, and fracture sequencing. These fractures demonstrate force direction and energy dissipation. While literature provides an understanding of the theoretical underpinnings that dictate bone's reaction to projectile trauma, the inclusion of skeletal analysis in a course's purview is imperative as exhibited by the author's successful analysis of cranial projectile trauma. The skull from this case study displayed internal beveling at the entrance, external beveling at the exit, and radiating fractures; all of which are consistent with high-velocity projectile trauma. Timing of the fracture was assessed as perimortem due to fracture characteristics and lack of healing. This experience allowed the student to gain skills as it allowed the application theoretical knowledge to a forensic scenario, which strengthened the ability to recognize trauma patterns, interpret skeletal evidence, and connect classroom concepts to practical casework.

P5-G Forensic analysis of hacksaw paint transfer in dismemberment Muthoni Thuku [1], *Sanjib Thapa [1], Rizalia Klausmeyer [1], Rohil Kayastha [1], Bernd Zechmann [1], Zhenrong Zhang [1], Joseph Ferraro [1] (1. Baylor University)* Dismemberment occurs in approximately 3% of homicide cases, with saw marks frequently observed on bones. Previous research details the relationship(s) between saw blade morphologies and kerf mark morphologies, resulting in typological schemes that facilitate class-based identification of saw types associated with specific marks. During dismemberment, paint traces from saw blades may be transferred to kerf walls. Here we report that kerf marks created by hacksaw blades can be identified to both saw type and commercial brand through integrated taphonomic and trace-evidence approaches. We simulated human dismemberment by sawing defleshed bovine remains using saws from five commercially available hacksaw brands under controlled laboratory conditions. We recovered paint residue from each kerf and created impressions of kerf marks using hydrophilic dental molding materials. Kerf molds were digitized using a laser scanning microscope (LEXT OLS5100) and identified to the hacksaw type using published procedures and morphological criteria. Reference paint samples were collected from each hacksaw blade. Paint residues from kerfs and those of reference samples were analyzed using Raman spectroscopy, with 532 nm and 633 nm laser excitation. Raman spectra of the reference blade paint residues were compared and matched with the bone-derived residues through correlation analysis on Origin software 2023 b. This forensic study aims to identify and match paint traces found in bone kerfs to specific hacksaw blade manufacturers. The study demonstrates that by integrating taphonomic and trace-evidence approaches, kerf marks created by hacksaw blades can potentially be identified not only to saw type (i.e., hacksaw) but also to commercial brand.

P6-U Recognizing Intimate Partner Violence in Forensic Anthropological Trauma Analysis: A Literature Review Sara Medeiros [1] *(1. Texas State University)* Forensic anthropologists are tasked with performing trauma analysis, as they are uniquely qualified to document and interpret skeletal injuries. Skeletal trauma analysis is critical in detecting signs of interpersonal violence in death investigations. A subset of interpersonal violence that results in skeletal trauma is intimate partner violence. Patterns of intimate partner violence are characterized by blunt force trauma to the head, neck, face, and upper extremities. Anthropologists are well poised to interpret interpersonal violence as they hold a complex understanding of skeletal trauma and societal influences that result in this type of violence. Interpersonal violence has been shown to display recurrent injury patterns at specific locations, for instance, the midfacial region. This author performed a literature review of medical and forensic work on skeletal trauma associated with interpersonal violence and its relationship to intimate partner assault and homicide. The result of this literature review synthesizes patterns of skeletal trauma typically detected in cases of interpersonal violence, such as frequent locations of fracturing and common mechanisms of force. This review demonstrates the importance for forensic anthropologists and other medicolegal professionals to be cognizant of skeletal trauma patterns indicating interpersonal violence. The benefits of competent skeletal analysis are the ability to reconstruct an antemortem history of trauma and perimortem events from a forensic perspective, to better understand the circumstances surrounding inflicted trauma. This literature review represents a foundation for detecting interpersonal violence through the analysis of skeletal trauma. Recognition of intimate partner violence is integral to victim advocacy, justice, and public safety.

P7-G Osteometric Measurements for Reassociating and Pair-Matching of Commingled Tali and Naviculars

Susanna Jones [1] *(1. Texas State University)*

When commingled human remains are found in an assemblage, it is the responsibility of forensic anthropologists to separate the bones according to the individuals to whom each bone belongs. The purpose of this is to increase the number of positive identifications made by identifying the minimum number of individuals represented in the assemblage. The correct matching of bones at the highest and most achievable level possible is crucial in showing respect for the dignity of decedents. However, smaller bones are often overlooked in this process, as they can be more difficult to reassociate and may be viewed as less important than the long bones despite being just as much a part of the body. Here I demonstrate an assessment of a method for reassociating and pair-matching commingled ankle bones, specifically the tali and naviculars. The goal of this assessment is to determine the utility of talo-navicular osteometrics (bone measurements) in identifying when these bones are from the same individuals within an assemblage. Furthermore, tests conducted on a sample with higher demographic diversity compared to one with lower diversity shed light on whether osteometrics can be applied to an assemblage with less human variation. These results demonstrate rates of accurate matches among commingled individuals and whether osteometrics become less reliable depending on the demographics of the individuals in the sample. These findings can inform how to adapt approaches when dealing with commingled assemblages in a variety of contexts.

P8-U Gene Expression Changes in Parkinson's Disease

Serena Ylostalo [1], *Joni Ylostalo [1] (1. University of Mary Hardin-Baylor)*

Parkinson's Disease (PD) is a neurodegenerative disease in which neurons gradually break down and die, causing loss of fine and gross motor control, the characteristic tremor, and speech changes. The underlying cause is unknown, but several factors have been noted to play a role including environmental triggers and genetic linkages. Many current treatment programs aim to target symptoms since the cause is yet to be discovered. Levodopa (L-DOPA) remains the cornerstone treatment for PD due to its significant efficacy in short-term motor symptom relief. The long-term neuroprotective potential involving advanced therapies remain unanswered. In this bioinformatics study, various PD samples were analyzed to identify expression changes in genes and pathways. The raw microarray data sets, including *in vitro* and *in vivo* animal and human samples, were obtained from the Gene Expression Omnibus data repository. The data sets were transferred into the Transcriptome Analysis Console (TAC) for normalization and quality control evaluation as separate data sets. Data sets were then analyzed with TAC to identify differentially expressed genes. Many genes previously identified to be important in PD were identified as differentially expressed. In addition, other genes and pathways were identified as differentially expressed. In conclusion, this study confirmed the gene expression changes in many PD-related genes and identified other genes that were either up- or down-regulated in the PD samples. Furthermore, general gene expression patterns and pathways potentially important in PD were identified.

P9-G Enhancing Monascus pigments production and application as a natural alternative to sodium nitrite in pork sausages compared with traditional food colorants.

Lakshmi Devi Chittepu [1], *Minji Jang [1], Behiye Ebru Sahiner [1], Krithika Maki [1], Boluwatife Ajayi [1], Md Ariful Haque [1], Md Abdur Razzak [1], Hye Kim [1], Wesley Osburn [1], Mathew Taylor [1], Seockmo Ku [1] (1. Texas A&M University)*

Increasing safety issues over the health risks of synthetic colors & additives have driven the demand for natural alternatives. *Monascus purpureus*, a filamentous fungus, produces excellent natural hues with bioactive benefits and has been used for over a thousand years in oriental fermented foods and in East Asian cuisine. However, it co- synthesizes citrinin, a mycotoxin limits the safe use of *Monascus* pigments in food applications. The current research was carried using *Monascus purpureus* ATCC 16365 strain to optimize pigment production in defined medium to enhance pigment production while reducing citrinin levels to ensure product safety. In this study we found that fructose & glucose-based medium produced higher pigments 378.05 AU/mL, 68.8 AU/mL and safer levels of citrinin respectively highlighting its potential for safe use in food applications. Results depicted that *Monascus* pigments, particularly at 2% (2mL in 100 g of sausage) concentration, improved sausage coloring, which is closest to the sodium nitrite treated sausages, indicating that this study develops a citrinin-reduced *Monascus* pigments that are used as clean-label natural alternative to conventional colors and additives. In this study, we achieved higher pigment production using fewer nutrients and a shorter fermentation period, making the process more efficient and sustainable. Future study will focus on evaluating the bioactive properties of the optimized pigments. Additionally, the best performing pigments with safer level or no citrinin will be applied as safer natural alternative to sodium nitrite in pork sausages compared with traditional dyes to assess color stability, storage quality, and microbiome dynamics.

P10-U Optimization of PVA, Ag Hydrogels: Effects of Heating and Freeze Thaw Crosslinking on Antibacterial Activity Against E. coli

Ethan Yager [1], *Milka Montes [1] (1. University of Texas Permian Basin)*

Poly(vinyl alcohol) (PVA) hydrogels infused with silver ions are promising antibacterial materials, but previous preparations showed inconsistent dissolution and degradation. This study aims to optimize PVA hydrogel preparation and evaluate how processing conditions affect antibacterial performance against *Escherichia coli* (E. coli). Here we show that heated hydrogels maintain stronger and more uniform antibacterial activity than freeze–thaw-crosslinked hydrogels. PVA was dissolved at 65 °C with continuous stirring for 40–90 minutes to prevent scorching and achieve complete dissolution. Two heated hydrogels (H1 and H2) were produced and sonicated for 30 minutes before adding 0.01 mM $AgNO_3$. Additional hydrogels (Fc1, Fc2, Fc3) underwent 1, 2, or 3 freeze–thaw cycles to increase physical crosslinking density. Water-only gels served as controls. Disk diffusion assays against *E. coli* showed that H1 and H2 produced strong and consistent zones of inhibition, indicating effective silver release. In contrast, freeze–thaw hydrogels shrunk on the agar surface, and antibacterial activity was restricted only to the areas where the hydrogel directly contacted the agar, producing partial and irregular clearance zones. This suggests that increased crosslinking limits silver diffusion and reduces antimicrobial effectiveness. Water controls showed no inhibition. To further investigate structural differences, portions of H1, H2, Fc1–Fc3 will be dried and analyzed using scanning electron microscopy (SEM) to compare porosity and crosslink morphology. These microstructural insights will help explain differences in silver release and antibacterial behavior. Overall, this optimized workflow improves PVA–Ag hydrogel reproducibility and demonstrates how preparation conditions influence antibacterial performance, supporting future expansion into CMC hydrogels.

P11-G Diversity and Prevalence of Non-Tuberculosis Mycobacteria in Texas *Maritza Estrada [1], Jennifer Honda [1], Joshua Banta [1] (1. The University of Texas at Tyler)* Non-Tuberculosis Mycobacteria (NTM) belong to the *Mycobacterium* genus, which also includes tuberculosis (*M. Tuberculosis*) and leprosy (*M.Leprae*), and require a host to survive and transmit from host to host. Whereas NTM are opportunistic pathogens commonly found in the environment, such as water, dust, and soil. Although most NTM exposures do not cause infections, people with lung abnormalities or immunocompromised systems are at higher risk. NTM infections can cause chronic lung disease, lymphadenitis, skin infections, or widespread disseminated disease. Their distribution is influenced by specific climate and environmental factors, like pH and temperature. Rising global temperatures, extreme weather, and altered hydrology have led to increased NTM exposure, with infection rates rising by approximately 4.0% and 4.1% per 100,000 persons per year. Because NTM distribution is influenced by climate and environmental factors, like pH and temperature, higher temperatures are likely to promote their growth and increase exposures. Our study aims to understand the current presence of NTM in the environment and future distribution across certain Texas regions.

P12-U Pedigree of a Rare Variant of the MYH7 Gene Associated with Cardiomyopathy *Danielle Felice Galon [1], Pheben Abebe [1], Joshua Brokaw [1] (1. Abilene Christian University)* Mutations in MYH7, which encodes the β-myosin heavy chain, are a well-established cause of hereditary cardiomyopathies, including hypertrophic (HCM) and dilated (DCM) forms. However, many rare variants remain insufficiently characterized, limiting our understanding of their penetrance, expressivity, and clinical relevance. In this study, we investigated a rare MYH7 variant in a multigenerational family after clinical genetic testing of the proband identified a deletion involving exon 40 and potentially adjacent regions. Subsequent Sanger sequencing defined the mutant allele as a unique 2,368 bp deletion encompassing most of the final MYH7 intron, all of exon 40, and more than 1 kb of the intergenic region between MYH7 and MYH6. Genotyping of available family members suggests a preliminary association between the variant and cardiomyopathic traits. Phenotypic variability was evident in the pedigree: some carriers displayed severe ventricular hypertrophy and trabeculation, whereas others were asymptomatic (but may not have undergone echocardiography and/or cardiac MRI), suggesting incomplete penetrance and variable expressivity if this mutation is the cause of the observed cardiomyopathies. By mapping inheritance and correlating genotype with clinical observations, this study contributes to understanding the pathogenic potential of rare MYH7 variants and highlights the value of family-based genetic analyses for risk assessment and counseling. These findings lay the groundwork for future functional studies of the variant and provide a useful case study for teaching genetic inheritance, variant interpretation, and clinical implications in an undergraduate research setting.

P13-U Screening Compounds for their Potential to Inhibit Growth of Leukemia cells (Molt-4) *Jiya Desai [1], Tina Prajapati [1], Rachna Sadana [1] (1. University of Houston-Downtown)* Cancer encompasses a group of diseases that occur when cells bypass cell-cycle checkpoints, allowing them to rapidly divide and invade surrounding tissue. Cancer is a common disease, affecting one in three people in the United States (American Cancer Society). It is considered a deadly disease because of how it can metastasize and how each type of cancer needs to be treated a little differently. Currently, we can treat cancer cells with hormone therapy, radiation therapy, and most popularly, chemotherapy. However, there are major disadvantages to chemotherapy, including nausea, fatigue, hair loss, neuropathy, diarrhea or constipation, and a low blood count, which warrants the discovery of new chemotherapeutic drugs with fewer side effects. Here, we screened a library of DKNR compounds from a partner lab in India and found that DKNR compounds 5, 8, 10, 11, and 13 successfully inhibit cell growth when tested using an MTT cell-proliferation assay. We have discovered how our DKNR compounds work compared to various cell lines. My project focused on Molt-4, a leukemia cell line. These select compounds will be further investigated for their impact on the expression of various genes using RT-PCR and cell cycle analysis using flow cytometry. We anticipate our research will lead to identifying new compounds with the potential to be anti-cancer drugs.

P14-U Discovering potential inhibitors of New Delhi metallo-β-lactamase 1 (NDM-1) using Computational Docking Laura Jung [1], *Josh Beckham [1] (1. University of Texas at Austin)* The antibiotic resistance crisis is a major public health concern. It reduces the effectiveness of antibiotics and increases the mortality of E. coli and Klebsiella pneumoniae. A key contributor to this crisis is NDM-1 (New Delhi metallo-β-lactamase 1). This enzyme confers resistance to many β-lactam antibiotics, including carbapenems, which are a last line of treatment. NDM-1 hydrolyzes the beta-lactam ring of antibiotics. Currently, there is no specifically approved therapeutic inhibitor of NDM-1. In this work, we seek to find small molecules to bind to this enzyme. We used GOLD (Genetic Optimisation for Ligand Docking), a computer program that predicts protein-ligand docking using genetic algorithms, to screen potential NDM-1 inhibitors. Several candidate ligands show strong predicted binding to the NDM-1 active site, with ZINCXXXX47 having the highest score of 71.98, above the positive control co-crystallized ligand, Ampicillin (PDB 5ZGE). In order to validate the compounds, NDM-1 was expressed via autoinduction in BL21, purified using nickel affinity chromatography, and characterized using SDS-PAGE and Differential Scanning Fluorimetry (DSF) thermal assay. One initial compound was assayed for binding in DSF, but results were inconclusive. We will continue testing additional compounds and performing further thermal assays. We anticipate that our list of possible NDM-1 inhibitors will serve as a foundation for developing novel antibiotic-inhibitor combinations. This work also emphasizes the use of computational tools to accelerate inhibitor discovery and address antibiotic resistance.

P15-U Evaluation of Cranberry-Loaded Hydrogels for Antibacterial Activity *Shayna Oliver [1] (1. Howard Payne University)* Chronic wounds and bacterial infections remain a major challenge in healthcare. Antibiotics are often required to stop infections, but with antibiotic resistance in bacteria increasing, they are becoming more difficult to treat. Finding a safe and effective alternative has become an important focus in biomedical research. Cranberries contain proanthocyanidins (PACs), polyphenols known for their antibacterial and antioxidant effects. Previous studies have shown that PACs can stop bacteria from sticking to tissues and beginning infections, a common danger with bacteria like E. coli and Staphylococcus epidermidis. Despite these promising properties, the potential of cranberry extracts in wound care has not been fully explored. This project observes the development of a cranberry-based hydrogel designed to deliver PACs for infection control and potential tissue repair. Here, I propose to incorporate frozen cranberries into a hydrogel composed of three different polymers and evaluate which serves as the most optimal and stable hydrogel. Then, using different extraction methods, incorporate the cranberry extract into the optimal hydrogels and evaluate antibacterial activity using agar plate assays. I expect that the cranberry-infused hydrogel will inhibit bacterial growth most effectively. These findings support the hypothesis that the compounds from cranberries can serve as an effective alternative to antibiotics and inhibit bacterial growth. This experiment builds on research around using natural compounds in research by testing a safer and sustainable way to prevent infection and inhibit bacteria, support wound healing, and lower dependence on antibiotics.

P16-H The Impact of BT2-Modulated BCAA Reduction as a Novel Therapeutic for Alzheimer's Disease *Shriya Sreeju [1], Tanisha Makam [1], Lara Makkapati [1] (1. Marcus High School)* Alzheimer's Disease (AD) is a neurodegenerative condition characterized by severe cognitive decline, with limited effective therapies available. Recent studies have connected elevated branched-chain amino acid (BCAA) concentrations to AD pathology. This study investigates the effects of 3,6-dichlorobenzo[b]thiophene-2-carboxylic acid (BT2), a small molecule that downregulates BCAA levels, on gene expression and cognitive behavior in AD mouse models. The four treatment groups were wild-type vehicle, wild-type with a 20mg BT2 dose, AD vehicle, and AD with a 20mg BT2 dose. Real-time quantitative polymerase chain reaction (RT-qPCR) was conducted on cortex tissue samples to measure expression levels of 17 genes associated with AD pathology. An Enrichr analysis was used to identify the biological pathways and processes associated with the genes affected by BT2 treatment. The results of a Y-Maze test were administered to gather behavioral data. For further analysis, an ANOVA statistical test was performed to correlate gene expression fluctuations with behavioral responses across the four groups, after BT2 treatment. Moreover, a Random Forest Regressor model was used to identify which gene expression changes predicted cognitive performance in AD mice based on Y-Maze results. Our results indicate that BT2 led to notable behavioral changes and differential gene expression, suggesting that BT2 may mitigate AD behavioral symptoms by modulating BCAA levels and altering cortical gene expression. Observed cognitive behavior improvements support BT2's candidacy for therapeutic intervention in AD by addressing BCAA-related dysfunction. This study provides a foundation for future research into BCAA-reducing drugs as potential treatments for AD.

P17-U Exploring natural anti-microbial and anti-virulence compounds with their mechanism of actions to combat drug-resistant pathogens *Nathaniel Pyenta [1], Santosh Kumar [1] (1. McMurry University)* The emergence of drug-resistant pathogens is worrying and requires the discovery of new therapeutic approaches. *Staphylococcus aureus* is a gram-positive bacterium and causes a wide range of invasive infections involving skin and soft tissue, pneumonia, endocarditis, and bacteremia. The global rise of multi-drug resistance strains like methicillin-resistant *S. aureus* (MRSA) is a major concern. To invade host cells and cause infections, *S. aureus* expresses a diverse set of toxins and virulence factors including hemolysins, lipases and nuclease. In our current study we are discovering plant-based compounds that can block the expression of virulence factors of *S. aureus*. Under the specific growth conditions, we are evaluating anti-virulence potential of pure phytomolecules including glabridin from licorice root, usnic acid from lichens, and eugenol from clove. Furthermore, utilizing OMICs and cell-based methods, we aim to gain insight into the molecular mechanisms of action of the selected compounds exhibiting antivirulence capacity to uncover novel targets and develop new therapeutic strategies to combat drug-resistant infections.

P18-H Inhibitron-LC - A Novel Multitarget Drug with Nanoparticle Precision for Triple-Negative Breast Cancer

Nikila Swaminathan [1] (1. Allen High School) Triple-negative breast cancer (TNBC) is a clinically aggressive subtype characterized by hypoxia-driven metabolic reprogramming, contributing to therapeutic resistance and poor prognosis. Two key metabolic enzymes, lactate dehydrogenase A (LDHA) and carbonic anhydrase IX (CAIX), are consistently overexpressed in TNBC and represent actionable targets for disrupting tumor adaptation under hypoxia. This study presents the computational design and in silico validation of Inhibitron-LC, a novel dual inhibitor that targets both LDHA and CAIX and aims to overcome the limitations of existing single-target agents such as FX11 and acetazolamide. Structure-based molecular docking demonstrated the high binding affinity of Inhibitron- LC for both targets. ADMET profiling indicated favorable absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties. A comparative evaluation against vorinostat, a clinically approved epigenetic modulator, revealed the potential for enhanced metabolic disruption and synergistic efficacy.To improve delivery and tumor targeting, PEGylated pH-responsive liposomal nanoparticles were designed for encapsulating Inhibitron-LC. Physiologically based pharmacokinetic (PBPK) modeling predicted improved tumor accumulation, reduced systemic toxicity, and an increased circulation half-life. These findings provide a compelling computational framework for a multitarget therapeutic strategy in TNBC, combining metabolic pathway inhibition with nanoparticle delivery. Future directions include in vitro cytotoxicity assays and translational preclinical studies.

P19-U Regulation of RumAB Mutagenic Activity by the Putative R391 Lon Protease *Caleb Hammons [1], Martín González [1] (1. Southwestern University)* Environmental stressors, such as DNA damage, induce a stress response in bacteria known as the SOS Response. Under extreme DNA damage, the SOS Response includes the activation of an error prone DNA polymerase, DNA pol V, which due to its decreased fidelity in replicating DNA increases the likelihood of mutations, possibly resulting in antibiotic resistance. One extremely mutagenic DNA pol V ortholog is encoded by the rumAB operon found in the mobile integrative conjugative element R391. This element is capable of moving within and between species through horizontal gene transfer. Extensive mutagenesis is almost certain to have detrimental effects on bacteria harboring R391. Therefore, regulation of RumAB activity is necessary at both the level of gene expression and after production of the RumA’2B, the DNA pol V ortholog. The purpose of the current study is to determine whether a putative Lon protease homolog encoded on R391 is capable of regulating the RumAB error prone polymerase. Results of histidine reversion assays suggest that the Lon391 protease negatively impacts the mutagenic activity of RumA’2B, thereby minimizing mutations in Escherichia coli strains under both inducing or non-inducing SOS response conditions. Degradation assays and western blot analysis are currently being performed to continue addressing the mechanism by which Lon391 contributes to the regulation of R391-mediated mutagenesis, particularly potential degradation of RumA or RumB by Lon391.

P20-U Role of DENN Domain-Containing Protein 5b (dennd5b) During Early Embryonic Development of Zebrafish *Khaled Mohamed Nassar [1], Alicia Mendoza [2], Magdalen Marston [2], Andre Gil [2], Sharmin Hasan [2] (1. Texas A&M International University, 2. Sam Houston State University)* Non-canonical Wnt signaling regulates cell polarity and morphogenetic movements through cytoskeletal rearrangements, with Dishevelled-associated activator of morphogenesis 1 (Daam1) acting as a key mediator. Overexpression or depletion of Daam1 disrupts gastrulation in Xenopus embryos and produces phenotypes characteristic of spina bifida. To further identify downstream effectors of Daam1, a yeast two-hybrid screen was performed, which identified DENN (Differentially Expressed in Normal versus Neoplastic cells) domain-containing protein 5 (*DENND5A*) as a binding partner. In zebrafish, two orthologues, *dennd5a* and *dennd5b*, are present; however, the developmental expression and function of *dennd5b* remain uncharacterized. Here, we report that zebrafish *dennd5b* shares 68.2% sequence similarity with human *DENND5B* and 68.6% with zebrafish *dennd5a*. Semi-quantitative

RT-PCR revealed maternal deposition of *dennd5b* transcripts at 0 hours post-fertilization (hpf), with expression persisting through gastrulation, somitogenesis, and into the larval stage. Spatial expression analysis by in situ hybridization showed ubiquitous distribution during cleavage and gastrulation, followed by restriction to the brain and neural tube during early somitogenesis, with brain-specific expression maintained throughout late embryogenesis and into larval stages. Functional perturbations of *dennd5b* using loss-of-function and gain-of-function approaches revealed compressed head and tail deformities and disrupted convergence and extension movements. These perturbations also impaired rhombomere patterning, neural plate morphology, somite organization, notochord integrity, and prechordal plate formation. Together, these findings establish *dennd5b* as essential for zebrafish embryogenesis, particularly in neural development, and highlight its conserved role downstream of Daam1 in non-canonical Wnt-mediated morphogenesis.

P21-U Discovery of potential novel inhibitors of Mycobacterium tuberculosis InhA (MtInhA) with virtual screening *Shriya Mukkavilli [1], Josh Beckham [1] (1. University of Texas at Austin)*
Tuberculosis (TB) is a disease that has killed millions throughout history and remains a major public health concern due to the rise of highly drug resistant strains. Countries with limited healthcare resources face the greatest morbidity and mortality from drug resistant TB. The causative agent, *Mycobacterium tuberculosis,* has a unique mycolic acid cell wall that allows the bacteria to escape immune system detection. The enoyl acyl carrier protein (ACP) reductase InhA (MtInhA) contributes to the construction of mycolic acid cell wall by synthesizing a precursor lipid. We aim to discover small molecules that can bind to the InhA enzyme and inhibit it at the NAD pocket of the active site. In order to identify potential inhibitors, we took the crystallography model of MtInhA from the Protein Data Bank (PDB: 4TRN) and used it for screening predictions with the docking software GOLD and ligand libraries. Compounds with scores above the original ligand score of 95 were utilized in biochemical assays. BL21 cells were used to express the protein via autoinduction from a pET based plasmid. The protein was then purified with nickel-NTA affinity chromatography and analyzed via SDS-PAGE for an apparent molecular weight of 29.49 kDa. Then, Differential Scanning Fluorimetry (DSF) thermal binding assay determined the melting point as 62°C. A binding assay carried out with one top compound (score = 98.53) indicates potential destabilization of the protein from this compound. Our methodology utilized the synergy of wet lab and computational analysis to efficiently discover novel inhibitors of MtinhA.

P22-U Novel DKNR Compounds Inhibit Proliferation in Triple-Negative Breast Cancer Cell Line *Ashley Espinoza [1] (1. The University of Houston-Downtown)*
Triple-negative breast cancer (TNBC) is one of the most aggressive and hardest to treat types of breast cancer, creating a strong need for new compounds that may help target it. In this study, we screened a newly synthesized series of DKNR compounds developed in collaboration with chemists in India against the TNBC cell line MDA-MD-231 using an MTT viability assay. Cells were treated with 20 μM of each compound for 24 hours, and percent cell survival was calculated relative to the PBS negative control to determine overall viability. Across the DKNR series, several compounds showed measurable reductions in cell viability when compared to the control. Among them, DKNR9 and DKNR10 consistently appeared as the most active members, lowering cell survival to approximately 53–56% across replicates. DKNR11 also demonstrated noticeable activity, reducing survival to roughly 60–70%. The remaining compounds in the series showed viability levels similar to the negative control, indicating low or no activity at the tested concentration.DKNR9 and DKNR10 emerged as the strongest candidates within the series, showing the most consistent and meaningful reductions in cell survival. These results suggest that certain DKNR structures may have potential for further exploration and optimization. Overall, these findings provide an early experimental foundation for continued development of DKNR-based scaffolds that may be useful in future efforts to target highly aggressive TNBC cells.

P23-H Validating the Specificity of Novel Primers for a Biofilm Study *Shijay Sivakumar [1], Athenia Oldham [1] (1. Odessa High School)* Biofilm formation: the resulting aggregate of bacteria, and quorum sensing: the communication process used in bacteria, are both essential to the survival of microbes. Such microbes, as seen in the environment in a ballast tank, change frequently, and thus coordination between group behaviors increases survival in a hostile or rapidly changing environment. It is inferred that from these naval ballast samples, both processes are inherent; however, empirical evidence for the presence of these processes in marine bacteria is in question. Here, we show that primers are specific for targeting genes, as tested using the bacterial strain P. aeruginosa. Using three different polymerase chain reactions (PCR) with the three novel primer sets targeting the algU, lasR, and clpP genes. These three genes were found to be present in the genomes of several isolated naval-ballast bacterial strains and are pivotal for biofilm formation, while lasR is specific to quorum sensing. Clear bands were observed at their expected sizes, indicating that the primers were sufficient and specific to their gene targets. Our results show how certain genes of these two bacterial processes are likely to function, and likely result in the ability for primers to be used on future bacterial isolates. Next, we anticipate validating the sequencing data by testing out the three primers on three of the genomically assembled and annotated bacterial isolates, to substantiate the existence of each process in marine bacteria.

P24-U Formin Binding Protein 1l (fnbp1l) plays an important role during early embryonic development of zebrafish (Danio rerio) *Ty Franklin [1], Michael La Fontaine [1], Alicia Mendoza [1], Sharmin Hasan [1] (1. Sam Houston State University)* The non-canonical Wnt signaling pathway is critical for vertebrate gastrulation and neural tube closure, with the formin protein Dishevelled-associated activator of morphogenesis 1 (DAAM1) acting as a central mediator of cytoskeletal rearrangements. However, the downstream effectors that link DAAM1 to actin regulation remain incompletely defined. In a screen for DAAM1interacting proteins, we identified Formin-binding protein 1 (FNBP1), a highly conserved regulator of actin dynamics, sharing >90% sequence similarity across humans, Xenopus, mice, and zebrafish (Danio rerio). Zebrafish possess three orthologues of human FNBP1, fnbp1a, fnbp1b, and fnbp1-like (fnbp1l), yet their developmental roles have remained unexplored. Expression analyses revealed that fnbp1a and fnbp1b are not expressed from 0 hours post-fertilization (hpf) through hatching (48 hpf). By contrast, fnbp1l transcripts are maternally deposited and persist from 0 hpf through gastrulation, somitogenesis, and into the larval stage. Spatial analysis demonstrated ubiquitous fnbp1l expression during cleavage and gastrulation, followed by restriction to the brain during early somitogenesis, with brain-specific expression maintained throughout late embryogenesis. Functional assays using CRISPR/Cas9-mediated knockout and mRNA overexpression revealed that fnbp1l disruption produces characteristic developmental phenotypes, including compressed head structures, consistent with impaired neural morphogenesis. Together, these findings identify fnbp1l as the sole embryonic fnbp1 paralogue expressed during early zebrafish development and establish its essential role in neural development. Our results highlight fnbp1l as a conserved downstream effector of DAAM1 in non-canonical Wnt-mediated morphogenesis. Future studies will define the biochemical interaction between DAAM1 and FNBP1L and test genetic interactions with other Wnt pathway components.

P25-U CUDC-970 induces epigenetic reprogramming and AKT dephosphorylation in peripheral T-cell lymphoma *Braden Samples [1], Alex Rodmanac [1], Marco Maples [1], Sophia Myers [1], Adam Chaudhary [1], Mamta Gupta [1] (1. Stephen F. Austin State University)* Introduction: Peripheral T-cell lymphoma (PTCL) is a clinically heterogeneous and aggressive group of non-Hodgkin lymphomas, representing 10%–15% of all cases. Recent therapeutic efforts emphasize targeting molecular and epigenetic vulnerabilities. Histone deacetylases (HDACs) and phosphatidylinositol 3-kinase (PI3K) signaling pathways are well-established contributors to hematologic malignancies. CUDC-970 is a novel dual-acting small molecule designed to inhibit both HDAC and PI3K activities. This study investigated the therapeutic potential and mechanistic effects of CUDC-970 in multiple human PTCL cell lines. Methods: PTCL cell lines (SR-786, Karpas299, SUDHL1, Hut-78, H9, and HH) were cultured under standard conditions in complete RPMI. Cell proliferation and viability were assessed using MTT assays and Annexin V/propidium iodide staining, respectively. Histone acetylation and protein phosphorylation were evaluated via western blotting with target-specific antibodies. Results: CUDC-970 (10–500 nM) significantly suppressed proliferation of all PTCL cell lines in a dose-dependent manner after 72 hours ($p < 0.0001$). Cell survival was markedly reduced, with an approximate LD50 of 100 nM ($p < 0.001$). Mechanistically, CUDC-970 increased acetylation of histone H3 at lysine 27 and lysine 14, consistent with HDAC inhibition. In parallel, the drug strongly suppressed PI3K pathway signaling, causing dose-dependent dephosphorylation of AKT at Ser473 and Thr308. These findings confirm potent dual-pathway inhibition. Summary: Our study demonstrates that CUDC-970 exerts strong antitumor activity in PTCL through simultaneous targeting of HDAC-mediated epigenetic regulation and PI3K-AKT signaling. Dual-pathway inhibition may offer a promising therapeutic strategy for PTCL as a single-agent approach.

P26-U Requirement of Hippo signaling for larval crawling muscle development in Drosophila. *Kevin Hernandez [1] (1. Sam Houston State University)* Skeletal muscle development requires precise regulation of gene expression to ensure proper tissue growth, organization, and function. Conserved signaling pathways coordinate this process, and disruption of these systems can result in developmental abnormalities. The Hippo signaling pathway is a regulator of transcriptional activity and tissue growth, yet its role in skeletal muscle development remains poorly understood. Diseases like cancer cachexia are associated with severe muscle wasting, and the early molecular events contributing to muscle deterioration are unclear. Examining the genetic regulation of muscle development may provide insight into mechanisms relevant to muscle disease. Traditional mouse models are widely used to study muscle disorders, however, these systems offer limited resolution of early developmental defects, creating the need for alternative genetic models. Fruit fly larvae provide an effective system to study muscle development due to their rapid development and conserved signaling pathways. The specific role of Hippo pathway components in larval muscle development has not been clearly defined. Disruption of Hippo signaling leads to abnormal larval muscle morphology and reduced tissue organization. Preliminary results indicate that the transcriptional co-factor Yorkie (Yki) is required for proper muscle development and that the transcription factor Scalloped (Sd) exhibits a repressive function in the absence of Yki. This supports a model in which Yki activates muscle gene expression through Sd, while Sd alone limits transcriptional activity during normal muscle development. These findings demonstrate that Hippo signaling is essential for larval crawling muscle formation and suggest that misregulation of conserved growth pathways may contribute to muscle pathology.

P27-G An Expressional and Functional Study of PDZ and Lim Domain Paralogs in Danio rerio *Andre Gil [1], Alicia Mendoza [1], Sharmin Hasan [1] (1. Sam Houston State University)* The non-canonical Wnt signaling pathway plays a critical role in regulating cell movement, morphology, and polarity during vertebrate development. Within this pathway, Dishevelled-associated activator of morphogenesis 1 (Daam1) mediates key interactions between Dishevelled and downstream cytoskeletal regulators. Among Daam1-interacting partners are the PDZ–LIM domain proteins, a family first characterized in 1995 through studies of cytoskeletal regulators in human and mouse muscle. Although PDZ-LIM paralogs have been described in *Homo sapiens*, *Mus musculus*, and *Xenopus tropicalis*, their roles in *Danio rerio* remain poorly understood. In this study, we investigated the developmental functions of *pdlim3a*, *pdlim3b*, and *pdlim4* in zebrafish using gain-of-function by mRNA overexpression and loss-of-function by CRISPR-Cas9 knockout approaches. Our results show that perturbation of *pdlim3b* resulted in consistent cardiac abnormalities, including pericardial edema and intracardiac blood pooling, accompanied by reduced heart rate and irregular cardiac contractions. These phenotypes reflect conserved roles for PDZ-LIM proteins in cardiac structure and function, consistent with findings from mouse models in which *Pdlim3* disruption contributes to cardiomyopathy. Together, our results highlight the importance of PDZ-LIM paralogs in early cardiac development and demonstrate that zebrafish provide a powerful system for dissecting the conserved molecular pathways underlying cardiac morphogenesis.

P28-U New Protocol for Genotyping Casper Zebrafish Mutants Using RT-PCR in a University Genetics Course *Pheben Abebe [1], Danielle Felice Galon [1], Joshua Brokaw [1] (1. Abilene Christian University)* The Casper zebrafish, defined by homozygous mutations in roy orbison (roy) and nacre (mitfa), provides a transparent model organism widely used in developmental biology and imaging research. However, straightforward, classroom-friendly molecular methods for distinguishing homozygous wild-type individuals from heterozygous carriers are limited. This project developed and validated a new RT-PCR-based genotyping protocol optimized for an undergraduate genetics laboratory. We designed primer sets flanking known lesion sites in roy and mitfa and incorporated melt-curve analysis to differentiate alleles based on sequence-dependent amplicon stability. Reaction conditions were refined for reliability using standard qPCR reagents and the Bio-Rad CFX96 platform. Students tested the protocol on crude genomic DNA lysates from zebrafish fin-clip samples and evaluated genotype calls using amplification curves, melting temperatures, and derivative plots. The protocol successfully distinguished wild-type, heterozygous, and homozygous mutant genotypes for both loci with clear and reproducible melt-peak separation. Implementation in a course setting demonstrated that students could complete the steps of the procedure within standard lab periods and interpret data accurately with minimal prior qPCR experience. This project establishes an accessible, cost-effective, and high-throughput strategy for teaching molecular genotyping while supporting research involving the Casper phenotype.

P29-U Screening Synthetic Compounds for Impact on Cell Viability of Pancreatic Cell Line *Vivian Do Nguyen [1], Tina Prajapti [1], Rachna Sadana [1] (1. University of Houston-Downtown)* Cancer is a type of disease characterized by rapid cell division that can invade nearby tissues and spread to other parts of the body through metastasis. Knowingly, pancreatic cancer is one of the most aggressive and therapy resistant cancers that presents a high risk in oncology. Because of lack of specificity of current chemotherapy drugs, these treatments damage both cancerous and healthy cells and have side effects. Goal of our research is to identify safer and more effective treatment options that primarily target cancer cells and reduce the risk of health complications. This study analyzes the cytotoxic effects of DKNR series compounds on the pancreatic cancer cell line named BXPC3. The compounds on DKNR 5,8,10, and 13 seem effective at reducing cell viability when tested using MTT cell proliferation assay, indicating potential to be an anti-cancer drug. Future studies will investigate the mechanism of how these select cytotoxic compounds cause cell death using biochemical caspase 3/7 activation assay and fluorescence microscopy assays.

P30-U Calibration matters: Refining protocols for reliable dose-response data *Noah Dyson [1] (1. Wayland Baptist University)*

The popularity of e-cigarettes has skyrocketed and continues to rise at an alarming rate, easily outpacing modern medical knowledge about their safety. Furthermore, there is not yet a comprehensive understanding of health consequences associated with e-cigarette use. Many of the common ingredients and flavorings used in modern vapes are currently under heavy scrutiny for health safety, particularly when inhaled, and diacetyl and other structurally similar diketones have already been strongly implicated as causative toxicants for cases of bronchiolitis obliterans (popcorn lung), a chronic lung disease. Standard toxicology studies rely on the MTT/MTS cell viability assays to collect data, but these methods are limited to singleplex functionality and only provide endpoint data. In contrast, the RealTime-Glo MT Cell Viability Assay™ generates continuous cell viability data and can be multiplexed. This study aims to optimize the RealTime-Glo MT Cell Viability Assay™ to create and examine the dose-response curves of e-liquid flavorings. A549 alveolar epithelial lung cells were selected to be the basis of our biological model and optimization of the assay has determined that 1250 cells per well in a 96 well plate produces a linear increase in luminescence over a 72-hour time-period. Additional optimization of our Cytation-1 microplate reader functionalities allowed us to collect images and perform cellular analysis on the plated cells to accurately estimate the total cell count per well and normalize luminescence. This study will allow for the generation of future dose-response curves to be used for toxicological analysis of vaping flavorings.

P31-G Expression and Functional Analysis of MTSS2 Isoforms (mtss1la/mtss1lb) During Early Embryonic Development in Zebrafish *Danielle Duncan [1], Braulio Sandoval [1], Andre Gil [1], Samira Alam [1], Alicia Mendoza [1], Amira Manry [1], Sharmin Hasan [1] (1. Sam Houston State University)* MTSS2 (Metastasis Suppressor 2), also known as MTSS1L or ABBA, is an actin-binding protein that regulates cytoskeletal dynamics and membrane remodeling through its I-BAR and WH2 domains. MTSS2 coordinates neural progenitor cell division and morphogenesis by functioning in RhoA and Rac1 signaling pathways. Recent clinical studies have identified *MTSS2* mutations as causative for a neurodevelopmental disorder characterized by microcephaly, intellectual disability, seizures, and craniofacial abnormalities. However, the developmental mechanisms underlying these phenotypes remain poorly understood. Zebrafish possess two orthologs, *mtss1la* and *mtss1lb*, yet their expression patterns and functions during embryogenesis are uncharacterized. Here we show that zebrafish *mtss1la* shares 65% sequence similarity with human *MTSS2* and 85% with zebrafish *mtss1lb*. RT-PCR revealed temporal expression of both paralogs from 0 to 48 hours post-fertilization (hpf), with expression persisting through gastrulation and somitogenesis. Functional analysis using CRISPR-Cas9-mediated gene disruption revealed that loss of *mtss1la* affected notochord formation and pigmentation, locomotor behavior, and brain morphology in developing embryos. These findings demonstrate the essential roles of *mtss1l* orthologs in zebrafish neural and structural development and establish a model for investigating molecular mechanisms underlying MTSS2-related neurodevelopmental disorders in humans, potentially identifying therapeutic targets for clinical intervention.

P32-U Evaluating Synthetic Compounds for Inhibition of Cell Proliferation in Lung Cancer Cell Line *Huriel Bautista [1], Rachna Sadana [1], Tina Prajapati [1] (1. University of Houston-Downtown)*
The traditional chemotherapy treatments/drugs often lack specificity and cause significant toxicity which results in side effects such as nausea, hair loss, neuropathic pain and this highlights the urgent need for new therapeutic options. Cancer cells proliferate uncontrollably because of mutations in cell-cycle regulation, which makes developing effective treatments. To explore potential chemotherapy treatments our lab tests newly synthesized compounds that are developed by our collaborators in India. This study focuses on DKNR Series. We analyzed thirteen synthetic compounds on lung cancer cell line (A549) using a colorimetric MTT Proliferation Assay, and found that DKNR 8, DKNR 10, and DNKR 13 reduced cell viability by over 50% when tested at 20µM concentration. Currently we are working on determining IC_{50} of these 3 compounds and future studies will look into mechanism of cell death (apoptosis or necrosis) caused of these compounds and expression levels of pro- and anti-apoptotic genes.

P33-G The protective role of oncomodulin from stress induced mitochondrial damage in auditory cells *Janith Halpage [1], Santha Ranganathan [1], Dwayne Simmons [1] (1. Baylor University)*
Progressive hearing loss is driven by increased oxidative stress, disrupted calcium homeostasis, and impaired mitochondrial function. Recent studies suggest that the calcium binding protein, oncomodulin (OCM), may protect against progressive hearing loss associated with either aging or noise damage. To investigate the potential of OCM under oxidative stress, we employed HEI-OC1 auditory cells as an in vitro model for studying cochlear pathology. Cells transfected with OCM were exposed to 1 mM H_2O_2, and we assessed viability, calcium signaling, apoptotic markers, and mitochondrial morphology. OCM expression significantly improved cell viability at early stress (2 h) but not at late-stage exposure (4 h), indicating a time-limited protective window. OCM-transfected cells exhibited reduced cytosolic Ca^{2+} accumulation, suggesting enhanced buffering and maintenance of calcium homeostasis. Correspondingly, OCM decreased expression of antioxidant enzyme SOD2 and suppressed mitochondrial Cytochrome C, supporting a reduction in mitochondrial oxidative damage and attenuation of intrinsic apoptotic signaling. Mitochondrial dynamics revealed increased mitochondrial number, decreased mitochondrial volume, and enhanced branching, consistent with elevated mitochondrial fission. Together, these findings suggest that OCM delays oxidative stress induced cytotoxicity in auditory cells by modulating calcium homeostasis, reducing ROS-associated signaling, and promoting mitochondrial quality control. OCM's early protective effects highlight its potential relevance for mitigating cellular damage associated with noise-induced and age-related hearing loss.

P34-U Dimethyl Terephthalate Effects on Adipogenesis in an OP9 Cell Model *Gustavo Zamora[1], Klarissa Martinez[1], Jennifer Heitmeyer[1], Danielle Grove[1] (1. Texas Lutheran University)*
The frequent usage of plastic products has sparked a growing health concern, specifically regarding plasticizers with endocrine-disrupting chemicals (EDCs). EDCs are a concern because of their relation to obesity and other hormonal imbalances. EDCs emulate the body's hormones. Exposure can be through direct contact, ingestion, and even inhalation. Phthalates comprise a family of EDC's and scientific research has shown exposure to phthalates may promote adipogenesis and interfere with metabolism. Dimethyl terephthalate (DMT) is a type of phthalate primarily used in manufacturing food and drink containers such as polyethylene terephthalate (PET) bottles. Due to the chemical structure of DMT, it may be released into the environment. However, the specific effects of DMT are unknown. In this study, the effects of DMT on adipogenesis and lipid accumulation were studied using a mouse OP9 cell model. The OP9 cells were treated with varying doses of DMT ranging from 0.0001nM up to 100nM. The cells were grown for four days, then treated and allowed to differentiate for 72 hours. After differentiating, DMT-treated cells were compared to cells treated with 0nM DMT as a negative control and 10nM rosiglitazone as a positive control. Within these two assays, interesting results were observed, supported by Oil Red O staining. Many concentrations showed a lower fold change than the control, except for concentrations ranging from 0.1nM to 10nM in assay 2. Overall, DMT may disrupt adipogenesis, highlighting the need for further research on manufactured items containing this chemical, such as PET plastics.

P35-U Post-translational Regulation of the MucA′$_2$B Error-Prone DNA Polymerase *Paige Djurdjevic[1], Martín González[1] (1. Southwestern University)* The bacterial SOS response occurs when environmental stressors cause DNA damage. In the event of severe DNA damage, the error-prone DNA polymerase V (DNA polV) is employed, which is mutagenic because of its low fidelity during DNA replication. An ortholog of DNA polV (UmuD′$_2$C) is encoded by the *mucAB* operon and is found on the naturally existing plasmid pKM101. Because this operon is on a plasmid and not part of the *Escherichia coli* chromosome, like the *umuDC* operon, it more readily transfers to other bacterial species via horizontal gene transfer, which has implications for bacterial adaptation like antibiotic resistance. While UmuDC is well-researched, the post-translational regulation of MucAB is less so. This study focused on the regulation of the MucA and MucA′ proteins, which play a role in the error-prone MucA′$_2$B multimer. The contributions to MucA and MucA′ cellular levels of the five *E. coli* ATP-dependent bacterial proteases were evaluated. The results suggest that the Lon and ClpXP proteases negatively affect the stability of both MucA and MucA′, and therefore play a role in regulating the MucA′$_2$B-mediated SOS mutagenic response. Interestingly, the MucA/A′ heterodimer complex is a much more stable pairing than the MucA′ homodimer, which differs from the unstable UmuD/D′ heterodimer which targets the UmuD′ protein for degradation. Future work will address the role of these proteases on MucB.

P36-U Troubleshooting GSK3β Purification and Optimizing Virtual Screening for Inhibitor Discovery *Xiya Chen[1], Saikrishna Gundlapalli[1], Josh Beckham[1] (1. University of Texas at Austin)*
This research focuses on improving the purification of the enzyme GSK3β and optimizing virtual screening methods to identify potential small-molecule inhibitors, supporting the discovery of stronger drug candidates for Alzheimer's disease. GSK3β is a central component of signaling pathways regulating cell fate, protein synthesis, metabolism, mobility, proliferation, and survival, and human GSK3β is particularly relevant to Alzheimer's disease because its abnormal activation drives tau hyperphosphorylation and neurofibrillary tangle formation. While virtual screening predicts potential GSK3β inhibitors, experimental validation requires a purified, stable protein with only its GST tag to test top docking-pose ligands. However, the protein often degrades, is partially lost, or has compromised tags, limiting downstream assays and slowing drug-discovery progress. Multiple strategies for troubleshooting GSK3β purification and identifying top ligands through virtual screening were explored. The virtual screening revealed a promising ligand, but many high-scoring candidates failed Lipinski's Rule of Five and had logP values above 3.5, indicating drug-likeness concerns. In the wet lab, GSK3β colonies rapidly died even at 4 °C, and gravity- or column-based purification outperformed centrifuge-based approaches. These findings refine both computational and experimental strategies for successful GSK3β characterization and highlight broader challenges in early drug-discovery pipelines, where strong computational hits may not meet medicinal-chemistry criteria and protein behavior can diverge from expectations. The combined strategies provide a foundation for more effective early-stage drug discovery and offer a framework to guide biochemical research and therapeutic development for Alzheimer's disease.

P37-U The Adipogenic Effects of Butylparaben on OP9 Mouse Cells *Natalie Osina[1], Caitlin Roach[1], Jennifer Heitmeyer[1], Danielle Grove[1] (1. Texas Lutheran University)* The presence of preservatives in everyday products, including the majority of personal care products, has been unavoidable for decades. Health concerns associated with these preservatives, specifically parabens, had been ignored despite their widespread use and human exposure. However, recent expansion in understanding endocrine disruptors has prompted research into endocrine disrupting effects of parabens. A concerning impact of endocrine disruptors is their contribution to obesity, an overaccumulation of fat in the body. Parabens have been discovered to promote adipogenesis but require additional research. Butylparaben is a specific paraben which is one of the most used preservatives in cosmetics, lotions, and shampoos. Butylparaben has been suggested to promote more adipogenesis than other parabens due to its structure. Furthering research of its adipogenic effects, OP9 mouse cells were treated with varying doses of butylparaben and monitored for lipid accumulation in these cellular assays. Each assay lasted seventy-two hours. Assays consisted of a negative control, a positive control (rosiglitazone), and seven different concentrations of butylparaben: 0.1nM, 1nM, 10nM, 100nM, 1000nM, 10000nM, and100000nM. Cells were assessed for lipid accumulation with an Oil Red O staining assay that included quantification with ultraviolet-visible spectroscopy. Three assays consistently showed increased lipid accumulation at each concentration in comparison to the control, although not as high lipid accumulation as in the positive control with rosiglitazone. Due to time constraints dictating this study, continuation of these assays and similar research are still required to better understand the effects of butylparaben on obesity.

P38-U Effects of p-Phthalate Dimethyl Terephthalate on OP9 Mouse Mesenchymal Stem Cells *Klarissa Martinez [1], Gustavo Zamora [1], Jennifer Heitmeyer [1], Danielle Grove [1] (1. Texas Lutheran University)* Endocrine disrupting chemicals (EDCs) are toxic chemicals that obstruct the normal functioning of the endocrine system. Phthalates, bisphenols, perfluoroalkyl substances, dioxins, and parabens are all different classes of EDCs that are encountered in everyday products. Most EDCs are known obesogens that affect metabolic pathways influencing fat storage through the differentiation of stem cells into adipocytes (fat cells). Obesity is a significant health concern globally with the World Obesity Atlas 2025 revealing that obesity rates will increase 110% from 2010 to 2030. One way to help decrease the obesity rate is to limit exposure to known obesogens and investigate unknown obesogens. Previous studies have shown that phthalates do have obesogenic properties. However, dimethyl terephthalate (DMT) is a phthalate and suspected obesogen used in the production of PET plastics to slow the rate of crystallization to allow for thicker and more sturdy sheets of plastics. Here we demonstrate a 72-hour assay of different concentrations of DMT ranging from 0.0001 nM to 100 nM tested on OP9 mouse mesenchymal stem cells to determine if low doses of DMT exhibit obesogenic properties. We found most of the DMT dosages resulted in lipid accumulations below that accumulated by negative control and nowhere near the level accumulated by the positive control, 10 nM Rosiglitazone, a banned obesogen. Our results may indicate that DMT inhibits adipogenesis. We anticipate DMT to be further investigated at different dosages and different assay time periods considering DMT is in PET plastics that are found everywhere.

P39-U OP9 Mouse Stem Cell Differentiation When Treated With Two Specific Types of PFHxS (PFAS) *Ryan Trevino [1], Nicole Bloodgood [1], Jennifer Heitmeyer [1], Danielle Grove [1] (1. Texas Lutheran University)* Endocrine disrupting chemicals (EDC) affect homeostasis or hormone production in the body. These chemicals can be found worldwide, even in products used in everyday life; most commonly in non-stick cookware, firefighting foam, drinking water, and food packaging. These chemicals are dangerous because of their many health effects, including obesity, and pervasiveness across many products; the focus of this study was on obesity and was conducted using different concentrations of two variants of PFHxS on mouse OP9 mesenchymal stem cells. This research aimed to support previous research using mouse 3T3-IL cells. Cells were plated in 6-well assay dishes, treated, and then differentiated for 3 days (72 hours). Concentrations of PFHxS used were 0.01nM, 0.1nM, 1 nM, 10nM, 100nM, 1,000nM, and 10,000nM for 7 total dilutions in differentiating media with insulin, IBMX, and dexamethasone. Negative and positive controls were included. The treatments were placed in 6-well assay plates and added to the cells in duplicate wells. They were in treatment for 72 hours. Cells were then stained with Oil Red O; lipid accumulation was quantified by UV-Vis spectrophotometry. Results for the two types of PFHxS were slightly different in adipose generation. Both had a bimodal trend; 0.01nM and 100nM being the most effective in lipid accumulation for Assay 1. The most effective doses in Assay 2 were 10nM and 10,000nM. In the end, this study suggests PFHxS promotes adipogenesis in OP9 cells, but further research is required to better understand the underlying mechanisms.

P40-U Microbiological Determination of Folate in Fermented Asparagus Using HPLC *Sanjana Rachala [1] (1. Texas A&M University)* Folate is an essential B-vitamin that supports DNA synthesis, methylation, and cell division, making adequate intake especially critical during pregnancy and fetal development. Many regions, however, remain underserved by folic acid fortification and supplementation programs; the need for accessible food-based folate sources is widespread globally. This study investigates kimchi-style fermentation of skin-on *Asparagus officinalis* as a potential functional food strategy to enhance naturally occurring folate. Fresh asparagus spears with skins intact were fermented for four weeks in a brine composed of water, salt, sugar, garlic, and chopped green onion under controlled conditions. Brine and vegetable samples were collected at defined timepoints throughout fermentation, stabilized to protect folate vitamers, and analyzed for folate content using a high-performance liquid chromatography (HPLC) method, enabling specific quantification of individual folate forms. Parallel measurements of pH and microbial growth will be conducted to track lactic acid fermentation progress and relate folate changes to microbial activity. It is anticipated that folate concentrations will increase over time as lactic acid bacteria synthesize and release folate into the fermenting matrix, demonstrating that skin-on asparagus kimchi can serve as a promising folate-rich functional food. These findings aim to support the development of low-cost, culturally adaptable fermented vegetable products to help address folate insufficiency in populations with limited access to fortified foods and supplements.

P41-U Differential Gene Expression in Human Bronchial Cells after Exposure to 3D-printer Emitted Aerosols *Dominic Pruss [1], Mahmud Shojiv [1], Taylor Jefferis [1], Jon Beard [1], Charli Worth [1], Joseph Taube [1], Mary Lauren Benton [1], Christie Sayes [1] (1. Baylor University)* The use of 3D printers, particularly fused filament fabrication (FFF) printers, has increased in residential, educational, and occupational spaces. These printers emit aerosols, including particulate matter and volatile organic compounds, which may cause toxic effects in humans when inhaled. The health effects after exposure have not been adequately characterized. This study analyzes RNA-sequenced data from an FFF printer exposed to a BEAS-2B lung cell model for five different filament types: black-colored acrylonitrile butadiene styrene (ABS), transparent ABS, blue-colored polylactic acid (PLA), transparent PLA, and a mixed steel-and-polymer. Differential gene expression (DEGs) and protein-protein interactions (PPIs) were compared at 1 and 4 hours of exposure. There was significant variability in the numbers and identities of DEGs and PPIs among the different exposure groups. The highest number of DEGs and PPIs was observed in the 4-hour exposure to the transparent PLA (401 DEGs and 474 PPIs), and the smallest number of DEGs was observed in the 1-hour exposure to the steel filament (12 DEGs and 0 PPIs). Only a few perturbed genes were common across exposure groups, possibly indicating distinct mechanisms of action induced by each aerosol exposure. This research emphasizes the need for further investigation into the underlying mechanisms of 3D-printer emission-induced toxicity.

P42-U Assessing the Adipogenic Effects of 1H,1H,2H,2H-PFHxS and PFHxS Using the OP9 Mouse Cell Line *Nicole Bloodgood [1], Ryan Trevino [1], Jennifer Heitmeyer [1], Danielle Grove [1] (1. Texas Lutheran University)* Global obesity rates have risen dramatically, leading researchers to consider how the environment/human practices lead to this health outcome, rather than caloric expenditure or diet alone. The NIEHS defines endocrine disrupting chemicals (EDCs) as “natural or man-made chemicals that may mimic or interfere with the body’s hormones.” EDCs are being explored as contributors to this problem, with the current study investigating the role of per-/poly-fluoroalkyl substances (PFAS) as “obesogens.” PFAS are used in grease-/water-resistant items, such as non-stick cookware and firefighting foams, and are omnipresent in the environment. We explored the extent to which two specific and similar PFAS give rise to adipogenesis (formation of fat cells). OP9 cells were treated with 1H,1H,2H,2H-perfluorohexanessulfonic acid and perfluorohexane-1-sulfonic acid (PFHxS) at concentrations of 0.01nM-10000nM, using 10nM rosiglitazone as a positive control. Two assays per chemical were performed, with Oil Red O staining and UV-Vis spectroscopy used to quantify lipid concentrations 72 hours post-treatment. 1H,1H,2H,2H-PFHxS demonstrated increased lipid accumulation compared to an untreated negative control at all concentrations, and was more effective than the positive control at 0.01nM-100nM (greatest effect at 0.01nM). PFHxS demonstrated increased lipid accumulation compared to the negative control at every concentration except for 10000nM, and was more effective than the positive control at 0.01nM, 1nM, and 100nM (greatest effect at 100nM). These trends suggest that their different structures (i.e., fully fluorinated carbon chain of PFHxS compared to four fluorinated carbon chains of 1H,1H,2H,2H-PFHxS) influenced treatment effectiveness, though both short-chain PFAS promoted adipogenesis at these low doses.

P43-G Visualizing Non-Centrosomal Microtubule-Organizing Centers in Drosophila Muscle Using Fluorescent Tools *Cody Griffin [1], Mardelle Atkins [1] (1. Sam Houston State University)*
The overall biology and function of microtubules (MTs) are well characterized across many model organisms, including their roles in cellular structure, transport, and signaling. In muscle cells, the non-centrosomal microtubule networks play central roles in maintaining cell structure and transport. This network is anchored to organelles, including the endoplasmic reticulum (ER) and the Golgi Complex (GC), at sites known as non-centrosomal microtubule-organizing centers (ncMTOCs). These ncMTOCs are essential nucleation sites for the MTs; however, the network is also required for organelle positioning, creating a potential feedback loop. Despite their importance for muscle homeostasis and development, the function and regulation of ncMTOCs are poorly defined. *Drosophila* larval muscles are large and easily accessible cells that can assist in visualizing ncMTOC assembly and dynamics. Yet, *Drosophila melanogaster* remains relatively underexplored as a system for studying microtubule dynamics and associated complexes, especially in larval muscle tissues. To address these gaps, this project aims to present fluorescent reagents to visualize regulators of the MT cytoskeleton and ncMTOCs, in addition to using markers of the GC and ER to assess if they function as ncMTOCs in *Drosophila* larval muscle, which is currently unknown.

These efforts will not only show the biology of microtubule organization in healthy *Drosophila* muscles but also provide a toolkit for studying these processes in our *Drosophila* tumor model, laying the foundation for future work in our lab on the regulation of ncMTOCs.

P44-U The microtubule network is altered prior to cachexic wasting in a Drosophila larval model *Chrislynn Harris [1], Mardelle Atkins [1] (1. Sam Houston State University)* Cachexia is a wasting disease that affects approximately 80% of cancer patients by causing muscle and fat loss, and unfortunately there are currently no effective treatments for it. *Drosophila melanogaster* larval and adult tumor models are an emerging platform for studying cellular changes that occur in cachexia. Previously, we observed that there are alterations in nuclear positioning and disorganization of sarcomeric proteins prior to the onset of muscle wasting in a larval model of tumor induced cachexia. It is known that nuclear positioning in muscles, organization, and trafficking of proteins to the sarcomere is heavily dependent on the microtubule (MT) network and the LINC complex. Therefore, we hypothesized that the MT network and LINC complex may be altered in pre-cachexic muscles. In tumor-bearing larvae, I observed decreased MT coverage of the fibers in pre-cachexic stages, but in fully cachexic stages, I observed robust MTs wrapping around the nuclei instead of interlocking with its surrounding networks. Surprisingly, these results reveal that the MT network responds differently in pre-cachexic and cachexic muscle. To examine the expression of the LINC complex, we selected Klarsicht (Klar) due to its involvement in nuclear positioning in striated muscle, where reduction of Klar results in defects. Surprisingly, we observed that Klar is strongly upregulated in pre-cachexic and cachexic muscle. Both results suggest that both the MT network and LINC complex are altered in both pre-cachexic and cachexic muscles meriting further exploration into both the MT network and the LINC complex, which we are currently testing.

P45-U Impact of azadiradione on DNA oxidation *Julia Jurewicz [1], Mariah Saenz [1], Mary Brintha Croos [1] (1. University of Mary Hardin-Baylor)* Oxidative stress causes significant damage to biomolecules such as proteins, lipids, and nucleic acids, contributing to cellular dysfunction and disease. It is also a major factor in the development of cancer and neurodegenerative disorders such as Alzheimer's and Parkinson's disease; therefore, understanding how oxidative stress affects these biomolecules is essential for identifying protective therapeutic strategies. This study evaluates the ability of azadiradione, a neem-derived compound, to reduce oxidative nucleic acid damage in *Escherichia coli*. Oxidative stress was induced using hydrogen peroxide (H_2O_2), and nucleic acid oxidation levels were quantified using an ELISA-based assay for DNA oxidative damage. Treatment of oxidized cells with azadiradione resulted in a measurable reduction in nucleic acid oxidation compared to stressed controls. These findings provide preliminary evidence that azadiradione exhibits antioxidant activity at the nucleic acid level and may serve as a potential natural compound for mitigating oxidative damage.

P46-U Improving temperature control for myoglobin oxidation kinetic studies *Eva Zohne [1], Nwankwo U. Dickson [1], Zechariah Hall [1], Destini Eidman [1], David E. Thompson [1] (1. Sam Houston State University)* Dimethyl trisulfide (DMTS) is a polysulfide compound proposed as a potential antidote for cyanide poisoning due to its ability to convert cyanide to thiocyanate through sulfur donation. Understanding how DMTS interacts with heme proteins such as myoglobin is important for evaluating its therapeutic potential. This work examines oxidation kinetics of myoglobin (Mb) in the presence and absence of DMTS across temperatures ranging from 25 to 42°C using UV-vis spectroscopy. Temperature fluctuations during initial experiments introduced uncertainty in measured rate constants. This poster presents the preliminary kinetic analysis with uncertainties and describes an improved experimental design using jacketed flasks with a recirculating temperature controller to enable tighter thermal regulation and determination of activation energy.

P47-U Discovering Novel Inhibitors for 3-Oxoacyl-(Acyl-Carrier-Protein) Reductase (FabG) in Plasmodium falciparum *Sam Vargas [1], Josh Beckham [1] (1. University of Texas at Austin)* Malaria, caused by the parasite *Plasmodium falciparum*, accounts for 600,000 deaths annually with a vast majority occurring in regions of Sub-Saharan Africa where antibiotic resistance has emerged. This development poses a major challenge in treating malaria as *P. falciparum* has developed resistance to most widely available treatments. This project aims to utilize both computational and experimental methods to discover novel inhibitors of the 3-oxoacyl-(ACP) reductase enzyme. This enzyme, which is an element of the type II fatty acid biosynthesis (FAS-II) pathway, is essential for parasite membrane formation. This pathway is critical for the survival of this parasite and presents a unique target for antimalarial drugs. A homologous structure containing coenzyme A was aligned to the PfFabG crystal structure 2c07 to define the binding pocket. This structure did not possess a ligand docked to active site, therefore the structure 5my0 was aligned with 2c07 to act as the ACP chain. This model was used for virtual screening of multiple compound libraries including ChemBridge. Virtual screening was performed by molecular-docking using the GOLD software program. Two high-scoring compounds were ordered and will be subject to differential scanning fluorimetry with the purified protein obtained from expression of BL21(DE3) competent cells. The protein was expressed through autoinduction, IPTG induction, and different competent cell types. The overexpressed protein was purified through Ni-NTA purification to a molecular weight of 27 kDa. These methods yielded impure samples and low yields, therefore, additional methods and previously described methods will be further utilized to obtain samples for future testing.

P48-U Comparing Dynamics of Fermentation and Probiotic Properties with American Kimchi *Justy Chung*[1]*, Jairus Wenzel*[1]*, Sehyeon Song*[1]*, Seockmo Ku*[1] *(1. Texas A&M University)*
Kimchi, a traditional Korean fermented food, has gained popularity within the United States; however, the capabilities of utilizing locally sourced ingredients in making kimchi are unknown. This study compared the fermentation parameters of two Texas-style kimchi styles, traditional (with Texas pepper powder) and white (no pepper powder added), prepared with locally sourced Napa cabbage and seasonings. Both kimchi types were salted, seasoned, and fermented at room temperature for 24 hours, then transferred to a fridge to ferment at 3°C. Samples were taken and analyzed over four weeks for their pH, titratable acidity, and lactic acid bacteria (LAB) counts through MRS and PCA plating. A 16s rRNA sequencing method was utilized to obtain data over specific bacterial strains. Results from both kimchi samples showed rapid pH decrease and increased acidity, with the spicy kimchi (containing Texas pepper powder) exhibiting lower pH and higher acidity throughout fermentation. LAB counts peaked early before declining with increased acidity, with higher counts also observed in the Texas kimchi. The findings indicated that spicy ingredients accelerated organic acid production and LAB growth as both kimchi types followed similar fermentation trends. The study displays the capabilities of Texas-grown ingredients in traditional kimchi fermentation, offering future opportunities in locally sourced probiotic foods.

P49-U Shifting Geometries: Octahedral Geometry and Electron Count Affect Electronic Communication *Jordan Ruppert*[1]*, John Gary*[1] *(1. Stephen F Austin State University)* Cooperativity between multiple redox sites is a strategy to utilize multiple cheap Earth-abundant metals to perform multi-electron chemistry when these metals often undergo one-electron redox radical reactions. Enzymes utilize metals, metal clusters, and amino acids in conjunction to perform these processes and the properties which allow for redox cooperativity are not well understood. In an effort to design new experimental model systems, computational chemistry is employed to understand the key design features. This poster will highlight how changing d-orbital electron count of the metal and the geometry at the metal can affect redox communication between sites. Specifically, how going from traditional square planar metal centers to octahedral change communication and allow for expanded possibilities in organic components. This expands the possibilities of future experimental systems which could be developed to perform this cooperative redox chemistry.

P50-U Biochar Production Through Microwave Pyrolysis: A Study of the Structure of Activated Carbon and Graphite Carbon. *Jemima Estrada*[1]*, Jessica Villarreal*[1] *(1. University of Texas Permian Basin)* Due to its low cost and efficiency, biomass has been used as the best method for the preparation of carbon-based materials through microwave pyrolysis. Activated carbon is a versatile material that can be used through a range of various applications such as green energy, water purification, and catalytic reactions. Its versatility comes from the strong electronegativity of the defected sites of the carbon mesh which makes it easy to attract positively charged atoms. While graphite is a great conductor of heat and electricity due to its unique physical structure. Consequently, graphite has been of high necessity for its various implementations in renewable energy and industrial applications. As such, the study aims to investigate the degree of graphitization as well as understand the differences in the structure of activated carbon and graphite carbon with two types of catalysts using microwave pyrolysis. Raman Spectroscopy was utilized to analyze the samples to determine both the degree of graphitization of graphite and the porosity and surface area of activated carbon for comparison in structure.

P51-U The Use of Microwave-Promoted Heating in an Undergraduate Organic Lab Activity: The Cannizzaro Reaction *Hayden Tolbert*[1]*, Russell Franks*[1] *(1. Stephen F. Austin State University)* The Cannizzaro reaction is a rare example of an organic disproportionation reaction, in which an aldehyde without enolizable alpha-protons is heated in alkaline medium to yield an alcohol and a carboxylic acid (after workup). This reaction is one that is commonly performed in undergraduate organic chemistry laboratories, but typically utilizing conventional heating sources, e.g. heating mantles. Since the reaction is performed in aqueous media, the Cannizzaro reaction is a good candidate for improvement using microwave heating. Microwave heating of organic reactions is more efficient, which allows reactions to be performed in a shorter amount of time and often with improved results. The purposes of this study are: (a) to explore the possibility of using microwave heating in a Cannizzaro reaction, (b) to explore the feasibility of using benchtop ^{1}H-NMR to analyze the reaction products, and (c) to develop and test a protocol for performing a Cannizzaro reaction in a multiple-batch reactor to be used with an undergraduate organic laboratory class. The purpose of these experiments was to produce the benzylic alcohol and benzoic acid products from *para*-chlorobenzaldehyde, *para*-nitrobenzaldehyde, *para*-anisaldehyde, and benzaldehyde. A Milestone SmartSynth laboratory microwave oven was used to heat reactions. A Magritek 60-MHz benchtop NMR spectrometer was used to analyze reaction products. Integration of the signal for the carbinol alpha-protons of the benzylic alcohol product was used for quantification. In single-batch reactions, aromatic aldehydes yielded results from 54 to >99 % conversion. Results from pilot studies using the multiple-batch reactor apparatus will be presented.

P52-U Exploring thermal selectivity for portable SERS-based methamphetamine detection in soil
Michaela Henson [1], Alicia Cortez [1], Samantha Martinez [1], Chizzy Obietikponah [1], David E. Thompson [1] (1. Sam Houston State University) Methamphetamine misuse continues to rise in the United States, driving demand for rapid, field-deployable detection tools. This research focuses on adapting a gas chromatography injection system for use in a portable device capable of detecting methamphetamine in soil. The injector includes a resistive heating cartridge interfaced with a proportional-integral-derivative (PID) temperature controller to enable precise thermal regulation. Controlled thermal ramping offers a key advantage: selective desorption of matrix interferents at lower temperatures before volatilizing methamphetamine at higher temperatures, improving detection specificity. This poster describes the system design, electrical interfacing of the heating and temperature sensing components, and the planned approach for thermal characterization.

P53-U Reflective Analysis of Inorganic Pigments
Clayton Engler [1], Holdin Price [1], Corey Thompson [1] (1. Texas Lutheran University) The Urban Heat Island (UHI) effect, characterized by elevated temperatures in urban regions compared to rural areas, poses a growing environmental and public health challenge. As the global population living in urban areas is projected to reach 6 billion by 2025, temperature deviations exceeding 12°C are reported in dense metropolitan regions. The need to develop sustainable, cost-effective cooling strategies has become increasingly urgent. This research investigates one of these strategies by altering building materials. We focused on the synthesis and characterization of inorganic near-infrared (NIR) reflecting pigments for application in cool paint coatings designed to reduce heat absorption from the sun's infrared rays. Our results demonstrate the viability of NIR-based inorganic pigment cool paints as a practical, sustainable approach to mitigating UHI effects. Here, we present the data from our experiments and optimization considerations to further enhance the cooling performance of our paints.

P54-U Pharmaceutical Contaminant Analysis in the Nacogdoches Wastewater Treatment Process using SPE-UHPLC-MS/MS
Brandon Lovell [1], Kefa Onchoke [1], Mike Ojemaye [1], Michael Janusa [1], Kadin Green [1], Jamie Humphries [1] (1. Stephen F. Austin State University) Pharmaceutical contaminants in municipal wastewater are recognized as persistent emerging environmental pollutants due to their biological activity and potential ecological risks at trace concentrations. Their resistance to conventional treatment motivates efforts to characterize compound-specific removal within wastewater treatment plants (WWTP) In this study, the fate of acetaminophen, fexofenadine, cetirizine, ketotifen, and pyridoxine across the treatment stages of the Nacogdoches Wastewater Treatment Plant to assess their behavior removal was examined. Triplicate samples collected from the influent, aeration basin, clarifier, chlorine contact chamber, and sulfur dioxide stages were pre-concentrated using SPE and quantified via UHPLC–MS/MS in positive-mode ESI. Removal efficiency of acetaminophen and pyridoxine 80% and 7%, respectively. In contrast, cetirizine and fexofenadine showed limited or no net reduction and instead demonstrated stage-to-stage variability consistent with strong persistence and possible desorption or re-formation from conjugated metabolites. Ketotifen, detected at low concentrations, displayed irregular fluctuations rather than a clear downward trend, reflecting its moderate stability and potential analytical variability. Collectively, these trends indicate that NWWTP effectively removes highly biodegradable pharmaceuticals but provides low removal for persistent antihistamines, which remain detectable through final discharge. This study highlights the compound-specific limitations of conventional treatment and underscores the need for targeted tertiary processes to address resistant pharmaceuticals in municipal effluents.

P55-U Thermally-controlled bypass valves for selective SERS detection of methamphetamine in soil
Samantha Martinez [1], Alicia Cortez [1], Michaela Henson [1], Chizzy Obietikponah [1], David E. Thompson [1] (1. Sam Houston State University) Clandestine methamphetamine laboratories generate significant quantities of harmful byproducts and waste, which are often dumped or buried, contaminating soil and water and posing environmental and public health risks. This has driven demand for on-site methods capable of detecting methamphetamine and its precursors in soil samples. However, the complexity of soil matrices presents analytical challenges, including contamination of sensing surfaces. This work describes the design, construction, and control of bypass valves for a SERS-based detection system aimed at minimizing substrate contamination. Temperature-triggered on/off controllers regulate valve position, directing sample vapor through a bypass path except within a temperature window corresponding to methamphetamine volatilization from soil. Within this target range, valves open to route vapor to the SERS substrate for detection. This approach is designed to enable selective concentration of methamphetamine onto the substrate while reducing interference from other matrix components. The system has been assembled and validated for mechanical function. Future work will focus

on determining the optimal temperature window and testing with soil samples.

P56-U GC-MS Analysis of Castor Oil *Anthony Ramos [1], Darrell Fry [1] (1. Stephen F Austin State University)* In this work, we quantitate the amount of various fatty acids in castor oil. Ricinoleic acid, is the most economically important fatty acid in castor oil; therefore, we will quantitate the amount of this acid. We employed a microwave-assisted transesterification (MAT) method developed, converting the fatty acids into their methyl ester derivatives. This modification lowers the boiling point of various fatty acids, enabling effective GC-MS analysis. The results confirmed that ricinoleic acid methyl ester was the predominant component, accounting for 80.% of the total peak area. A small amount of unreacted ricinoleic acid remained in its carboxylic acid form, suggesting that the MAT process could be further optimized. Potential sources of error include incomplete transesterification and residual byproducts from earlier steps. Future work should focus on improving the MAT protocol and selecting GC-MS column with a higher temperature maximum.

P57-U Fluorescent polarization is superior to BIOMOL® for measuring RecA binding affinity *Emma Scott [1], Robert Moore [1] (1. Wayland Baptist University) Mycobacterium tuberculosis* is an extremely widespread and dangerous disease that has become increasingly drug resistant. Previously, using chemiluminescent electrophoretic mobility shift assays (EMSAs), we observed that the DNA repair protein RecA binds more weakly to certain sequences that when mutated lead to drug resistance in comparison to sequences immediately before and after the codon of interest. These EMSAs were only semi-quantitative, low throughput, and could not reasonably be used to compare RecA binding of one mutation site to another. In this work, we evaluated two methods which could potentially be used for rapid characterization of RecA binding affinity to single-stranded DNA: a phosphate detection system using BIOMOL® Green and fluorescent polarization. The BIOMOL® reagent was sensitive to the ATP concentration in the assay, but showed no sensitivity to the presence of RecA. This makes this approach unsuitable for evaluating RecA-DNA interactions. Conversely, fluorescent polarization was 3-4 times greater when fluorescein-tagged DNA was incubated with RecA compared to free fluorescein-tagged DNA. Additionally, in the presence of ADP, polarization decreased. This suggests that ADP could serve as an inhibitor of nucleoprotein filament formation and thus useful in differentiating RecA binding strength to various DNA sequences. As such, we recognize fluorescent polarization could be a valuable quantitative tool in studying RecA binding affinity, substantially increasing workflow throughput over chemiluminescent EMSAs.

P58-U Analysis of contaminant metals in tampons and evidence for metal mobility *Sage Bartlett [1], Naomi Moody [1], Alison Bray [1] (1. Texas Lutheran University)* Women commonly use tampons to absorb menstrual fluids during their reproductive years. Given that tampons are inserted vaginally, understanding any potential contaminants, such as trace metals in tampons, is essential to their safe use. Shearston et al. (2024) found that 12 of 16 metals they studied were present in 100% of regular and super-absorption tampons. To confirm these results, in this study, 0.5-gram samples of the absorbent core from a variety of conventional and organic brand tampons were analyzed. The samples were acid digested and analyzed by ICP-MS to determine levels of arsenic, lead, cobalt, chromium, cadmium, selenium, and vanadium. In conventional tampon brands, multiple trace metals were detected; however, lead had the highest average concentration (197.0 ng/g) among the samples. In the organic brand samples, lead also had the highest average concentration (116 ng/g). To test the mobility of metals present in the tampons, three tampons from four conventional brands were soaked in 18 Mega-ohm water. The samples sat in a warm bath to simulate body temperature for 8 hours. The water was extracted from the tampons and analyzed for the previously stated metals. The results showed 100 percent of samples had detectable amounts of lead and chromium. Chromium also had the highest average concentration among the four brands. These results suggest that contaminant metals are not only present in tampons but, in some cases, appear to be mobile under simulated human body conditions.

P59-U Green Synthesis of a Cross-linked Polymerized Hydrogel Containing NDGA-Capped Gold Nanoparticles for Skin Lesion Treatment *Areej Khodair [1], Milka Montes [1] (1. University of Texas of the Permian Basin)* Masoprocol, also known as nordihydroguaiaretic acid, is an antineoplastic drug that inhibits skin growths and holds anti-inflammatory properties. Currently, methods for the development of skin treatment drugs that are ecofriendly, low cost, convenient and sustainable are imperative as the demand for such treatment increases. In this work, we aim to describe the synthesis of a cross-linked gold nanoparticle-polymer network, in the form of a protective hydrogel containing nordihydroguaiaretic acid (NDA), which can be extracted from the plant *Larrea tridentata*. The hydrogel was prepared using poly vinyl alcohol (PVA), which is an excellent polymer widely used for its biocompatibility in biomedical applications. NDA-capped gold nanoparticles were synthesized and incorporated into the hydrogel to produce a wound dressing. The results demonstrate that metallic gold nanoparticles can readily integrate into a cross-linked polymer and function as a drug delivery system for the topical treatment of skin lesions.

P60-U Pyranone Generation By Way of Substituted Oxetanes

Denali Rubio [1], Michael Ruane [1], Sheldon Peters [1] (1. Texas Lutheran University) Pyranones are oxygen-containing heterocyclic molecules found in numerous natural products and commonly used as building blocks for synthesizing more complex organic materials. Traditional pyranone syntheses often rely on strongly basic conditions, such as those used in aldol or Claisen-type condensations, which cyclize a linear chain to form the six-membered ring. This approach contrasts with the fundamentally different mechanism explored in the current project, which focuses on expanding the ring of a lactone using aldehydes and/or alcohols. In this project, a substituted lactone with dibenzyl titanocene to form an oxetane molecule. The oxetane can then be opened using a Lewis acid (boron trifluoride) in the presence of lithium bromide. The ring could then reform and expand using aldehydes to cyclize and form a substituted pyranone. Considering that chiral b-lactones have been generated via asymmetric synthesis, and stereochemistry has been controlled via intermediates, such as the Zimmerman-Traxler intermediate, considerable stereo-control can be exerted on four different carbons in a small number of steps. This method when successful will creates a more modular route for constructing complex pyranones using lactones as a precursor. More trials are necessary in order to fully assess the degree to which this process has succeeded.

P61-U Phytochemical Modulators of Cancer Metabolism: Docking Analysis of Flavonoid Interactions with 6-Phosphogluconate Dehydrogenase

Alicia Trejo [1], Thanh Tien Dao [1], Georgetta Zuo [1], Bidisha Sengupta [1] (1. Stephen F. Austin State University)
The pentose phosphate pathway (PPP) is essential for maintaining cellular health because it produces NADPH, a molecule required for growth, repair, and protection against oxidative stress. Within this pathway, the enzyme 6-phosphogluconate dehydrogenase (6PGD) catalyzes the formation of ribulose-5-phosphate while generating NADPH. Cancer cells often rely on elevated 6PGD activity to support rapid proliferation and maintain redox balance. However, the ability of naturally occurring phytochemicals to interact directly with 6PGD is not well understood. Here we examine whether selected flavonoids can bind to 6PGD and potentially influence its activity. Using computational docking, we show that four plant-derived compounds, naringenin (a flavanone), kaempferol (a flavanol), luteolin (a flavone), and daidzein (an isoflavone), bind favorably to the active site of human 6PGD. These ligands display predicted binding affinities comparable to or stronger than the natural substrate 6-phosphogluconate (6PG), suggesting competitive occupancy of the catalytic pocket. These findings add to existing knowledge by identifying specific flavonoids capable of directly engaging a key metabolic enzyme required for tumor survival. Because cancer cells depend heavily on NADPH to withstand oxidative stress and sustain anabolic growth, modulation of 6PGD activity represents a promising therapeutic strategy. This work establishes a computational foundation for future biochemical studies to test whether these phytochemicals can inhibit 6PGD and potentially contribute to targeting metabolic vulnerabilities in cancer.

P62-U Flavoring chelation properties influence the quantity of metals in vaping aerosols

Anna Perez [1], Clancy Collom [1], Gregory Smith [2] (1. Wayland Baptist University, 2. Angelo State University)
E-cigarettes have seen an increase in popularity over the last two decades, along with an awareness that e-cigarettes negatively affect user health. However, no clear mechanism of action has been proven to cause these health effects due to the large variability amongst vapes and e-liquids. E-cigarettes contain a metal coil that heats up to aerosolize e-liquids for inhalation by the user. Previous research has demonstrated the presence of metals in the parts-per-billion (ppb) range in e-cigarette emissions resulting from the leaching of metals from the coil into the e-liquid, but research correlating flavorings and metal intake is slim or nonexistent. Therefore, our project investigates two popular flavoring agents, vanillin and ethyl vanillin, that are analogous but differ by the length of their alkoxy group. Additionally, vanillin is a known chelator, whereas ethyl vanillin is not. Thus, we expect to see more metals from vanillin-containing aerosols than from aerosols with ethyl vanillin. To investigate metal aerosol content, lab-made e-liquids with varying vanillin or ethyl vanillin content were aerosolized with an e-cigarette, collected via simple distillation, and analyzed for metal content with inductively coupled optical emission spectroscopy (ICP-OES). The vanillin-containing aerosols had a higher observed nickel content than the samples with ethyl vanillin. Further studies are necessary to evaluate the significance of this difference and to determine if the decrease in aerosolized metals makes ethyl vanillin a safer flavoring. This study is the first step in establishing that known metal chelation of flavorings impacts the amount of metal exposure to e-cigarette users.

P63-U Investigation of Naturally Fluorescent Materials Using Fluorescent Microscopy

Ian Cortez [1] (1. Howard Payne University)
Microplastics (pieces of weather plastic less than 5 mm) were imaged under a fluorescent microscope utilizing the stain Nile Red. While this stain is commonly utilized in literature, its overall cost may make imaging too expensive for some laboratories. As such, stains extracted from plants and their fluorescent properties were investigated to determine whether they could adhere to microplastic plastic particles for imagining. Additionally, these stains have never been found in literature, and they were also investigated to see if they allow for imagining of cell structure. These stains were compared to

commercially available stains in their effectiveness to image both samples. The first plant extract allowed for the determination of both microplastics and cell presence; however exact interactions are inconclusive at this time. In comparison, the second plant extract did show some capabilities, but the overall quality was not very effective for making the microscopic plastic fluorescent.

P64-U Tuning Hydrogen Bonding for Designing Colorimetric Sensor for Heavy Metals *Andrew Do [1], Rashid Mia [1], Jack Weeks [1] (1. Stephen F. Austin State University)* A molecular cleft shaped ligand, aniosolbis(imine-hydroxyanisole) (ABIHA) has been designed and synthesized to enhance sensitivity for metal recognition via optical spectroscopy. Molecular cleft **ABIHA** was synthesized by coupling 3,4-diaminoanisole and 2-hydroxy-m-anisaldehyde in methanol. Incorporating imine moiety adjacent to phenolic hydroxyl group allows cleft shaped probe to form two new six-membered rings through resonance-assisted hydrogen bonding (RAHB). In contrast, the purpose of incorporating electron donating methoxy group (- OCH_3) in each benzene ring is to build up positive inductive effect on imine-N and phenolic-H atoms to destabilize (weaken) the hydrogen bonding so that a minute amount of metal can disrupt the RAHB and metals can easily coordinate to increase sensitivity. In DMSO, sensor solution produced a blue color with a shoulder at 280 nm and a broad absorption band at 350 nm and emission at 474 nm (λ_{ex} = 345 nm). Upon addition of CH_3COO^- anion, no optical response observed both in UV-vis and fluorescence, suggest that there is no hydrogen bonding between imine and phenolic group or RAHB is extremely weak. Upon the addition of various metals, Zn^{2+}, Cd^{2+}, Hg^{2+}, Co^{2+}, and Cu^{2+} ions show optical response, absorption spectra 280 and 350 nm disappeared by red-shifting to three major area 305-325 nm, 359-369 nm, and 406-439 nm. The emission spectra at 474 nm ratiometrically shifted to 435 nm for Zn^{2+}, to 383 nm for Hg^{2+}, to 494 nm for Cd^{2+} and quenched for Cu^{2+} and Co^{2+} ions due to metal ligand charge transfer (MLCT) and chelation quenched fluorescence (CHQF) mechanism.

P65-U Delta-8 or Delta-9? Testing the Truth Behind THC Gummies *Abby Henderson [1], Dennis Gibson [1] (1. Howard Payne University)* As cannabis-infused gummies grow in popularity, many are marketed as containing Delta-8 THC, a less potent and legal alternative to its CBD-derived counterpart, Delta-9 THC. This study examines THC gummies from a local smoke shop and an online retailer to determine the actual type of THC present, evaluate labeling accuracy, and explore Nuclear Magnetic Resonance (NMR) spectroscopy for a faster, one-pot testing method. Thin Layer Chromatography (TLC) confirmed THC presence in each sample, and NMR analysis identified chemical shifts consistent with Delta-8 THC. This one-pot reaction removes the need for various laboratory equipment and has an analysis time of 2.5–3 hours without disrupting accuracy. These findings suggest that our gummies contain Delta-8 THC, and that a streamlined, one-pot method is possible. This research could further support method development towards analyzing these materials for consumer safety amid a growing unregulated market.

P66-G Innovative and Timely Cell-Free Assays: A Novel Approach/ Methodology in Toxicity Testing *Sabrina Shahjabeen Alam [1], Christie Sayes [1], Amanda Charlton-Sevcik [1] (1. Baylor University)* New approach methodologies (NAMs) can enhance chemical safety assessments by providing biochemical models that do not rely on animal testing. Here, we have developed a rapid enzymatic activity model (REAM) that can be used as a cell-free screening tool to inexpensively and quickly elucidate the possible mechanisms of toxicity for environmentally relevant chemicals, such as pesticides. Using REAM, we have tested six commonly used pesticides- avermectin B1, atrazine, cypermethrin, cyantraniliprole, fipronil, and glyphosate. Each chemical is a growing environmental health concern due to its frequent use and potential exposure to humans and the environment. While most of them have been associated with neurotoxicity, the exact toxicological mechanisms remain unknown. We investigated two necessary neuronal enzymes: acetylcholinesterase (AChE) and butyrylcholinesterase (BChE). AChE is important for regulating neurotransmission, whereas BChE plays a crucial role in regulating acetylcholine levels in the brain and peripheral nervous system. Using REAM, we evaluated the effect of the pesticides at different concentrations (from 0.1 to 100 mM) on the activity of these enzymes. Statistical significance was analyzed using two-way ANOVA with pesticide type and concentration as factors, followed by Tukey's post-hoc test to compare group differences. At all tested concentrations, atrazine and glyphosate significantly inhibited AChE activity. For BChE activity, both pesticides showed significant reductions at higher concentrations, while they did not cause statistically significant inhibition at the lowest concentrations. The REAM model provides a novel, rapid, and humane alternative screening assay that can be extended to other toxicologically relevant enzymes involving environmental contaminants.

P67-U Utilizing Free Fatty Acids to Inhibit Bacteria in Eyedrops
Bethany Blair [1], Bailey Nobles [1] (1. Howard Payne University) Individuals who are affected by autoimmune diseases, such as Sjrogenssyndrome, must consistently use preservative-free eye lubricants because repeated exposure to preservatives could case eye deterioration. However, preservative-free eye drops are more expensive, have a shorter shelf life, and can become contaminated easily. In May of 2022, there was a strain of drug-resistant, gram-negative bacteria, pseudomonas

aeruginosa, that contaminated a brand of eye drops. Consequently, the FDA has recommended that 28 commonly-used eye drops should be avoided. In our research, four free fatty acids, Linoleic acid, Lauric acid Linolenic acid, and Palmitic acid were used as natural bacteria inhibitors in lieu of preservatives in eye drops. Their effectiveness was tested against staph (gram-positive) and E.coli (gram-negative) bacteria and yeast (gram-positive). So far, results have been inconclusive, as none of the concentrations are inhibiting the bacteria. The only true inhibiter is bleach, which is the control.

P68-U Investigating Various Deep Eutectic Solvent Solutions in Chitin Extraction *Addysage Seay [1], Dennis Gibson [1], Philips Agboola [1] (1. Howard Payne University)* Traditional chitin extraction from shrimp shells often relies on concentrated acids and bases, which pose environmental hazards and degrade the polymer's structural integrity. This study investigates natural deep eutectic solvents (NADES) as greener, milder alternatives. Shrimp shells, processed as whole and ground samples, were treated with four choline chloride-based NADES formulations using malic acid, lactic acid, and urea as hydrogen bond donors at a 1:2 molar ratio. These solvents were synthesized and applied under mild thermal conditions to facilitate demineralization and deproteinization. Fourier-transform infrared spectroscopy (FTIR) confirmed successful chitin extraction, while bomb calorimetry provided insights into thermal stability and energy content. Among the solvents tested, the urea-based NADES demonstrated superior performance, particularly with whole shells, yielding strong FTIR signals and favorable thermal properties indicative of minimal polymer degradation. The extracted chitin exhibited physicochemical characteristics comparable to commercial-grade chitin. FTIR results underscore the potential of NADES, especially malic acid mixtures, as sustainable and efficient alternatives for chitin extraction with structural preservation.

P69-U Virtual Screening–Driven Identification of Inhibitors Targeting MtFabG in Mycobacterium tuberculosis *Manal Saad [1], Mahdia Rahman [1], Sharon Rong [1], Josh Beckham [1] (1. University of Texas at Austin)* Tuberculosis (TB), caused by *Mycobacterium tuberculosis* (Mt), remains a leading cause of infectious disease mortality worldwide. The rise of multidrug-resistant TB highlights the urgent need for new therapeutic strategies. This project focuses on the enzyme 3-oxoacyl-ACP-reductase (MtFabG), an NADPH-dependent oxidoreductase that catalyzes the reduction of 3-oxoacyl-ACP to 3-hydroxyacyl-ACP in the fatty acid synthase II (FAS-II) pathway, a crucial step in the biosynthesis of mycolic acids. These mycolic acids help form the lipid-rich cell wall of M. tuberculosis, contributing to its impermeability, and antibiotic resistance of the bacterium. This NADPH binding site was defined as the active site for GOLD software docking.The crystal structure of MtFabG was obtained from Protein Data Bank (PDBI 3LLS) for use in structure-based virtual screening of over 100,000 compounds from the Maybridge HitFinder and in-house libraries. Molecular docking was performed using GOLD software to identify high-affinity ligands, which were prioritized based on docking scores and interactions within the NADPH-binding site. Experimental validation is ongoing through differential scanning fluorimetry (DSF) and spectrophotometric NADPH-consumption assays using Ni-NTA purified MtFabG expressed in E. coli BL21(DE3) cells via autoinduction with lactose and the T7 promoter in a pET plasmid.Ultimately, this work integrates computational and biochemical approaches to identify MtFabG inhibitors as potential antitubercular lead compounds. Targeting the FAS-II pathway provides a selective strategy for overcoming resistance and addressing the global TB drug-development gap.

P70-U PEG-BSA hydrogels: release and diffusion studies
Averi Felan [1], Jenna Slussler [1], Jacques Jean-Francois [1] (1. Texas Lutheran University) Hydrogels are biocompatible biomaterials made to interact with our living systems for diagnostic or therapeutic purposes. These hydrogels are formed with polymers of natural or synthetic origin to create a porous structure that allows for the diffusion and release of molecules. PEG-BSA hydrogels have two components: poly (ethylene glycol) (PEG), a synthetic polymer with good mechanical properties, and serum bovine albumin (BSA), a biocompatible natural polymer. The PEG-BSA hydrogel results from the chemical crosslinking between PEG and BSA and has a high-water content (more than 90%). To evaluate the impact of PEG architecture (PEG 2-arms, PEG 4-arms, PEG 8-arms) on the porosity of the hydrogel, release studies using quinine and diffusion studies using ovalbumin-FITC and dextran-FITC were conducted. Quinine release studies by fluorescence showed that hydrogels made of PEG 2-arms have the highest quinine release that plateau after an hour unlike the other hydrogels that plateau after forty minutes. Diffusion of ovalbumin (45kDa)-FITC and dextran (10kDa)-FITC were evaluated by confocal microscopy. Results showed a higher diffusion rate of the smaller molecular weight dextran-FITC in PEG 2-arms and PEG 4-arms hydrogels. These preliminary results highlight the importance of the pore sizes on the ability of our hydrogels to release molecules of different sizes.

P71-U Are FTIR and mass changes a good way to determine the degradation of plastics? *Kirstin Van Nostrand [1] (1. Schreiner University)* In this study, we investigated plastic degradation using FT-IR and mass comparison in order to determine time-based degradation of polyvinyl chloride and polyethylene in water. Samples were evaluated every 80 days over a period of 360 days, approximately a year. Samples remained submerged in

50.0+/-2.0°C water between sampling periods, while the control was stored at room temperature isolated from ultraviolet light exposure. FT-IR was used to monitor the potential chemical changes for both polyvinyl chloride and polyethylene. With data obtained from the FT-IR, we selected characteristic peaks for observation and calculated the percent change in absorbance between the different sampling periods (ie. 0-80day, 80-360day). Each of the 17 experimental sample masses was recorded, averaged, and compared to the control. Preliminary results indicate that chemical modification occurred based on individual IR peaks evaluated in sample spectra in both polyvinyl chloride and polyethylene. Mass comparison revealed that there was a directional decrease in mass observed in both polyvinyl chloride and polyethylene when compared to control over the same period. We aim to inform the public of the possibility of degradation of these high-use materials in waterways using this data. However, further investigation into this subject is required.

P72-U Redox-Sensitive GFP to Monitor the Impact of Carbon Monoxide on Cellular Redox Status in Saccharomyces cerevisiae
Jessica Villarreal[1], Nin Dingra[1] (1. University of Texas of the Permian Basin) Redox chemistry plays an essential role in numerous metabolic pathways. This study examines the impact of carbon monoxide on redox status in *Saccharomyces cerevisiae* using carbon monoxide releasing carboxyborane, CORCB-1, as a CO source. Redox-sensitive GFP protein was used to track the cellular oxidation state. Our results indicate that exposure to CO significantly influenced the redox balance of the yeast cells by shifting it to a more reduced condition. This study offers valuable insights into the role of CO in altering cellular redox balance. Understanding the impact of CO on cellular processes has broader implications for disease research and therapeutic applications, particularly in areas related to oxidative stress and redox signaling.

P73-U Discovering novel inhibitors of D-alanine D-alanine ligase in Yersinia pestis *Raina Patel[1], Mahitha Simhambhatla[1], Josh Beckham[1] (1. University of Texas at Austin)* The Plague, caused by Yersinia pestis, led to devastating epidemics in the 1300s and remains a public health concern due to its persistence in rural regions of the western United States, Africa, and Asia, and its capability as a bioterrorism agent. This project aims to identify new compounds that could treat Yersinia pestis infections by inhibiting D-alanine-D-alanine ligase (YpDalaDala), using small-molecule drug discovery strategies. YpDalaDala catalyzes the formation of D-alanyl-D-alanine for peptidoglycan synthesis and lacks human homologs, making it an ideal target. This project uses virtual screening and wet lab techniques to identify novel inhibitors of YpDalaDala. GOLD (Genetic Optimization for Ligand Docking) software and a YpDalaDala crystal structure (PDB ID: 5C1P) were used to screen 120,000+ compounds and identify those with high predicted binding affinity to the active site. Two high-scoring compounds that followed Lipinski's Rule of 5, ZINC14993443 and ZINC14741400, were selected. Functional protein for testing was created using a YpDalaDala expression plasmid that was transformed into E. coli BL21(DE3), expressed via autoinduction, purified using Ni-NTA affinity chromatography, and characterized with SDS-PAGE to verify protein identity and purity. A thermal melt assay using differential scanning fluorimetry (DSF) was conducted to assess denaturation and repeated with compounds to identify thermal shifts indicating binding. Enzyme assays will measure the function of the protein and its inhibition by the compounds. The results of this project will contribute to developing new treatments for Yersinia pestis, as current treatments target early stages of the disease, and antibiotic resistance remains a concern.

P74-U Foraging Responses of Hummingbirds to Nectar Concentration in an Andean Cloud Forest
Mercy Nnaeme[1], Andres Vasquez[2], Mark Brown[3], Joshua Banta[1] (1. University of Texas at Tyler, 2. Tropical Birding, 3. University of KwaZulu-Natal)
Variation in floral nectar concentration is thought to reflect selective pressures imposed by avian nectarivores, yet how hummingbirds allocate foraging time across nectar concentrations remains poorly resolved. We examined nectar concentration use by hummingbirds in a montane cloud forest of northwestern Ecuador using a simultaneous three-choice feeding experiment. Free-living birds were offered sucrose solutions at three concentrations (10%, 20%, and 30%) and allowed to forage freely among all options. Total visitation declined with increasing sugar concentration, whereas energetic intake rate ($\text{kJ g}^{-1}\text{ h}^{-1}$) increased sharply with concentration. This pattern is consistent with birds adjusting feeding duration in response to energetic reward, such that higher concentrations require less foraging time to achieve similar caloric intake. We discuss the implications of these results for hummingbird foraging behavior in Andean cloud forest communities and for selective pressures on nectar concentrations of hummingbird-pollinated flowers.

P75-U Comparison of Bird Species in Various Habitats in Weston Ranch *Natalie Garcia[1] (1. Texas Lutheran University)*
Our purpose was to evaluate the diversity of bird species at Weston Ranch during the 2025 summer breeding season, to expand on prior research conducted. Bird species were recorded using both visual and auditory observation techniques, including binoculars for sight identification and the Merlin Bird ID app to record songs and calls. To determine which birds were accurately present, we decided rare birds had to been seen to be counted. A total of 43 different bird species were recorded. Each of the five sites had 15 to 35 species. The

most commonly observed species were *Cardinalis cardinalis* (Northern Cardinal), *Mimus polyglottos* (Northern Mockingbird), *Passerina ciris* (Painted Bunting), *Thryomanes bewickii* (Bewick's Wren), which were found consistently across all sites, *Thryothorus ludovicianus* (Carolina Wren), *Dendrocygna autumnalis* (Black-bellied Whistling-Duck), *Tyrannus forficatus* (Scissor-tailed Flycatcher), *Coragyps artratus* (Black Vulture), *Molothrus ater* (Brown- headed Cowbird), and *Haemorhous* mexicanus (House Finch). We expected to observe a similar variety of species based on the previous year's checklist. The top three species (by occurrence) in both 2024 and 2025 were Northern Cardinals, Northern Mockingbird, and Painted Bunting, suggesting that the area supports a stable bird community during the summer breeding season in the area.

P76-G Investigating the Conservation Statuses of Native Texas Crayfish Species Through Distribution Analysis and Ecological Niche Modeling *Elizabeth Croft [1], Jared Dickson [1], Archis Grubh [2], Ryan Shartau [3], Joshua Banta [1] (1. University of Texas at Tyler, 2. Texas Parks and Wildlife, 3. Washington State University)* Crayfish have essential roles in ecosystems since they are ecosystem engineers and keystone species. However, crayfish species are threatened by degradation and loss of habitats, introduction of invasive species, and high levels of endemism. Unlike many other states, Texas provides no legal protections for *specific* crayfish species, despite its high diversity. This absence hinders targeted conservation efforts, such as designating critical habitat tailored to the ecological needs of vulnerable species. Crayfish are also understudied as compared to other taxa, and comprehensive distributional assessments are hard to find. This study plans to change that by creating distribution maps for all 52 crayfish in Texas using all available data from literature, field sampling, and citizen science. Once the distribution maps are established, ecological niche models using soil data, and current and future climate data will be created for certain crayfish species to determine current needs and future threats. This study will compare historical, present, and future distributions of crayfish species to see how they have or will change over time. The overall goal of this study is to clarify the conservation statuses of native Texas crayfish species and to better understand their distributions.

P77-G Aggregation and collation of Texas crayfish museum specimens to determine their current conservation statuses
Adrian Alvarez [1], Archis Grubh [2], Joshua Banta [1], Ryan Shartau [3] (1. University of Texas at Tyler, 2. Texas Parks and Wildlife, 3. Washington State University) Crayfish are macroinvertebrates that remain largely understudied in Texas despite their ecological significance. They account for over half of the macroinvertebrate biomass in many ecosystems and serve as crucial bioindicators because of their behavioral and physiological adaptability to environmental changes. Their presence in aquatic systems often signifies healthy water quality. Despite being home to approximately 52 native crayfish species, Texas currently lacks protective regulations for any of them. This gap mainly results from insufficient information about the distribution and occurrences of crayfish species in the state, including a lack of Species of Greatest Conservation Need (SGCN) statuses. This study will compile museum records of crayfish across Texas and compare them with more recent field survey data to address these knowledge gaps and recommend SGCN status updates. This document aims to provide a comprehensive starting point for researchers seeking background information on Texas crayfish and a foundation for future research.

P78-G Environmental tolerances and habitat association of three critically imperiled crayfish species in Texas *Andy Walker [1], Ryan Shartau [2], Joshua Banta [1] (1. University of Texas at Tyler, 2. Washington State University)* Globally, crayfish play a significant role in freshwater systems as ecosystem engineers, indicator species, and a food source for avian, terrestrial, and aquatic predators. Crayfish are considered one of the most threatened taxa due to factors including pollution, habitat loss, and climate change. The Jackson Vale ecoregion of Southeast Texas is home to three species of understudied endemic crayfish, two of which are listed as Species of Greatest Conservation Need by the Texas Parks and Wildlife Department, *Procambarus* fayetti, Procambarus, nueces, and Procambarus texanus. My Research will consist of performing physiological tests on these three species as well as the widespread crayfish *Procambarus* acutus. I will evaluate the environmental tolerances of temperature (CTmax), hypoxia (Pcrit), and water chemistry (pH) through dynamic loss of equilibrium experiments. I hypothesize that the widespread *P.* acutus will have a broader tolerance of these parameters than the three geographically restricted endemic species and that the narrower tolerance ranges of the three endemics will make them more susceptible to environmental changes. Findings from these experiments will inform wildlife managers on the conservation status of these species as well as highlight similarities and differences in habitat limitations among the four species. These findings could be useful in modeling habitat suitability in relation to future climate trends.

P79-N Resilient Biodiversity: Guadalupe River Flooding Update
Chris Distel [1] (1. Schreiner University) The July 4, 2025 flood in the upper Guadalupe River took over 100 lives and impacted many thousands more. The unique combination of a concentrated, high-energy storm and the location of heaviest precipitation in the uppermost watershed meant that the volume and velocity of flood waters in the main river channel across Kerr County attained destructive power unprecedented in this system.

Using a combination of original survey data and iNaturalist records, biodiversity was assessed before and after the flood, with a focus on fish, amphibians, and reptiles. The river channel was inaccessible for surveying for approximately two months after the flood. As surveys became possible, biodiversity detections indicated that most species were resilient to the flood, with numerous species exhibiting breeding in the river by October. Local distributions of some species were affected, and a small number of species have yet to be detected since the flood. However, given the intensity of this flood, most local species appear to persist.

P80-U Utilization of an eDNA ddPCR assay on two SGCN mayfly species. *Jace Douglas [1], Matthew Blow [1], James York [2], Marsha Williams [1], Archis Grubh [2], Lance Williams [1], Matt Greenwold [1] (1. University of Texas at Tyler, 2. Texas Parks and Wildlife)*
Macroinvertebrate Orders Ephemeroptera, Plecoptera, and Trichoptera (EPT) are important water quality indicators that are often used in bioassessments. Two mayfly species (*Tricorythodes curvatus* and *Sparbarus coushatta*) are listed as Species of Greatest Conservation Need (SGCN) by Texas Parks and Wildlife Department indicating that their current status is either uncertain or threatened. Furthermore, field sampling and the morphological identification of mayflies is difficult and time consuming, so there has been a push to develop alternative sampling methods such as environmental DNA (eDNA). Environmental DNA is defined as DNA shed by organisms into the surrounding environment (water, sediment, air, etc.) and can be used for the detection of species using noninvasive methods. Previous work on these two mayflies produced an eDNA assay for these two species using Quantitative Polymerase Chain Reaction (qPCR), but it failed to amplify the target species from eDNA. Recent studies have shown that Droplet Digital PCR (ddPCR) is better at detecting lower quantities of DNA when compared to qPCR. Droplet Digital PCR utilizes oil emulsification of a typical qPCR reaction mixture to form upwards of 10,000 discrete reactions. This allows for the dilution of PCR inhibitors and the potential for direct quantification using a Poisson distribution. This project is focused on developing a functional eDNA assay for our two target species using ddPCR. Preliminary results indicate that we can detect *S. coushatta* from eDNA. We will report on our full testing of both species. We envision this data to be useful for future researchers when designing eDNA assays.

P81-G Life histories of two SGCN Procambarus Species in East Texas *McKenzie Adkins [1], Matthew Blow [1], Katrin Kellner [1], Matt Greenwold [1], Jared Dickson [1] (1. University of Texas at Tyler)*
Numerous Texas crayfish in the Procambarus genus are listed as species of greatest conservation need (SGCN) by the Texas Parks and Wildlife Department (TPWD). Crayfish are an ecologically important fauna, so being able to understand their ecology, including habitat requirements and life history characteristics is essential in developing conservation and management plans. The two species of interest are *Procambarus nigrocinctus* and *Procambarus nechesae*, which are both endemic to the state of Texas. These two species have only two documented samplings since 1990 and have differing classifications under the Endangered Species Act due to the lack of research. The goal of this project is to determine habitat association, as well as life history traits for each of the target species. Three sample sites were chosen for each of the two target species, and samples were taken once a month for twelve months beginning in January 2025. Sampling included the use of baited minnow traps, kick seine, and water chemistry parameters. During each sampling event, individuals from the target species had a set number of parameters recorded for later analysis. We hope to present the full twelve months of results and overall provide a better understanding of these two species life histories.

P82-U Playing by the numbers: Comparing microplastic estimates from summation and extrapolation *Sarah Berver [1], Emma Flores [1], Jordan Emerson [1], Romi Burks [1], Andre Felton [2] (1. Southwestern University, 2. University of Texas San Antonio)*
Forty million tons of US plastic waste a year contributes to increasing microplastic (< 5 mm) prevalence. Shed microfibers (mf) from frequently washed synthetic fibers are the predominant microplastic morphotype found in surface waters. We investigated how extrapolation from filtering different volumes influenced estimation of microfibers L-1, working towards a long-term plan of creating a loading index for site-to-site comparisons in Texas for labs with varying methodologies of volumes processed and data extrapolated. In our June pilot (N=6), we filtered different volumes from 1-L samples collected from a lake or stream. We hydrolyzed (30% H2O2) samples for 24-hrs and then added an equivalent volume of 1 M NaCl solution. To compare extrapolations of 2x or 8x the original volume, we either filtered four 250-mL subsamples on separate filters or 250 mL on one filter. Our June pilot found similar low, albeit variable, microfiber abundance (0 - 32 mf L-1), but extrapolation failed to account for no microfibers on individual filters. We repeated the study in November, adding a fully counted sample (1-L) to compare methods on stream microplastic estimations. In our follow-up, every sample contained microfibers, but noticeably higher variability occurred with extrapolated samples which ranged from 32 - 264 mf L-1. Fully extrapolated samples did not appear statistically different from summed ones (42 - 88 mf L-1), but combining summing and extrapolation (28 - 84 mf L-1) may slightly underestimate abundance. This work underscores the need for consensus on methods to estimate microfiber abundance to increase comparability across sites.

P83-U Thermal Sensitivity Patterns in Urban and Rural Austin Streams Jaalah Shand [1], *Amber Clark [1], Mary Poteet [1] (1. University of Texas at Austin)* Thermal regimes in streams are driven by interactions among solar radiation, atmospheric conditions, groundwater inputs, and riparian vegetation. Urbanization alters these drivers by reducing canopy cover, modifying hydrology, and increasing impervious surfaces that absorb and radiate heat. These changes contribute to localized warming associated with the urban heat island effect and may diminish the natural thermal buffering provided by surface waters. Although urban stream warming is well documented, the degree to which *thermal sensitivity*—the strength of the relationship between air temperature and stream temperature– varies across urban and rural settings is poorly understood. We installed paired air and water sensors at three urban and three rural creeks across Austin, TX. Based on preliminary analysis we expect that urban creeks will exhibit higher thermal sensitivity, with tightly coupled air-water temperature and faster stream responses to atmospheric fluctuations compared to rural streams. The availability of paired air and water temperature data is essential for detecting these patterns, as it allows us to isolate the relative influence of atmospheric forcing from watershed- and channel-scale controls. By having paired air and water temperature data we can begin to tease apart the drivers of thermal regimes and their shifts corresponding to surrounding urbanization. We hope that our study can be utilized as a tool to help riparian restoration and management strategies to mitigate thermal loads in creeks.

P84-G Spatiotemporal analysis of metazoan community from the subterranean estuaries of the Yucatan Peninsula and Cozumel island through metagenomics Danielle Bragg [1], *Elizabeth Borda [2], Fernando Calderón-Gutiérrez [1] (1. Stephen F. Austin State University, 2. Texas A&M University-San Antonio)* Subterranean estuaries are characterized by vertically stratified water layers (freshwater-to-saline) and are typically accessible via land-locked sinkholes, locally known in the Yucatan Peninsula as cenotes. Subterranean estuaries present a high endemism rate of cave adapted metazoans in response to the extreme environment of no sunlight, low oxygen, and limited organic inputs. The subterranean estuaries of the Yucatan Peninsula and Cozumel Island are among the "best known" and offer a unique study case by limiting geographical variation yet remaining geologically independent of each other. Most of the biodiversity assessments conducted so far rely on direct collection followed by morphological identification. Molecular tools allow for non-invasive biodiversity assessment of these poorly known communities. Particularly, genome skimming circumvents PCR bias, one of the biggest caveats in genomic studies. In this study, we will conduct a spatiotemporal analysis of the metazoan community using genomics to further characterize the biodiversity of these understudied ecosystems. New records and potential novel taxa of metazoans inhabiting subterranean estuaries are likely to be identified, with micro-metazoans expected to encompass most novel records. Metagenomic analyses of the community are expected to identify structure based on geographical and environmental parameters, but no, or poor structure is expected to be explained due to the temporality. The results of this study will greatly broaden our limited understanding of the metazoan communities in these overlooked subterranean estuaries.

P85-U Phenotypic Diversity of Escherichia coli from Water Samples in North and East Texas Christian Buford [1], *Wei-Chin Ho [1] (1. The University of Texas at Tyler) Escherichia coli* is found in the environment and the intestines of most livestock mammals and poultry. Although it typically supports gut health, some strains can be harmful, affecting livestock, wildlife, and humans. Understanding how benign and harmful strains vary across seasons and spread through water bodies is important for wildlife managers, farmers, and ranchers. This research aims to study *E. coli* diversity in North and East Texas. Particularly, seven sites were sampled across North and East Texas. These counties include Collin, Hunt, Kauffman, Madison, Navarro, and Smith. At each site, temperature and pH values were also measured, and water samples were collected. By plating water samples on Mueller-Hinton (MH) agar plates supplemented with 16 ng/mL ampicillin or streptomycin, we found five samples showed resistance to ampicillin, while only three showed resistance to streptomycin. To further focus on *E. coli* or fecal coliform microorganisms, we isolated single colonies by identifying green/purple colonies on eosin-methylene blue agar. Antibiotic resistance phenotyping was then performed on these isolates by disc diffusion assay with MH agar. The results are that all the samples exhibited susceptibility to the six antibiotic treatments (Penicillin, Streptomycin, Erythromycin, Tetracycline, Nalidixic Acid, and Sulfamethoxazole-trimethoprim), while the lab strain (K-12 derivative) showed resistance to all. The finding helps inform wildlife management strategies by identifying patterns of *E. coli* diversity in the wild. Additionally, it provides insight into environmental antimicrobial resistance for clinical applications. Our future plan includes sequencing the isolates and identifying their genetic diversity.

P86-U Using Grass Shrimp to Evaluate Mercury Concentrations of Texas Lake Systems Robert Albin [1], *T.J. Boyle [1] (1. McMurry University)* A population study was taken on *Palaemonetes kadiakensis*, commonly known as grass shrimp, to determine how size classes of the population correlate to mercury concentration. Mercury deposition in freshwater ecosystems can be measured using bioindicators. Samples were drawn from Fort Phantom Lake, Hubberd Creek Lake, Lake Eastland, and Middle Bosque River headwater of Lake Waco. Grass shrimp were measured in length, width, and weight to classify size classes. Data of size classes were compared to mercury concentrations with the hypothesis that the larger size classes would have greater concentrations. By developing size class and mercury concentration relationships, characteristics of each reservoir can be compared. The data will aid future studies to review the use of grass shrimp as bioindicators of mercury contamination.

P87-U Assessing white bass (Morone chrysops) population characteristics in two central Texas lakes across season and size classes *Caleb Fry [1], Yessenia Edgecomb [1], Caroline Vanderburg [1], Mervin Narito [1], Jason Locklin [1] (1. Temple College)* Relative weight, *Wr*, provides a practical and noninvasive estimate of fish body condition in populations over time as well as an assessment tool to estimate energy allocation across fish length classes. White bass (*Morone chrysops*) are popular among recreational anglers because of their conspicuous schooling activities in lakes and immense spawning runs upstream during the spring. The relative weight of two white bass populations in central Texas lakes, Lakes Belton and Stillhouse Hollow, are being assessed monthly in 2025-2026 to estimate current population condition compared to data from the early 1990s. In this presentation, we discuss the preliminary data from the first half of this ongoing study. We sampled each lake monthly by accompanying a licensed fishing guide during routine client trips. All white bass captured by angling were weighed (W, g) and measured for total length (TL, mm) to compute relative weight ($W_r = 100 \times W / W_s$), where standard weight (W_s) was taken from the published the species-specific length–weight equation, $\log_{10} W_s = -5.066 + 3.081 \log_{10} \mathrm{TL}$, $r^2 = 0.999$. All fish were released immediately after processing. Preliminary results suggest that *Wr* differs between the two populations at only at mid size classes (255-356 mm) and both population W_r values in 2025 exceed those observed in both lakes in 1991. Continuing monthly sampling through April 2026 will evaluate temporal stability, quantify variance among size classes, and establish a yearlong baseline to support future comparisons, population assessments, and fisheries management decisions.

P88-U Signs of Decline in Texas? Zebra Mussel Population Density and Condition Across Invasion Timelines *Kaylyn Wolf [1], Mervin Narito [1], Peyton Sen [1], Jason Locklin [1] (1. Temple College)*
Zebra mussels (*Dreissena polymorpha*) are among the most invasive freshwater bivalves in North America, first introduced from Europe into the Great Lakes about 37 years ago. They have since spread extensively throughout the Mississippi River Basin and into adjacent regions. The species reached Texas in 2009 and has since established reproducing populations in at least 34 lakes across the state. At southern latitudes like Texas, zebra mussels exhibit elevated growth rates and two annual spawning events, leading to rapid establishment and the formation of dense populations over short time periods. Although high densities are common soon after invasion, anecdotal evidence suggests that declines may be occurring in Texas over time. Understanding these potential reductions is important for researchers and management agencies when developing long-term mitigation strategies. In this study, we surveyed 14 infested Texas lakes representing a range of invasion timelines to estimate current population densities and to evaluate the populations' physiological conditions. The lakes spanned from the earliest invaded system (Lake Texoma, 2009) to one of the most recent (Hords Creek, 2023). Adult zebra mussels were not observed in three of the 14 lakes. Among those systems with mussels present, densities ranged from as few as 3 mussels/m² in Lake Ray Roberts to as many as 911 mussels/m² in Hords Creek. Mussels from recently invaded lakes exhibited higher physiological condition than those from older populations, suggesting that declining densities over time may be associated with reduced physiological condition. These findings provide valuable guidance for managing newly infested Texas lakes.

P89-U Visualizing the First Flush Temperature Effect in Austin, Texas *Rhianna Saini [1], Mary Poteet [1] (1. University of Texas at Austin)* Thermal pollution due to stormwater runoff can have detrimental effects on aquatic organisms. First flush, or the initial 30% of stormwater runoff volume flowing into creeks, significantly alters stream temperature. First flush typically cools streams in rural watersheds due to inputs of relatively cool overland flow; however, studies of urban creeks report inconsistent results, likely reflecting interactions among impervious surfaces, stormwater infrastructure, and seasonal hydrology. In this study, we quantify the direction and magnitude of temperature changes due to first flush in an urban creek in Austin, Texas, over a seven-year period (2017 to 2024). Continuous stream temperature measurements were paired with discharge and precipitation data from a nearby USGS gauge to identify storm events and evaluate thermal responses across seasons and hydrologic conditions. Data were visually evaluated for changes in temperature in response to discharge and precipitation during storm events. Our data show that the temperature response of creeks to first flush is dependent on season and amount of discharge. Storm events that led to low discharge tended to increase creek temperature during first flush. However, storm events that led to high discharge tended to decrease creek temperature during first flush. These thermal disturbances have important ecological implications, including physiological stress of temperature-sensitive organisms. Understanding the drivers and variability of this first flush temperature effect is essential for predicting biological impacts and for designing stormwater and urban infrastructure that mitigates rapid thermal pollution in urban streams.

P90-U Characterizing the K-Pg Boundary in Central Arkansas, USA *Matthew Smith [1], Mindy Faulkner [1] (1. Stephen F Austin State University)* The Cretaceous-Paleogene boundary (K-Pg) is an important geological marker that represents a major mass extinction event that signified the end of the Mesozoic Era. Central Arkansas has several locations that have Cretaceous and Paleogene rocks in outcrop that could contain fossil and mineralogical evidence of the asteroid impact in the Yucatan Peninsula. An uptick in iridium, one of the rarest occurring elements in the Earth's crust with background concentrations of 10-12 ppb, is often used as a marker for the K-Pg boundary. Recent field investigations in Central Arkansas have yielded interesting results. Stratigraphic measurements across the K-Pg boundary and laboratory analyses were used to determine the presence of iridium spikes at known outcrops with Cretaceous and Paleogene rocks. Microfauna characterization and guide fossils were used to determine ages of formations and boundary definitions. Forty samples in three locations were collected and analyzed using a Thermo Scientific hRF instrument. These data were used to create a series of litho- and chemo-stratigraphic correlations of elements of interest including lanthanum, niobium, barium, silver, uranium, and others. Laser Ablation-Inductively Coupled Plasma-Mass Spectroscopy (LA-ICP-MS) analyses were conducted on ten of the forty powdered samples, which yielded quantifiable concentrations of various elements including iridium. The analyses did report several samples with a greater mean concentration of iridium than the average concentration within the Earth's crust. These data could represent sediment transported into the study site from areas with a greater concentration of iridium.

P91-G Evaluating Sulfate-Reducing Potential of Native Wetland Plant Species in a Coal Ash Disposal Area, Panola County, Texas, USA *Cari Mitchell [1], Mindy Faulkner [1], Jenny Rashall [1] (1. Stephen F Austin State University)* The Martin Lake Steam Electric Station (MLSES) A-1 Disposal Area in Panola County, Texas, is a designated site where coal combustion residues (CCR) from the MLSES are stored and managed after combustion. Trace elements found in coal ash leach into holding ponds and must be treated before release into the environment. At the MLSES A-1 Disposal Area, prior combustion and treatment have created an excess of sulfate in the effluent water. This site is exceeding its regulatory limit of sulfate concentrations and is in need of a cost-effective and sustainable solution to this problem. This study proposes to model treatment wetland cells using native plant species in a system of 20-quart plastic tubs placed outdoors. The wetland cells will be used to investigate sulfate removal potential of East Texas native plant species. Three species will be utilized: *Juncus effusus*, *Schoenoplectus tabernaemontani*, and *Scirpus divaricatus*. Each individual species, as well as each possible combination of species, will be tested by using a system of three plastic tubs and 1,000 ppm sulfate water to measure the efficacy of sulfate reduction. Each week, water will be circulated to mimic water movement through the effluent pond system at the disposal facility. Sulfate concentration, pH, electroconductivity, and dissolved oxygen will be analyzed in situ weekly before the water is circulated. This study will highlight the efficacy of these East Texas native wetland plant species for reducing sulfate concentration in effluent water in hopes of developing a sustainable strategy for mitigating the environmental impacts of CCR.

P92-U Insights into the Large Mammal Fossils from Phillips Paleo Cave, Crockett County, Texas *Angelica Reyes [1], Stacie Skwarcan [1] (1. University of Texas at Austin)* The Cretaceous carbonates of Texas played an important role in the formation of caves on the Edwards Plateau in the central portion of the state. Those caves preserve the remains of Quaternary vertebrates and allow us to understand the large mammals that were present on the plateau during the Pleistocene. However, our knowledge of which taxa of large Pleistocene mammals inhabited the Edwards Plateau during that time is biased towards the better-studied eastern and southern portions of the plateau. The discovery of Philips Paleo Cave, situated on the western end of the Edwards Plateau in Crockett County, Texas, provides a glimpse into the vertebrate fauna of the western side of the plateau during the Pleistocene. Excavations and surface collection activities in 2012, 2013, and 2021 yielded numerous Pleistocene age vertebrate fossils. A number of specimens of complete and partial teeth of larger mammals were identified through comparison with modern osteological material and published diagnoses for each taxon. The specimens record the presence of *Nothrotheriops, Canis, Hemiauchenia, Capromeryx, Odocoileus,* and *Equus* in the cave deposits. Diagnostic features are absent on five of the more fragmentary specimens. Further evaluation of the specimens from Phillips Paleo Cave will contribute to our understanding of how faunal composition varied geographically and temporally across the Edwards Plateau, a region which today encompasses the transition from the humid eastern portion of North American to the arid western portion of the continent.

P93-U Staging the embryogenesis of male-pregnant Gulf pipefish (Syngnathus scovelli) using optic development. *Kimble Gould [1], Aniston Lovetinsky [1], Sunny K. Scobell [1] (1. Southwestern University)* Individuals within the Syngnathidae Family (seahorses, seadragons, and pipefish) exhibit the unique characteristic of male pregnancy, ending with the release of self-sufficient offspring. Reproduction of Gulf pipefish (Syngnathus scovelli) involves gestation within the brood pouch of the male until the release of juvenile individuals. Previous embryonic development studies of fishes within the Syngnathidae Family have described specific developmental stages of embryos based on the features present to determine the progress of development. In members of the family Syngnathidae, optic development follows three distinct phases: optic vesicles, optic cups, and eye pigmentation, however, no standardized method exists at this time to classify the stages of embryogenesis in S. scovelli. One notable feature present is the development of the eyes. Eyes are one of the earliest features to appear and their formation serves as a reliable marker for an embryo's stage. The objective of this work is to analyze and describe embryonic development of the gulf pipefish, utilizing eye formation as a stage-specific indicator. This study aims to provide insight into the developmental staging of species within the Syngnathidae family and provide researchers within the field with a model for classifying developing embryos based on optical developmental markers.

P94-U Characterizing embryonic development in the pregnant male pipefish, Syngnathus Scovelli, using snout formation as a morphological marker *Aniston Lovetinsky [1], Kimble Gould [1], Sunny K. Scobell [1] (1. Southwestern University)* The Gulf pipefish, Sygnathus Scovelli, a member of the Syngnathidae Family (seahorses, seadragons, and pipefish), exhibits the rare phenomenon of male pregnancy. During reproduction, females transfer eggs into the brood pouch of the male, where fertilization and embryonic development occur until the release of fully formed offspring. Previous research on syngnathids have described general patterns of embryogenesis; however, there are no studies that have established a standardized system for classifying developmental stages within S. scovelli. Because the elongation and shaping of the snout are defining features within this species, snout morphology provides a useful indicator of developmental progress. The objective of this study is to characterize and describe the stages of embryonic development in the gulf pipefish, using snout formation as a morphological marker. This work aims to enhance understanding of developmental staging within the Syngnathidae family and to provide a framework for identifying embryonic progression based on craniofacial features.

P95-U A Longitudinal Study: The Abundance and Disease Status of Starlet Corals in Roatán, Honduras *Gloria Dominguez [1], Ashley Tejada [1], Kaylee Aguilar [1], Xaile Garza [1], Ana Quintinilla [1], Leon Rosales [1], Annie Mowry [1], Ashlyn Kennedy [1], Matthew Hicks [1], Racheal Gomez [1], Traesha Robertson [2], Stephanie Randell [1], Stephanie Lockwood [3], Jacqueline Dove [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University)*

Coral reefs support 25% of marine life, protect shorelines, and are increasingly threatened by anthropogenic factors such as climate change. These stressors have led to increased coral disease and bleaching. Starlet corals are native to the Mesoamerican Barrier Reef (MBR) and are affected by two key diseases - Dark Spot Syndrome (DSS) and Stony Coral Tissue Loss Disease (SCTLD). Dark Spot Syndrome produces non-lethal lesions which weaken coral while SCTLD begins with lesions which quickly spread, causing rapid tissue decay and coral death. This study assessed the abundance and disease status of starlet corals *Siderastrea siderea, Siderastrea* radians, and *Stephanocenia intersepta* on the MBR in Roatán, Honduras from 2023 to 2025. Relative abundance was 71% for *S. siderea*; 20% for *S. radians*; 9% for *S. intersepta*. Since 2023, disease prevalence in *S. siderea* increased by 93% (n=374) and by 11% (n=108) *for S. radians*. Disease prevalence decreased by 53% for *S. intersepta.* In 2025, three *S.siderea* were observed with both DSS and SCTLD. Dive sites Bears Den and Mandy's Eel Garden had the greatest disease prevalence in 2023; Fish Den and My Choice in 2024; and Pillar Coral and My Choice in 2025. Percentages of dead coral decreased for all species; damage and bleaching were observed across all three years. Though there was a 91.6% damage rate, this percentage remained stable for all species and dive sites. These findings suggest that damage to starlet corals is more prevalent than disease. Future research should explore environmental factors influencing coral health.

P96-U The Role of Symbiodiniaceae Identity in Mediating Pathogenic Bacterial Effects on Exaiptasia *Emily Ryan [1], Tanya Brown [1] (1. University of Texas at Tyler)* Coral reefs are vibrant ecosystems often being called the rainforests of the sea. Corals are the main architects of reefs and are known to harbor specific clades of symbionts. The symbionts provide food to the coral host by way of photosynthetic products.During times of stress corals have been shown to shuffle symbionts. The sea anemone, *Exaiptasia diaphana* is a model system for coral symbiosis as it can have associations with different symbionts. *E. diaphana* were rendered aposymbiotic by having the anemones expel their symbionts and subsequently kept in dark conditions. Before different clades of symbionts were provided to *E. diaphana*, aposymbiotic anemones were placed in the light for a month to confirm that they were indeed symbiont free. Results from the light trials showed no sign of recolonization of *E. diaphana* with symbionts, confirming that the anemones were aposymbiotic. Currently aposymbiotic *E. diaphana* strain H1 where fed non native symbionts from strain CC7 anemones. These anemones will be used in future studies to explore resistance to microbial challenge with the known coral pathogen *Vibrio coralliilyticus*. Results from this work will be fundamental in understanding how shuffling symbionts may aid corals in fighting pathogens.

P97-U Echinoderm Diversity in Roatán, Honduras *Anna Contreras [1], Yuto Goto [1], Harrison Wolf [1], Sarah Lucas [1], Hannah Kaye Windwehen [1], Traesha Robertson [2], Annie Mowry [1], Ashlyn Kennedy [1], Jacqueline Dove [1], Stephanie Lockwood [3], Stephanie Randell [1] (1. McLennan*

Community College, 2. College of Coastal Georgia, 3. Texas Tech University) Echinoderms are marine invertebrates that function as predators, prey, filter feeders, and detritivores, filling diverse ecological roles supporting habitat structure, nutrient cycling, and biodiversity across marine ecosystems. There has been a lack of data on echinoderm diversity which limits the ability to detect ecological shifts. This study was conducted to document echinoderm diversity in Roatán, Honduras. Data was collected from 27 - 30 May 2025, using the Randell Robertson Marine Survey Technique (RRMST) for shore and reef surveys. A total of 645 echinoderms were recorded with substrate preference across six sites. The most abundant classes were Echinoidea (74.9%), Crinoidea (14%), Ophiuroidea (9.9%), and Holothuroidea (1.2%). Overall, substrate preference by class was Rock for Echinoidea (85.9%), Coral for Crinoidea (93.3%), Rock for Ophiuroidea (42.2%), and Sand for Holothuroidea (100.0%). The most dominant species by class were *Echinometra lucunter* (80.8%) for Echinoidea, *Davidaster rubiginosus* (58.9%) for Crinoidea, *Ophiocoma echinata* (48.4%) for Ophiuroidea, and *Holothuria mexicana* (62.5%) for Holothuroidea. Chi-square tests revealed significant associations between echinoderm species and sampling method. Shore snorkeling surveys had the highest species richness and abundance. Significant relationships were found between class and substrate type, and within classes, Echinoidea and Ophiuroidea exhibited significant substrate associations, while Crinoidea did not. Sea urchin species with shorter lifespans such as *Echinometra lucunter* should be monitored for population declines since they serve as bioindicators for ecosystem stability. Given the ecological significance of echinoderms and growing environmental pressure, this study establishes baseline for future reef health assessments and conservation efforts in Roatán, Honduras.

P98-U Association of Diversity and Health of Scleractinian Corals with Macroalgae in Roatan, Honduras Hannah Dawson [1], *Zoe Hilliard [1], Harrison Wolf [1], Christopher Allovio [1], Traesha Robertson [2], Anne Mowry [1], Ashlyn Kennedy [1], Jacqueline Dove [1], Stephanie Lockwood [3], Stephanie Randell [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University)* Anthozoans in the Caribbean face increased stressors from climate change, increased sedimentation, eutrophication, overfishing, ocean acidification, and disease. Coral coverage in the Caribbean has been declining with coral depauperate reefs typically dominated by macroalgae. Macroalgae can negatively impact the health of stony corals by altering the coral microbiome via allelochemicals, shading, and by harboring pathogens. Algal phase shifts alter reef structure and reduce biodiversity causing further coral coverage decline which could be irreversible for the ecosystem. In 2014, Stony Coral Tissue Loss Disease emerged and spread from Southeast Florida to the Caribbean. By 2021, *Meandrina meandrites, Dendrogyra cylindrus,* and *Orbicella faveolata* were considered endangered by the global IUCN Red List. This study was done to assess Scleractinian coral diversity and health in association with macroalgae coverage. Four dive sites were surveyed in Roatan, Honduras May 27 – 30, 2025. Data indicated significantly higher macroalgae coverage in comparison to coral coverage. Average coral coverage per dive site was 4.18% and average macroalgae coverage was 85.74%. Dead coral was frequently observed covered with macroalgae, with macroalgae completely shading the reef structure in some cases. Disease prevalence was too low to assess any association between macroalgae coverage and disease. Only two sampled quadrats had measurable diseased areas, the diseased coral only made up .02% of live coral coverage. There was an association between reduced coral coverage and macroalgae coverage - as macroalgae coverage increased, coral coverage decreased. These data suggest the reef is undergoing a phase shift to a coral depauperate reef system.

P99-U Associations of algal species with sponge disease in Roatán, Honduras Paola Vallejo [1], *Virginia Fuentes [1], Grettel E. Ramirez [1], Traesha Robertson [2], Annie Mowry [1], Ashlyn Kennedy [1], Jacqueline Dove [1], Stephanie Lockwood [3], Stephanie Randell [1] (1. McLennan Community College, 2. College of Coastal Georgia, 3. Texas Tech University)* Sponges play essential roles in coral reef ecosystems by facilitating nitrogen cycling, filtering water, serving as a food source for certain fish, and providing substrate for primary producers such as algae, although no direct association between algae and sponges has been established. These organisms are increasingly threatened by factors including pollution, climate change, and other environmental stressors, which contribute to diseases such as bleaching and orange band syndrome. Common Caribbean species, *Xestospongia muta* and *Aiolochroia crassa*, are integral to reef health due to their ecological functions. To address these questions, this study was undertaken to investigate the association of algal species with sponge disease in Roatán, Honduras. This study was conducted in May 2025 at four established dive sites. The data analysis demonstrated no association between algal species and sponge diseases. Among the 24 *X. muta* sponges surveyed, 42% were found to be diseased ($p = 0.007$), while only 4% of the 47 *A. crassa* sponges showed signs of disease ($p = 0.027$). Across all dive sites, Bears Den had the highest number of diseased sponges, while My Choice exhibited the highest algal species diversity. *Dictyota* was the most prevalent algal species found throughout all dive locations. Future studies should incorporate water testing to assess for nutrients associated with algal overgrowth or for potential chemical run-off that may affect sponge disease status.

P100-U MoRocco – A Secure Exam Operating System for Academic Integrity Rocco Guevara [1] *(1. McMurry University)*
Academic institutions increasingly face challenges in maintaining exam integrity as students gain access to advanced AI tools, remote assistance technologies, and operating-system–level workarounds. Traditional lockdown browsers restrict applications at the software layer but remain vulnerable because they depend on the security of the host environment. As a result, universities require a more robust solution that isolates the testing environment from the underlying system while still supporting programming tasks, technical assessments, and classroom-scale deployment. In this project, we introduce MoRocco, the Modular Restricted Operating Computing Core OS, a lightweight secure exam operating system designed specifically for controlled academic testing. To support modern computing courses, MoRocco incorporates an Object Oriented Programming approach that improve maintainability and extensibility. Additional supporting utilities are developed using Python and shell scripting to enable efficient integration with Linux kernel features and provide proper restrictions. The operating system provides only essential tools such as a code editor, compiler, and terminal, all governed by a strict security policy that validates binaries and enforces a zero-trust runtime. MoRocco can run locally on low-spec university laptops as a virtualized or containerized image, eliminating dependency on network speed or cloud resources. Instructors prepare exam materials through a secure packaging utility, ensuring that exam files, datasets, and auto-grading scripts become available only after the OS boots and remain isolated from the host. Preliminary evaluations demonstrate that MoRocco offers a tamper-resistant, resource-efficient, and pedagogically flexible testing environment that surpasses traditional lockdown solutions.

P101-U Comparing the Effectiveness of Two Common Lichen Sampling Methods Courtney Shuman [1], *Chad Cryer [1], Martha Hartt [1] (1. Temple College)* Lichen density surveys aim to find the amount and diversity of lichens present in an area. These surveys are important in determining the effect that pollution and other variables are having on the health of lichen communities. The information collected from them can be used in fields of study such as bioclimactic modeling and finding zones of environmental quality. Various methods of collecting data on lichen density are possible, but may lead to conflicting results. Here we show the differences between the results of two collection methods. Where they have previously been used interchangeably, we compare the two methods on the basis of their accuracy and usability. This assessment identifies clear areas of reliable performance for each method and proposes when each should be used to obtain useful data on lichen coverage. Our study uncovers and analyzes the strengths and weaknesses of each of the two sampling methods. We anticipate that making methods more consistent will allow accurate information on lichen abundance, diversity, and distribution to be collected and compared over time. Up to date and correct information on lichen presence will help overall environmental trends and characteristics to be identified.

P102-U GRACE – Gesture Recognition for Augmented Cultural/Religious Expression Daniil Kochkonbaev [1] *(1. McMurry University)* Religious practices often involve deeply symbolic gestures that express faith, devotion, and reverence. However, these gestures are rarely integrated with modern technology in a way that preserves their cultural and spiritual meaning. When worshipers interact in temples, churches, or mosques, their physical expressions such as kneeling, bowing, or folding hands carry profound significance. Yet, technology in sacred spaces is often limited to static audio or visual aids, which do not respond dynamically to human presence. In this project, we introduce GRACE, which stands for Gesture Recognition for Augmented Cultural/Religious Expression. GRACE is a robotic prayer companion that recognizes devotees' gestures and responds with appropriate actions. For example, when a person kneels, the robot may light a lamp or recite a short prayer. The system is built using an RGB camera and a Yahboom ROS depth camera for gesture recognition, a Raspberry Pi 5 as the main processing unit, and servo motors connected through a "PCA9685" driver to perform physical actions. Speakers are used to deliver prayers or chants, and LED lamps provide visual feedback when gestures are detected. Our software framework is developed in Python using TensorFlow for real-time gesture detection and control integration. GRACE serves as both an engineering and cultural exploration, demonstrating how technology can respectfully enhance religious experiences without replacing human or spiritual elements. Preliminary experiments show that GRACE can accurately identify and respond to common devotional gestures, offering a meaningful connection between tradition and innovation within sacred environments.

P103-H Q-Safe: Mitigating Quantum Threats with Lattice-Based Cryptography Nikhitha Swaminathan [1] *(1. Lowery Freshmen Center)* Modern encryption relies on mathematical problems difficult to solve with conventional computers. One widely used method, RSA, is based on the challenge of factoring large numbers. However, quantum computers and algorithms like Shor's algorithm threaten RSA's security by making factorization far faster and more efficient, necessitating quantum-resistant alternatives. This study hypothesizes that lattice-based cryptography, particularly Kyber KEM, offers stronger quantum resistance and greater computational efficiency than RSA, making it a practical option for future encryption systems. Lattice-based cryptography remains secure even against quantum attacks. Specifically, it examines Key Encapsulation Mechanisms (KEMs) based on the Learning With Errors (LWE) problem, highly resistant to both classical and quantum attacks. The study compares RSA, Kyber KEM, and FrodoKEM, focusing on encryption/decryption speed, key sizes, and scalability. Performance metrics, including encryption/decryption time, key size, and ciphertext size, were gathered using Python scripts. The research also introduces a mathematical model for an adaptive framework that dynamically selects Kyber or FrodoKEM based on security needs and computational constraints, improving efficiency while maintaining strong security. Results show RSA decryption at 8192-bit key size takes 53.79 ms, while Kyber operates roughly 20× faster than FrodoKEM and uses smaller ciphertexts, confirming its real-world efficiency. Mathematical analysis and computational testing confirm Kyber and FrodoKEM as secure post-quantum alternatives to RSA, demonstrating how mathematical hardness underpins modern encryption and its quantum-resistant evolution.

P104-U Location of AVT neurons within the seahorse and pipefish pituitary *Rachel Ling [1], Sunny K. Scobell [1] (1. Southwestern University)* Arginine vasopressin (AVT) is a nonapeptide hormone released by the posterior pituitary and is found in nearly all fish species. In teleost fish species, it has been known to influence courtship behaviors as well as play a significant role in sex change in fish such as the blue-head wrasse. In the pre-optic area of some species of fishes, differing concentrations of AVT receptors in parvo-, magno-, and gigantocellular subpopulations of neurons appear to have a significant impact on social behavior and dominance in competing males. However, very little is known about its functions within the brains of syngnathids (seahorses, pipefishes, and sea dragons), especially in sex-role reversed species such as pipefish. We used multi-fluorescent immunohistochemistry to label AVT expression in the pituitaries of the pipefish, Syngnathus fuscus, and the seahorse, Hippocampus erectus. AVT expression was concentrated in the pars nervosa on the dorsal side of S. fuscus and H. erectus pituitary glands with extensions of the expression leading ventrally into the proximal pars distalis. This indicates that syngnathid species exhibit similar locations of AVT expression as that of other fish families. Expression levels were compared between the species and the sexes. Further investigations will examine the pre-optic area of the hypothalamus to determine whether AVT plays a role in regulating social behavior in syngnathids as it does in other teleosts. We anticipate our study will provide more information about the driving mechanisms of syngnathid social behavior.

P105-G Assessing Cell Death in a 6-Hydroxydopamine Zebrafish Model *Yushe N Islam [1], Roha Qureshi [1], Nolawit Tilahun [1], Ayman Hamouda [1], Brent Bill [1] (1. The University of Texas at Tyler)*

Parkinson's disease (PD) is characterized by progressive loss of dopaminergic neurons caused by dopamine dyshomeostasis, oxidative stress, protein aggregation, and mitochondrial dysfunction. There is no known cure for the disease suggesting a need to identify new potential treatments. Positive Allosteric Modulators (PAM) of the α4β2 nicotinic acetylcholine receptor are a new class of drug that are an ideal target for investigation. These drugs are good candidates because their specificity, they modulate rather than open the ion channel, and are expressed in the dopaminergic neurons critical for the pathogenesis of PD. In zebrafish, oxidative stress-induced loss of dopaminergic neurons can be studied using 6-hydroxydopamine (6-OHDA), a neurotoxin that enters neurons via the dopamine transporter and generates reactive oxygen species. We have optimized a 6-OHDA exposure paradigm based on behavioral and molecular features, but have yet to verify if our protocol induces cellular stress or cell death as observed in other zebrafish larvae protocols. We hypothesized that our paradigm would alter the viability of DA neurons; therefore, our goal was to assess neuron viability using acridine orange (AO), a fluorescent vital dye that selectively labels apoptotic nuclei to quantify cell death via fluorescence intensity. Larvae were exposed to 6-OHDA with or without a PAM and stained 24 and 48 hours post initial exposure (Hpie). Qualitatively, we observed increases in cell death in our 6-OHDA treated animals. Future work will focus on quantitative assessment and determination of cell type.

P106-U An analysis of the dopaminergic pathway in the brain and pituitary of male-pregnant pipefish and seahorses *Madeleine Thomas [1], Sunny K. Scobell [1] (1. Southwestern University)* The Family Syngnathidae (seahorses, pipefish & seadragons) is the only group of vertebrates exhibiting male pregnancy. Males fertilize eggs from females and incubate them in a specialized ventral brood pouch. In most vertebrates, reproduction and pregnancy are regulated by the hypothalamic-pituitary-gonad (HPG) axis via the ultimate release of sex steroids that alter reproductive function. In syngnathids, an additional axis should be considered: the hypothalamic-pituitary-pouch (HPP) axis. To investigate the HPP-axis and hormonal regulation of male pregnancy, key neuroendocrine regulators of pituitary hormones should be considered. However, syngnathid neuroanatomy remains largely unexplored. Our neuroanatomical studies of the Northern pipefish, Syngnathus fuscus, and the closely related lined seahorse, Hippocampus erectus, revealed tyrosine hydroxylase (TH - an enzyme in the dopaminergic pathway) reactivity in the brain and pituitary. These dopaminergic neurons were prevalent in the hypothalamus, and projections were observed in the pars intermedia (PI) and proximal pars distalis (PPD) of the pituitary. In other fish, dopamine is a potent inhibitor of prolactin and GnRH1, two hormones that are likely involved in the regulation of male pregnancy. However, little is known regarding the functions of the dopaminergic system in syngnathids. Our goal is to create an atlas of dopaminergic neurons and projections in the brain and pituitary of seahorses and pipefish. Mapping the dopaminergic cells of these species will help to elucidate the role of dopamine during the reproductive cycle in male syngnathid pregnancy.

P107-G Exploring the Role of Angiotensin Receptor Blockers in the Management of Traumatic Brain Injury: A Review of Mechanisms and Therapeutic Potential *Manaal Salman [1], Kayley Stroupe [1], Lora Talley [1] (1. University of the Incarnate Word School of Osteopathic Medicine)* This review aimed to evaluate the neuroprotective potential of Angiotensin Receptor Blockers (ARBs) related to traumatic brain injuries (TBIs), with a focus on mechanisms of their neuroprotective effects. TBI remains a leading cause of mortality and long-term disability, characterized by secondary cascades of injury due to oxidative stress, blood-brain barrier (BBB) disruption, excitotoxicity, and neuronal apoptosis. Current strategies focus on supportive care and intracranial pressure management, but there is an interest in agents that can prevent secondary injury mechanisms. ARBs, used for cardiovascular conditions, have emerged as potential neuroprotective agents in TBI. We conducted a literature review using the terms "traumatic brain injury, PPAR-γ, ARBS, astrocyte, and neuroprotective." We selected 24 publications that support the hypothesis that ARBs induce neuroprotective effects through angiotensin 1 and 2 receptor (AT1 & 2) modulation, resulting in PPAR-γ agonism following TBI, thus reducing excitotoxicity and neuronal apoptosis. Preclinical models of TBI have demonstrated that blood-brain barrier-crossing ARBs reduce cerebral edema, improve BBB integrity, reduce dysfunctional remodeling, and attenuate neuroinflammatory markers by controlling angiotensin II and AT1 & 2 receptors. AT1 receptors and PPAR-γ have an inverse effect: by inhibiting AT1 receptors, there's an upregulation of PPAR-γ. PPAR-γ reduces proinflammatory cytokines, mitigating the effects of oxidative stress and apoptosis in cerebral tissue. ARBs represent a promising class of neuroprotective agents in TBI management due to their multifaceted role in modulating neuroinflammation and vascular dysfunction. Future research should prioritize clinical trials, biomarker-guided treatment strategies, and investigation into the synergistic effects of ARBs with other neuroprotective agents.

P108-U Investigating AHDC1 Loss and Retinal Development in a Zebrafish Model of Xia-Gibbs Syndrome *Adedire Owulebaja [1] (1. University of Texas at Tyler)* Many neurodevelopmental disorders are caused by mutation within genes that control early brain development. Xia-Gibbs syndrome is a neurodevelopmental disorder characterized by developmental delays, low muscle tone, autism-spectrum behaviors, and vision problems such as strabismus and refractive errors. Harmful dominant nonsense mutations in the gene AHDC1. AHDC1 produces the protein Gibbon that is hypothesized to be a DNA binding transcription factor. Despite recurrent symptoms in patients, the eye phenotype shows variability. In addition the anatomical changes and mechanism of the eye defects are not well understood. This project's goal is to further characterize changes in the eye at the anatomic level. To do this, we will utilize a zebrafish knockout/knockdown. We have designed CRISPR and Morpholino reagents to reduce ahdc1 levels in zebrafish embryos and then use immunohistochemistry to observe AHDC1 expression and important retinal cell markers. We hypothesize that lowering ahdc1 expression will lead to alteration in retinal anatomy and the fish will display strabismus. In our pilot study, we observed a lack of sensitivity to touch at 2 days post fertilization (dpf); however, this was not apparent at 3dpf. This could suggest a developmental delay phenotype, or it could be related to reports of sensory issues observed in XGS patients. Overall, this model will help us better understand how AHDC1 affects eye development and may guide future research on vision and sensory problems in Xia-Gibbs Syndrome.

P109-G Prefrontal Transcranial Photobiomodulation in Autism Spectrum Disorder: Cognitive, Behavioral, and Neurophysiological Effects Across Age Groups *Sarah Diaz [1], Hunter Dutkiewicz [1], Gabriela Guimaraes [1], Nicole J. Moore [1], Isabelle Rose [1], Douglas Barrett [1], F. Gonzalez-Lima [1] (1. The University of Texas at Austin)* Autism spectrum disorder (ASD) is a prevalent neurodevelopmental condition characterized by difficulties in social communication and interaction, as well as restricted interests and repetitive behaviors. These core features are often accompanied by challenges with sustained attention and impulsivity, which can significantly affect daily functioning and quality of life. Transcranial photobiomodulation (tPBM) is a non-invasive brain stimulation technique that uses low-level, near-infrared light to enhance mitochondrial bioenergetics. When applied to the right prefrontal cortex (PFC), tPBM has been shown to improve attention, working memory, impulsivity, and emotional regulation in both healthy and clinical populations. Given evidence implicating mitochondrial dysfunction in the pathophysiology of ASD, right prefrontal tPBM shows potential for improving cognitive and behavioral symptoms. While previous studies have shown promising effects of tPBM in ASD, research in this area is still in its early stages. This double-blind, sham-controlled, randomized study investigates the effects of daily right prefrontal tPBM over eight weeks in children, adolescents, and adults with ASD. Participants complete cognitive testing, behavioral questionnaires, and undergo functional near-infrared spectroscopy (fNIRS) to evaluate changes in prefrontal activation and connectivity. Randomization is stratified by age, sex, and ASD level to evaluate effects across groups. Weekly check-ins monitor safety, compliance, and subjective responses to treatment. Data collection is ongoing. We hypothesize that participants receiving active tPBM will show cognitive and behavioral improvements accompanied by improved prefrontal activation and functional connectivity. This study aims to establish tPBM as a novel, low-risk, and accessible alternative intervention for ASD. Supported by Vanguard Charitable.

P110-U Investigation of the role of Drosophila gene CG12299 in the circadian controlled locomotive activity in fruit flies Annie Trinh [1], *Aimalohi Edeghere [1], Yuan Yuan Kang [1] (1. University of Houston-Downtown)* The circadian rhythm is a phenomenon observed in many organisms and accounts for physical, mental, and behavioral changes over the course of 24 hours. Fruit flies are a commonly used model organism in genetic research due to their having a large percentage of genes that are homologous to humans. In fruit flies (*D. melanogaster*), circadian controlled activity can be monitored using the *Drosophila* Activity Monitor (DAM) to identify circadian behavior and the genes responsible for them. CG12299 is a *Drosophila* gene predicted to enable DNA-binding transcription repressor activity, RNA polymerase II-specific, and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. The goal of my project was to identify whether this gene influenced circadian-controlled locomotion in flies and investigate its expression in fly tissue at different developmental stages. Our results suggested that when this gene was knocked down using the yeast GAL4/UAS binary system and the RNA interference approach in neurons, night activity and evening anticipation were affected, consistent with what we observed in CG12299 mutants. Furthermore, immunostaining showed that CG12299 gene was expressed in the neurons of the fly brain at the embryonic, larval, and adult stages, supporting that CG12299 is a candidate gene required by neurons to regulate circadian controlled locomotive activity

P111-U Blueprints of the Brain: Fetal Cortical Development and the Shadow of Gestational Diabetes
Riya Jadeja [1] (1. University of Texas at Austin) Maternal metabolic health during pregnancy plays a central role in shaping fetal development, particularly the maturation of the brain. Gestational diabetes mellitus (GDM) is increasingly prevalent and has been associated with neonatal complications and later-life neurocognitive differences, yet the mechanisms linking maternal glucose regulation to fetal cortical development remain poorly understood. Cortical thickness, surface area, and gyrification undergo rapid and tightly regulated changes during gestation, making them sensitive indicators of neurodevelopmental integrity. This study addresses how maternal glycemic status influences fetal cortical maturation across gestation. Longitudinal fetal MRI data from the Maternal Abdominal Morphology Assessment (MAMA) study were analyzed to evaluate associations between maternal glucose regulation and cortical morphology across three prenatal timepoints and a one-year postnatal follow-up. Mixed-effects modeling was applied to compare fetuses from pregnancies with no diabetes, GDM, temporary versus persistent GDM, and pregestational diabetes, with adjustments for maternal BMI, gestational age, and pancreatic changes measured through abdominal MRI. Preliminary findings indicate that altered maternal glucose patterns correspond to measurable differences in cortical folding trajectories and regional thickness development. These observations extend previous knowledge by leveraging a rare longitudinal fetal-imaging dataset to identify early neurodevelopmental deviations that may emerge under metabolic disregulation. More broadly, this work integrates maternal-fetal medicine with developmental neuroscience and illustrates the potential of non-invasive fetal MRI to identify early biomarkers of neurodevelopmental vulnerability. Understanding how maternal physiology shapes early brain development may inform future screening strategies and clinical interventions aimed at improving long-term neurological outcomes.

P112-G Effects of Repeated-Session Transcranial Photobiomodulation on Prefrontal Oxygenation and Impulse Control in Adults with Attention-Deficit/Hyperactivity Disorder
Farzad Salehpour [1], Patrick O'Connor [1], Douglas Barrett [1], Isabelle Rose [1], Ayla Farzamnia [1], Monique Tran [1], Amir Emamian [1], Haeun Yeo [1], F. Gonzalez-Lima [1] (1. University of Texas at Austin) Attention-deficit/hyperactivity disorder (ADHD) is a neurodevelopmental condition with a prevalence of approximately 6% among U.S. adults. Neuroimaging studies consistently show reduced hemodynamic responses in the right prefrontal cortex (PFC) of individuals with ADHD during tasks requiring inhibitory control. Transcranial photobiomodulation (PBM) is a non-invasive neuromodulation technique that enhances PFC metabolic activity. This ongoing double-blinded, randomized, sham-controlled trial investigates the behavioral and cerebral oxygenation effects of repeated-session transcranial PBM in adults with ADHD. Eligible participants are adults aged 18–44 years with a verified medical diagnosis of ADHD, either on stable medication or not taking medication. Fifty-two participants will be randomly assigned to receive either active PBM or sham stimulation. Each participant will undergo three weekly sessions of transcranial PBM targeting the PFC using a 1064 nm laser. Participants complete the continuous performance task to assess sustained attention and cognitive control, and the 2-back task to evaluate working memory. Functional near-infrared spectroscopy is used to measure cerebral oxygenation in PFC regions. ADHD symptomatology is assessed using the Adult ADHD Self-Report Scale at baseline, post-treatment, and four-week

follow-up. Nine participants have been enrolled to date. We hypothesize that participants receiving active PBM will demonstrate improvements in cognitive performance, enhanced PFC hemodynamic responses, and stronger functional network interactions across prefrontal subregions. We also predict progressive reductions in ADHD symptoms across time points in the active PBM group. This study is supported by the Oskar Fischer Project and the Elhapa Foundation.

P113-U Investigation of the role of Drosophila gene polyhomeotic proximal in the circadian controlled locomotive activity in fruit flies *Pedro Rodriguez Navarro [1], Yuan Yuan Kang [1], Delwin Sunil [1] (1. University of Houston-Downtown)* Animal species show fluctuating locomotive activities based on the 24-hour circadian rhythm, with high activity during the day and lower activity during the night, with peaks around the light-dark or dark-light transitions. While the neural basis for the circadian control of locomotive behavior is known, the genetic mechanism has not been fully explored yet. In our lab, we conducted quantitative trait locus (QTL) mapping and identified candidate genes for morning and evening anticipation. One candidate gene associated with morning anticipation is called polyhomeotic proximal (ph-p), which encodes for a transcription factor, as a member of the Polycomb group (PcG) protein. To validate the role of this gene in locomotion, we tested ph-p mutants and knocked down its function using neural specific Gal4 drivers and RNAi interference. Then we performed the *Drosophila* Activity Monitor (DAM) Assay to measure day and night activity, morning and evening anticipation. Our results showed that while the ph-p mutants showed lower night activity and lower morning anticipation, the pan-neuronal knock-down of ph-p led to lower night activity only. Interestingly, we observed sexual dimorphism in morning anticipation where female and male mutants displayed opposite phenotypes. The above work is the first line of evidence to show the potential role of the ph-p gene in regulating circadian controlled locomotive activity. Therefore, our ongoing work involves further characterization of the neurons the ph-p gene is required in and specific roles the ph-p gene might play in circadian rhythm.

P114-U Antidepressants and Lung Toxicity: A Narrative Review *Ariana Azimi [1], Elakiya Jayaramen [1] (1. University of Texas at Austin)* Pulmonary toxicity is a serious yet frequently under-recognized complication of antidepressant therapy. With the continued rise in prescriptions, awareness of potential respiratory adverse effects is crucial. This review outlines documented cases of lung injury linked to various antidepressant classes, including selective serotonin reuptake inhibitors (SSRIs), serotonin-norepinephrine reuptake inhibitors (SNRIs), atypical antidepressants, serotonin modulators, tricyclic antidepressants (TCAs), and monoamine oxidase inhibitors (MAOIs). A wide range of manifestations, such as interstitial lung disease, eosinophilic pneumonia, acute respiratory distress syndrome, and alveolar hemorrhage, occurring at both standard dosages and in overdose situations, have been documented. Clinicians should remain vigilant for respiratory symptoms emerging during treatment and pursue timely evaluation and management to minimize the risk of long-term pulmonary complications and improve clinical outcomes.

P115-H Can Deep Learning Models Trained on Cosmological Simulations Predict the Signatures of Early Supermassive Black Hole Seeds Formation Scenarios? *Hitaishi Chillara [1], Ryan Farber [2] (1. University of North Texas, 2. University of Purdue Fort Wayne)* The origin of supermassive black holes (SMBHs), which reside at the centers of most massive galaxies, remains a pivotal unresolved question in modern astrophysics. Two primary hypotheses dominate the debate: "light seeds" formed from Population III remnants and "heavy seeds" formed from direct collapse. Distinguishing between these scenarios requires robust theoretical predictions testable by next-generation observatories. In this work, we present a novel framework combining large-scale cosmological hydrodynamic simulations (SIMBA) with high-resolution accretion simulations (Athena++) to generate synthetic observations for the Vera C. Rubin Observatory (LSST) and JWST. We employ forward modeling to convert simulated physical properties into observable diagnostics, accounting for AGN spectral energy distributions, host galaxy contributions, and dust extinction. Our synthetic data shows excellent agreement with LSST Data Preview 1 (DP1) observations, validating the pipeline. We further develop Deep Learning (DL) models trained on this synthetic dataset to classify SMBH seed types. Our Random Forest classifier achieves 99.9\% accuracy in distinguishing between light and heavy seeds based on photometric properties, while a regressor predicts LSST magnitudes with an R^2 score of 0.997. These results demonstrate that machine learning, trained on physically grounded synthetic data, can effectively identify the observational signatures of early SMBH seeds, bridging the gap between theoretical models and upcoming multi-messenger observations.

P116-U Using 3D Printing in a Research Lab *Montserrat Menchaca [1], Rosa Cardenas [1], Ileana Lane [1] (1. University of the Incarnate Word)* 3D printing is now more accessible than ever before. Its affordability has made it possible to create parts useful in multiple scientific capacities. The accessibility of these instruments in effect brings a machine shop to small universities where resources are limited and there is no access to the service from a machine shop. Parts created with commonly available vat photopolymerization 3D printer are described for use with vacuum systems. In addition to this, the advantages and disadvantages of the parts created with 3D printers have been studied.

P117-U Under the Soil: Effects of Diquat Herbicide on Tomato Root Complexity and AM Fungi Symbiosis

Michaela Stelzer [1], Annabel Ferniza [1], Honey Golden [1] (1. Temple College) Arbuscular mycorrhizal (AM) symbiosis is a widespread phenomenon among various plant taxa. This relationship can be established between most terrestrial vascular plants and fungi in the phylum *Glomeromycota*. AM hyphae create vast networks of mycelium, with a special ability to establish a symbiotic relationship with host plants in the form of arbuscules. These intracellular structures allow a free flow of nutrients to plant roots and offer a promising role in regenerative agricultural practices aimed at minimizing the effects of industrial agriculture on soil health. However, it is unknown whether the commercial non-selective herbicide diquat dibromide affects AM fungi symbiosis. Here we show the effects of spraying a diquat dibromide Roundup formulation on soil to treat weeds prior to transplanting gold nugget cherry tomatoes (*Solanum lycopersicon*). Our investigation assesses the effects of diquat dibromide on tomato plant root complexity and soil health indicators in the presence and absence of AM fungi inoculation. Our results demonstrate that root health and complexity are significantly impacted by the diquat dibromide herbicide, even in the presence of AM fungi symbiosis. We anticipate that these results will help elucidate the effects of commercial herbicides, and warrant further caution in their use and application.

P118-U Heat stress response in Sorghum halepense: tolerance decreases with exposure time but is consistent across seasons

Ashley Cantu [1], Mandy Payan [1], Daniel Odejimi [1], Michael Tobin [1] (1. University of Houston-Downtown) Heat waves are becoming more frequent with climate change, raising concerns about how rising temperatures affect growth and mortality of grasses. We investigated how temperature and exposure duration combine to cause tissue damage in grass leaves. Further, we tested whether the relationship between temperature and exposure duration changed seasonally. We hypothesized that higher temperatures and longer exposure duration at the same temperature would lead to great tissue damage, but that temperature increases would have a greater impact. We also hypothesized that heat tolerance curves would shift to higher temperatures from early spring to late summer. We addressed these hypotheses by constructing heat-tolerance curves for Johnson grass (*Sorghum halepense*) using ion leakage as an indicator of tissue damage. Mature leaves were collected in early spring and again in late summer and exposed to a series of temperatures (28°C, 42°C, 48°C, 52°C, 54°C, 56°C) for four durations (10, 20, 45, and 90 minutes). Ion leakage was measured after each sample after treatment and again following maximum damage after a 98°C treatment, allowing percent damage to be calculated. Across seasons, temperature was the dominant driver of ion leakage, with steep increases in damage at the highest temperatures, while longer exposure times decreased temperature tolerance. Comparisons between spring and late-summer samples revealed minor seasonal shifts between temperature and exposure duration relationships, consistent with a modest acclimation of heat tolerance. Together these results show how temperature, exposure duration, and sampling season interact to determine heat tolerance of leaf tissue in Johnson grass.

P119-U Modest increase in photosynthetic heat tolerance occurs across leaf developmental stages in Johnson Grass (Sorghum halepense)

Mary Robles [1], Diana Diaz [1], Jacqueline Cervantes [1], Shaimaa Obaid [1], Michael Tobin [1] (1. University of Houston-Downtown) A plants photosynthetic heat tolerance determines its ability to maintain photosynthetic function during heat waves. Some grasses continually grow new leaves throughout the summer, potentially exposing leaves to heat stress during development. In this study, we examined whether photosynthetic heat tolerance in *Sorghum halepense* leaves varies during expansion and development or is stable throughout this period. We hypothesized that photosynthetic heat tolerance increases progressively, with immature leaves having the lowest tolerance, and mature, fully expanded leaves having the greatest tolerance. To test this, leaves at three developmental stages (immature, intermediate, and mature) were collected for *S. halepense* and exposed for 20 minutes in water bath treatments to temperatures ranging from 28℃ to 60.5℃ in 2.5 increments. The chlorophyll fluorescence parameter Fv/Fm was measured after heat treatments to assess the photosynthetic response of the leaves. Curves of temperature induced declines of Fv/Fm exhibited modestly greater tolerance at later leaf developmental stages. These results suggest that photosynthetic heat tolerance in *S. halepense* gradually increases as leaves mature, but increases are limited. For plants which flush leaves continually during the growing season rather than during spring when heat waves are rare, maintaining heat tolerance throughout development could protect leaves from damage during unpredictable heat waves.

P120-U Heat-induced ion leakage curves similar across leaf developmental stages in Johnson grass (Sorghum halepense)

Daniel Odejimi [1], Mandy Payan [1], Ashley Cantu [1], Jacqueline Cervantes [1], Michael Tobin [1] (1. University of Houston-Downtown)

Intense heat waves can greatly affect the growth and survival of grasses. Grasses continuously grow new, expanding leaves throughout the vegetative growth period. High temperatures may affect expanding leaves more than fully flushed mature leaves. To determine whether heat waves affect younger leaves more than older leaves, we measured tissue damage caused by exposure to high temperatures for immature, intermediate, and fully expanded leaves. We exposed leaves of Johnson grass (*Sorghum halepense*) to 20-minute temperature treatments ranging from 28°C to 60.5°C in 2.5°C increments in 14 water baths. We quantified heat-induced tissue damage by measuring ion leakage, which is a measure of the ions leaking out of the treated samples. Curves of temperature-induced increases in ion leakage were similar among the immature, intermediate, and mature leaves. These results suggest Johnson grass has consistent tissue heat tolerance across leaf developmental stages, from small expanding leaves until leaves are fully expanded and mature. Instead of younger leaves being more sensitive, all leaf developmental stages experienced comparable membrane damage from short-term heat exposure. For plants that flush leaves throughout the growing season rather than solely during spring, maintaining heat tolerance throughout development could protect expanding leaves from tissue damage should a heat wave occur.

P121-U Sanger sequencing of microsatellite loci to characterize contributions of non-tandem indels to allelic diversity in Mentzelia pectinata. *Hannah Anthony [1], Ana Rodriguez [1], Joshua Brokaw [1] (1. Abilene Christian University)* Microsatellite markers are short, tandemly repeated DNA sequences (typically 2–6 bp) that vary in repeat number among individuals. These markers are widely used to assess genetic diversity in plant populations due to their high mutation rates and polymorphism. While variation is usually attributed to differences in the number of tandem repeat units, non-tandem insertions and deletions (indels) within regions flanking the microsatellite may also contribute significantly to allelic diversity, but these contributions are frequently overlooked. In this study, we used Sanger sequencing to characterize allelic variation at multiple microsatellite loci in Mentzelia pectinata, an annual wildflower native to southwestern California of ecological and conservation interest. PCR-amplified loci were sequenced from multiple individuals across geographically distinct populations. Sequence analysis revealed that, in addition to variable numbers of tandem repeats, non-tandem indels within flanking regions accounted for a substantial proportion of observed allelic differences, suggesting their role in shaping overall microsatellite diversity. These findings highlight the importance of incorporating sequence-level analysis in microsatellite studies to avoid underestimating or misinterpreting allelic variation. By linking sequence variation to population-level diversity, this work provides insights into the evolutionary dynamics of microsatellite loci and helps to establish the molecular toolkit for future studies of M. pectinata. Furthermore, this project demonstrates a cost-effective, student-friendly approach for integrating molecular techniques and population genetics in a genetics teaching laboratory leading to undergraduate research opportunities.

P122-U Using database searches and new collections to document the floristic diversity of the Independence Creek Preserve, TX
Olivia Fischer [1], Edmundo Avalos [1], Matt Allen [1] (1. Wayland Baptist University) The Nature Conservancy's Independence Creek Preserve (ICP) protects a spring-fed tributary of the lower Pecos River that supports unique plant communities within the broader Chihuahuan desert ecosystem. Efforts to document the area's floristic diversity began at least 80 years ago, but to date, no comprehensive flora has been published. Here we describe a project to create a flora for the preserve, both through new plant collections and searches of herbarium databases for plant specimens. Photos and collection data of ICP plants will be digitally archived in the Texas Oklahoma Regional Consortium of Herbaria (TORCH) database as a part of an ongoing WBU digitization project. Plant specimens will be housed in the WBU herbarium and in a newly established herbarium at the ICP. Since summer 2025, we have collected 97 plant species. Preliminary TORCH searches have yielded approximately 700 plant specimens previously collected in the area of the ICP. These specimens represent approximately 400 taxa. Survey efforts in 2026 will attempt to focus on areas of the preserve underrepresented among extant collections. Additionally, we will work to refine database search parameters to better identify plants collected within the current bounds of the ICP.

P123-U Revisiting Zygnema: assessing diversity and systematics using publicly available sequence data
Monserrat Alvarez [1], Anna Crowell [1] (1. University of Houston-Downtown) Freshwater green algae are ecologically important primary producers in freshwater habitats, contributing to nutrient cycling, oxygen production and supporting aquatic food webs. Within this diverse group, the genus *Zygnema* (Zygnematophyceae, Charophyta), exhibits extensive morphological and genetic diversity. This variation makes it a useful system for understanding evolutionary relationships among algae and exploring patterns of species diversification across different regions and environments. This study investigates the systematics of *Zygnema* isolates collected from various Californian watersheds. We retrieved rbcL gene sequences from GenBank, aligned them using MUSCLE, and constructed maximum likelihood phylogenetic trees in Geneious Prime. The resulting trees were examined to explore genetic relationships among the sampled isolates, identify well-supported clades, and compare patterns across different sequences and species annotations. By working directly with publicly available sequence data, we evaluated the utility of rbcL sequences for reconstructing *Zygnema* phylogeny and explored practical challenges such as variable sequence lengths, inconsistent annotations, and the need to generate reproducible phylogenetic trees. This analysis demonstrates how molecular data can complement

traditional morphological approaches, providing a framework for resolving species-level relationships in complex algal groups. Overall, this project presents an approach for investigating the genetic diversity of *Zygnema* using existing sequence resources. The findings emphasize the broader application of phylogenetic methods in understanding evolutionary and ecological relationships among freshwater algae and underscore the importance of careful data curation and reproducibility when using publicly available molecular sequences for biodiversity research.

P124-U The use of the rbcL gene to identify relationships among Nitzschia palea strains (Bacillariophyceae) Ambivalencia Bonilla Love [1], *Anna Crowell [1] (1. University of Houston-Downtown)* *Nitzschia palea* is a prevalent freshwater diatom, commonly used as a bioindicator to assess the health or quality of an environment due to their variable resiliency. Previous research has shown that *N. palea* represents a diverse strain complex and played an important role in diatom evolutionary history as an endosymbiont. Additionally, the ubiquity of *N. palea* allows it to be used as a reliable bioindicator throughout a wide range of freshwater ecosystems. However, its extensive diversity has left many aspects of its evolutionary history and genetic relationships unresolved. Here we show a maximum likelihood tree demonstrating the evolutionary nuances within the *N. palea* strain using the *rbc*L gene. Sequences were retrieved from GenBank, aligned using MUSCLE, and analyzed through maximum likelihood trees created in Geneious Prime. Our analyses revealed that the *rbc*L gene showed a more discriminative relationship between *N. palea* strains than previously used sequences such as *cox*1. Furthermore, we found a more nuanced relationship between the *N. palea* strains under study than previous research indicates. The *rbc*L gene alone did not fully resolve relationships within this complex, suggesting that multi-gene or genomic approaches will be necessary to capture the full extent of genetic divergence. These results highlight both the utility and limitations of *rbc*L for diatom phylogenetics and underscore the need for more comprehensive molecular datasets.

P125-U Understanding Evolutionary History Within Genus Amphora Using the rbcL Gene *Justino Gonzalez [1], Anna Crowell [1] (1. University of Houston-Downtown)* Diatoms are diverse microalgae, an important group that contributes substantially to global primary production, playing essential roles in aquatic food webs and biogeochemical cycles. Within this group, the genus *Amphora* (Bacillariophyceae) exhibits a wide range of morphological diversity, which makes it a useful model for studying species relationships and evolutionary patterns. Traditional classifications of *Amphora* have relied primarily on morphological characters, however, convergent traits limit the reliability of morphology in constructing evolutionary history. Here, we show the investigation of the evolutionary relationship among several *Amphora* species using the *rbc*L gene. Sequences were retrieved from GenBank, aligned using MUSCLE, and maximum likelihood phylogenetic trees were constructed in Geneious Prime. We examined the resulting trees to explore genetic relationships among sampled isolates, assessed clade support, and compared molecular groupings with existing morphology-based classifications. Our analysis demonstrates the utility of publicly available *rbc*L sequences for phylogenetic patterns within the genus *Amphora* and shows how molecular evidence can reveal structure not apparent from morphology alone. While some clades correspond with morphological groupings, other relationships remain unresolved, highlighting the limitations of single-gene analyses. Overall, this project presents a reproducible framework for leveraging existing molecular resources to investigate *Amphora* diversity and emphasizes the importance of integrating molecular and morphological data to improve our understanding of diatom systematics. By combining these approaches, this study contributes to a more accurate foundation for interpreting species relationships within the genus *Amphora*, informing taxonomy and future molecular sampling efforts.

P126-U Phylogenetic relationships among Sheathia species (Batrachospermales, Rhodophyta) *Alfredo Aldana Lopez [1], Anna Crowell [1] (1. University of Houston-Downtown)* Freshwater red algae are key contributors to stream ecosystems, serving as foundational species that provide food and habitat to aquatic macroinvertebrates. Within this group, the genus Sheathia (Batrachospermales, Rhodophyta) can be found in five continents, excluding South America, and exhibits considerable morphological and genetic diversity. Species within Sheathia are distinguished from other members of the Batrachospemales by unique morphological features and rbcL gene sequences, which have proven useful for resolving species relationships in molecular systematics studies. Here, we re-examine these morphological characters and evolutionary relationships among Sheathia species. We retrieved rbcL sequences from GenBank, aligned the sequences using MUSCLE and constructed maximum likelihood trees using Geneious Prime. Previous studies have found only a 6% sequence divergence of the rbcL gene among Sheathia species, revealing eight distinct clades and identifying heterocortication as a synapomorphy for the genus. In this study, our phylogenetic reconstruction of the genus Sheathia further explores genetic relationships among Sheathia species, reinforcing the earlier findings and contributing to a better understanding of the diversity and evolutionary history of this genus. Overall, our work highlights the value of molecular systematics using publicly available data for clarifying taxonomy and examining the biodiversity of freshwater red algae. This study has significant impact because it establishes

Sheathia into one of the larger genera in the Batrachospermales and provides a clearer understanding of the molecular similarities among its species.

P127-G Potential for Acorn Morphometric Analysis in Quercus Identification Zoe Matranga [1], *Juan Daza [1] (1. Sam Houston State University)* Oak trees (*Quercus* spp.) are famously difficult to identify, and exhibit both phenotypic and genotypic plasticity. Acorn morphology can be used to help distinguish between species, but descriptions are often limited or subjective. Here we used high resolution computed tomographies (HRCT) to analyze, quantify, and compare the acorn components (cupule, pericarp, and seed) between two closely related and frequently confused oak species (*Q. nigra* and *Q. arkansana*). Each acorn component was separated in the computer program Avizo Lite to create digital models, observe internal structure, and obtain volumetric data, with the goal of documenting significant morphological differences. Correctly identifying these trees matters because *Q. nigra* is common in Texas and beyond (S5, NatureServe), whereas *Q. arkansana* is ranked as critically imperiled in Texas (S1, NatureServe) but is frequently cut down because it is assumed to be *Q. nigra*. Results from this test could help distinguish between these species and aid conservation efforts. Additionally, if successful, morphometric analysis of acorns could expand beyond these two species and become another tool for untangling some of the more convoluted oak complexes.

P128-N AI/VR Digital Twin Prototypes for Supply Chain Operations Education Maria Burns [1], *Suresh Kumar Peddoju [1] (1. University of Houston)* This pilot study develops and evaluates Virtual Reality (VR)-based digital twins for the STEM education of supply chain operations. We will design small-scale virtual environments simulating supply chain security scenarios and test them with 75 undergraduate students to assess knowledge retention and engagement. Our prototype platform develops digital-twin modules for supply chain operations at a maritime seaport and a global distribution center. Students interact with these virtual replicas while AI/ML models track decisions and provide automated feedback within simulations. This novel methodology will enable real-time adaptive learning pathways based on individual performance patterns. We compare immersive digital-twin training with traditional lecture-based instruction, and simulation performance metrics reveal patterns in skill development. Data from 50 undergraduate students, divided into AI/ML/VR-trained and traditionally trained groups, inform analysis of learning differences. This study establishes the technical feasibility and pedagogical effectiveness of AI-enhanced digital twins for education on global supply chain security. Initial findings will guide improvements in simulation design, AI integration, and assessment methods, providing foundational evidence for scaling VR/AI training platforms, advancing experiential learning technologies in supply chain education, and informing future development of STEM curricula. **Keywords:** STEM education, digital twins, supply chain technologies, AI, VR, American workforce.

P129-U Improving Math Readiness for General Chemistry Through the Development of an Online Bootcamp Alfonso Lena Ordaz [1], *Ariyana Fisher [1], Lindsey Niehof [1], Lance English [1] (1. Temple College)* General chemistry is a gateway course with traditionally high attrition rates, and math readiness is consistently identified as a strong predictor of student success. Many students entering college chemistry lack proficiency in key mathematical concepts, which are assumed but not typically taught at the college level. A popular tool to assess readiness is the Math-Up Skills Test (MUST), a 20-item exam covering arithmetic and algebraic topics essential for general chemistry. A study across six Texas universities found the MUST to be a consistent predictor of chemistry success, with stronger correlations when the exam was administered without a calculator. To address the gaps identified by the MUST, we are developing an online bootcamp hosted on D2L and aligned with both MUST topics and Texas high school TEKS standards. Each module includes a brief primer, an open-access textbook chapter, curated video tutorial links, and a large set of Python-generated practice problems. Here we present the development and implementation of the first 16 modules, which were piloted with two general chemistry sections in Fall 2025. After completion of the remaining modules and expansion of topics based on student feedback, the bootcamp will be made available to all general chemistry sections and any other students seeking additional preparation. While similar content is available through publisher-integrated platforms, this project offers an open-access, low-cost, and scalable alternative to strengthen general chemistry readiness.

P130-U Bringing Biochemistry into Organic Chemistry through an LLPS-Based CURE Module Lila O'Donnell [1], *Lindsey Niehof [1], Ariyana Fisher [1], Luis Rodulfo [1], Steven Whitten [2], Lance English [1] (1. Temple College, 2. Texas State University)* Liquid–liquid phase separation (LLPS) is a biophysical phenomenon not commonly covered in lower-level chemistry courses; however, it offers a unique opportunity for chemistry educators to connect a wide-range of organic chemistry topics with biologically relevant systems. This study builds on previous work to develop a protein structure-driven CURE module for second-semester organic chemistry. The goal of the module is for students to investigate the effects of different cellular conditions or small-molecule supplements on the phase-separating (PS) potential of a model protein. A bioinformatics screen previously identified the intrinsically-disordered region of ZNF-326, which shows strong PS potential. The protein expresses well, purifies in a single step via Ni-NTA chromatography, and remains stable for months at -20°C. Here we evaluate the effects of L-arginine and hexane-1,6-diol–two small molecules thought to enhance and inhibit LLPS, respectively–as initial options for an inquiry-based lab. Surprisingly, L-arginine decreased PS-potential and was quantifiable via UV absorbance of the dilute phase. Hexane-1,6-diol increased PS-potential, but separation by centrifugation was incomplete, requiring a qualitative turbidity analysis. This limitation, combined with the time constraints of an undergraduate lab period, has motivated the development of a visible-range turbidity assay that eliminates the need for centrifugation. This approach also increases accessibility by enabling the use of handheld visible-range spectrophotometers instead of a limited number of shared benchtop UV-Vis instruments, supporting the feasibility of incorporating protein-driven LLPS experiments into organic chemistry lab curricula.

P131-G Engineering Lassi by Exploring How Common Ingredients Shape Fermentation and Quality Haran Prasad [1], *Hye Kim [1], Md Ariful Haque [1], Jaehyun Ahn [2], Seockmo Ku [1] (1. Texas A&M University, 2. University of Florida)* Fermented dairy beverages such as *Lassi* are important components of traditional diets and are increasingly examined for their microbial stability and physicochemical properties. Although plain *Lassi* has been studied previously, the effects of flavoring agents on its microbiological and chemical attributes remain poorly characterized. In this study we evaluated how four formulations, which included a control sample, salt added *Lassi*, sugar added *Lassi*, and mango fortified *Lassi*, influenced key microbiological and chemical parameters following traditional fermentation. All samples were prepared using identical starter cultures and identical fermentation conditions so that the specific effect of each formulation could be isolated. Here we show that the addition of sugar and mango increased post fermentation lactic acid bacteria counts, while the addition of salt resulted in comparatively lower microbial growth. Chemical analyses further demonstrated that pH declined the most in sugar and mango formulated samples, which was consistent with enhanced fermentative activity. Titratable acidity, total soluble solids, and protein stability varied significantly across the treatments, with mango fortified *Lassi* showing the highest total soluble solids and the most pronounced change in acidity. These results demonstrate that common flavoring ingredients can substantially influence both microbial behavior and chemical characteristics of *Lassi*. This challenges the assumption that these additions only modify taste without altering fermentation outcomes. In a broader context, this work highlights opportunities to optimize *Lassi* formulations to improve microbial viability, product stability, and consumer appeal, supporting the development of value added fermented dairy products.

P132-U From Concept to Cosmos: Cultivating The Next Generation of Our Future Space-STEM Workforce *Brett Jacobsen [1] (1. University of Texas Permian Basin)* Presented by the WEX Foundation and in partnership with NASA, the New World Awaits You (NWAY) program is dedicated to enriching the Space-STEM workforce by inspiring the next generation of innovators. The program sparks interest in pursuing post-secondary education and careers within the STEM field by empowering students in predominantly underserved and underrepresented communities. NWAY directly addresses the gap in these communities by implementing project-based learning (PBL) centered on authentic NASA challenges, such as the Artemis Lunar missions. There is a need for accessible, rigorous, and relevant out-of-school and in-school programming that equips historically underserved students for careers down the Space-STEM pipeline. Therefore, a curriculum focused on lunar habitation design, implemented through diverse young leaders, successfully engages hundreds of students and educators in the Engineering Design Process (EDP). These designs are effective motivators that bring excitement to the STEM field, delivering high-impact and hands-on education that connects students directly to space exploration. With a focus on middle schoolers, NWAY lays the foundation for building a critical pipeline that enables students to develop their curiosity about pursuing scientific research. Increased engagement in the field of STEM through student educators at the university level not only connects the younger generation but also provides the necessary education to those students with limited resources.

P133-U Creek to classroom: Exploring biodiversity through hands-on ecological investigation *Edmundo Avalos [1], Matthew Allen [1] (1. Wayland Baptist University)* Experiential learning has consistently demonstrated its value in meaningfully engaging students through active learning and directed inquiry in STEM. It aligns well with the Texas Education Agency’s “Effective Schools Framework” that emphasizes effective instruction. In the summer of 2025, we completed a research project at the Independence Creek Preserve, TX investigating streambed plant communities. Elements of that research could be directly adapted into a ninth-grade biology lesson that addresses TEKS B.13(D) which focuses on how environmental change affects biodiversity and ecosystem stability. This presentation will focus on ideas for how that research can be translated to the classroom through hands-on investigations of plant diversity. In those investigations, students will gain firsthand experience with how environmental change impacts biodiversity, granting them opportunity to develop their data-collection, graphing, and scientific reasoning skills.

P134-U Enhancing STEM Education Through Micro-Credentialing: Fostering Instrument Proficiency and Career-Ready Skills Corey Hobbs [1], *Darrell Fry [1] (1. Stephen F. Austin State University)* In the rapidly evolving landscape of STEM education, traditional curricula often fall short in providing hands-on experience with advanced laboratory instrumentation and fostering essential soft skills. This poster presents a micro-credentialing framework designed to bridge these gaps by integrating targeted training on technical instruments such as Gas Chromatography-Mass Spectrometry (GCMS) and Ultraviolet-Visible Spectroscopy (UV/Vis) with skill-building assessments. The program's core objective is to cultivate deep conceptual understanding of these instruments through modular, competency-based modules. Students engage in individual assessments to build self-autonomy, master basic instrument operation, improve data analysis, and build confidence troubleshooting independently. Group-based projects simulate real-world collaboration, enhancing teamwork while exposing participants to a broader array of laboratory machinery, including HPLC and FTIR systems. By emphasizing practical lab immersion, the initiative aims to equip students with a versatile skill set—encompassing technical expertise, critical thinking, and adaptability—directly aligned with industry demands. Preliminary implementation in undergraduate cohorts has shown increased confidence in instrument handling and improved career preparedness, as evidenced by participant feedback and skill proficiency metrics. This micro-credentialing approach not only democratizes access to high-end STEM tools but also promotes lifelong learning, preparing graduates for diverse careers in research, pharmaceuticals, and environmental science. Future expansions could incorporate digital badges for broader recognition and scalability, physical incentives for an increased student participation, and collaboration in with instrument manufacturers and industry leaders.

P135-U Cost-Effective Spectrophotometry for K-12 Victoriano Cooper [1], *Dennis Gibson [1], Bobby Womack [1], Wade Ashby [1] (1. Howard Payne University)* The purpose of this research is to develop a cost-effective method for analyzing the sugar content of solutions. This research focuses on the K-12 teaching setting and schools that struggle with underfunding. The goal is to develop a setup similar to a spectrophotometer by using a phone and computer coding. It was found that Texas public schools rank 41st in the nation for fiscal health. This prevents teachers from investing money in expanding their curriculum. One instrument that can be particularly useful is a spectrophotometer, a machine used to measure the intensity of light that passes or reflects from a sample. This tool can be useful in K-12 schools across various disciplines, including chemistry and statistics. This instrument can also cost up to $1,000 for the machine, software, and maintenance costs. The discussed research for a cost-effective method can drastically decrease the cost of the machine while also increasing access to technology similar to a spectrophotometer. The cost-effective method will still be useful in chemistry and statistics, but will also be geared toward upcoming engineers and computer programmers. To develop this technique, a spectrophotometer was used to confirm that the cost-effective method can make an acceptable calibration curve and quantify the sugar content in solution. In future experiments, the cost-effective method will be tested more extensively for reproducibility and reliability.

P136-G Girl Scout STEM Education and Engagement through Field Activities Kendall Kinsey [1], *Steven Koether [1], Diane Neudorf [1] (1. Sam Houston State University)* We are creating a science, technology, engineering, and math (STEM) field activity that seeks to grow Girl Scouts' interests and attitudes towards STEM. There are knowledge gaps between STEM interests and attitudes with this demographic and setting (i.e., age group, Girl Scouts, non-formal). The hour-long activity will be associated with field ornithology to improve the participants' experience with competition, collaboration, creation (making), discovery, teaching, and performance skills. This will be accomplished through a ten-minute lecture, a group hands on bird nest deconstructions exercise, and a presentation by the participants on their findings. We will be using the framework for observing and categorizing instructional strategies (FOCIS) survey to compare participants' interests and attitudes in the seven main modes of active learning. This survey will be given pre-/post-activity. Our study will help leaders of non-formal education experiences cultivate the next group of scientists.

P137-N Bridging the AI Literacy Gap: STEM Student Perspectives on Artificial Intelligence in Higher Education

Wendi Wolfram [1], Liz Fitzgerald [1], Shama Grimmage [1], Jenna Odeh [1], Josh Lackey [1], Naseeba Abdeljaber [1] (1. Purdue Global University)

As artificial intelligence (AI) transforms a variety of tools used in higher education, understanding how STEM students perceive and engage with these tools is essential to developing an informed curriculum design. While AI technologies are developed to enhance efficiency, creativity, and access, the uneven trends in AI literacy across student populations present a growing challenge to equitable learning outcomes. This study explores AI perception and use among undergraduate and graduate students in STEM disciplines. Using survey data from multiple institutions, we analyzed student knowledge, confidence, and ethical concerns related to AI use in academic settings. Results indicate that while many students use AI in some capacity, many lack a clear understanding of its true capabilities, limitations, and the responsible application of its use. Additionally, significant gaps emerge between traditional and adult learner populations, highlighting the influence of prior educational experience and digital exposure on AI confidence and trust.

Here we show that targeted AI literacy instruction, particularly emphasizing transparency, critical evaluation, and ethical awareness can help close these gaps and improve student engagement and success. These findings provide evidence-based recommendations for embedding AI literacy into existing STEM curricula and faculty development initiatives. In viewing AI tools as not just technological innovations but as a critical literacy, this research underscores the need for universities to prepare students for an evolving digital ecosystem where human insight and machine intelligence intersect.

P138-U A Taxonomically and Ecologically Diverse Marine Vertebrate Assemblage at the end of the Cretaceous in Texas (USA) Kieu Nguyen [1], *Thomas Stidham [1] (1. Austin College)*

The late Maastrichtian Corsicana Formation exposed in eastern parts of Texas contains significant accumulations of marine vertebrate fossils that have not been examined in detail. The uppermost Corsicana Formation fauna includes a minimum of 29 taxa spread across 19 families including sharks, rays, and bony fishes. The shark fauna is the most taxonomically diverse with members of Lamniformes (including white sharks Lamnidae and sand sharks Odontaspididae), Carcharhiniformes (including cat sharks Scyliorhinidae and requiem sharks Carcharhinidae), Hexanchiformes (cow sharks Hexanchidae), Squaliformes (dogfish Squalidae), and Orectolobiformes (carpet sharks Orectolobidae and collared carpet sharks Parascyllidae). The rays and relatives include species of Torpedinidae (electric rays), Dasyatidae (whiptail rays), Ganopristidae (extinct sawskates), Myliobatidae (eagle rays), and Rhinobatidae (guitarfish). Most bony fish skeletal fragments remain unidentified, but identified teeth include Enchodus (Enchodontidae) and Albula (Albulidae). At present, the teeth of Enchodus and Scyliorhinidae are the most common among the identified specimens. Six of the catshark specimens were identified at the species level. The scyliorhinidae species consisted of Platrhizoscyllium jaegeri, Porodermoides spanios, and Cretascyliorhinus. This diverse latest Maastrichtian fauna suggests that the mid-Campanian marine extinction either did not significantly impact this region or that marine vertebrate diversity rebounded prior to the end of the Cretaceous. This fauna would not support the proposal of a sustained decline in marine vertebrate faunal diversity leading up to the mass extinction. However, the fauna includes a mixture of taxa that did not survive into the Paleocene, taxa with a reduced Cenozoic diversity, and diverse clades living today.

P139-U Examining the survival and initial recovery of fish after the Cretaceous mass extinction of the Kincaid Formation in Texas. *Diana Kettler [1], Emma Potts [1], Thomas Stidham [1] (1. Austin College)* The early Paleocene sediments exposed on the Brazos River record the initial aftermath and recovery after the mass extinction 66 million years ago. Fossils deposited ~200,000 years after the extinction include diverse invertebrates and vertebrates, particularly the bones and teeth of fish, rays, and sharks. Here we show the identification of nearly 200 dental specimens demonstrates the presence of sharks (Triakidae, Ginglymostomatidae, Scyliorhinidae, and Odontaspididae), rays (Dasyatidae, Rajiformes, Myliobatidae, and Rhombodontidae), and bony fish (Enchodontidae and Albulidae). The most common taxa in the fauna are benthic durophagous rays including *Dasyatis, Delpitia reticulata, Dasyrhombodus bondoni,* and *Atlantobatis weltoni.* The presence of diminutive specimens of the Texas endemic rajiform *A. weltoni* increases known survivorship and contrasts with the global pattern suggesting little rajiform survival. The shark teeth derive from small-bodied individuals of *Palaeogaleus* and *Scyliorhinus*. The shallow water shark fauna were largely benthic predators, supporting a global shift from larger bodied sharks (mostly lamniforms) to smaller, bottom feeding, non-durophagous Carcharhiniformes. Among the identified bony fish are bonefish (*Albula*) and *Enchodus*, two lineages that survived the extinction. The earliest Paleocene vertebrate fauna exhibits many taxa that appear to have survived locally, and their overall small size suggests a post-extinction lilliput effect.

P140-U Morphological differences in among populations of Amphisbaenians from Puerto Rico *Minji Kim [1], Juan Daza [1], Oscar Ospina [2], Camilo Linares-Vargas [1] (1. Sam Houston State University, 2. Johns Hopkins All Children's Hospital)* Amphisbaenians or worm lizards are a bizarre group of lizards that live underground. Today there are four species of amphisbaenians living in the Island of Puerto Rico. A recent study discovered genetic differences between the populations of *Amphisbaena caeca*, and some external differences in scales. In this project we are using skeletal characters to find additional characters that can be used to resolve the taxonomic status of some of these populations. We are using X-ray and CT Scan data to study members from different populations. In this study we are also using 3D morphometrics using landmarks in the skull to capture slight variations on cranial morphology. The parietal bone has an anterolateral flange in one population. We want to be able to quantify this variation in the parietal bone margin, to determine the validity of this character as a potential taxonomic character.

P141-U Comparative study of male aggression of food generalists and specialists in Drosophila species *Yuliana Santos Ventura*[1], *Abdulrahman Omar*[1], *Laurie Neuman*[1], *Yuan Yuan Kang*[1] *(1. University of Houston-Downtown)* Animals often display aggressive behaviors to secure food, mates and territory—behaviors that can be modeled in *Drosophila*. While *D. melanogaster* and *D. simulans* are dietary generalists, *D. sechellia* is a specialist that feeds almost exclusively on the noni fruit (*Morinda citrifolia*). We investigated how food source influences aggression in these species and whether these behavioral responses can be shaped by epigenetic modification across generations. Previous work from my lab found that the food specialist *D. sechellia* displayed higher aggression when placed on noni-containing food, while generalists showed similar levels of aggression regardless of food type. We hypothesized that this food-specific aggression was subject to epigenetic modifications and provided evolutionary advantages for food specialists competing in their natural environments. To test this, we reared *D. simulans* and *D. sechellia* on their non-preferred diets for at least ten generations. Single pairs of male flies from the same species (intra-species) were socially isolated and loaded into behavioral arenas containing normal or noni fruit. Aggressive behaviors (lunging, chasing, fencing) were scored on and off food across multiple trials. Preliminary results raised the possibility that prolonged exposure to non-preferred diets may alter the food-specific aggression displayed by *D. sechellia*. To test whether this aggression has significance in the ecological environment where *D. simulans* and *D. sechellia* coexist, we simulated the competition using interspecies pairing. Our data from the interspecies fighting between *D. simulans* and *D. sechellia* suggested a higher level of competition on noni food, consistent with our hypothesis.

P142-U Spontaneous Mutations on Antibiotic Resistance in Escherichia coli *Julian Ramirez*[1], *Brent Orji*[1], *Christian Buford*[1], *Natalie Zarate*[1], *Wei-Chin Ho*[1] *(1. The University of Texas at Tyler)*
Evolution is driven by random genetic changes known as spontaneous mutations, but we still have limited information about how mutations arise. For example, environmental conditions might influence which types of mutations occur. Gaining insight into this process is key to predicting how microbes adapt to new environments. Usually, the evolution of traits like antibiotic resistance results from a combination of mutation, natural selection, and genetic drift. However, the relative contribution of each factor is not always clear. This uncertainty makes it difficult to predict or control how quickly and in what way resistance will develop in bacterial populations. In this research, we aimed to isolate the impact of mutations alone by repeatedly streaking single bacterial colonies. Doing this helps maintain random mutations, increases genetic drift, and reduces selective pressure. Using this approach, we focus more on how mutations alone affect the development of antibiotic resistance. Specifically, we cultured E. coli on nutrient-rich media, both with and without the antibiotic's ampicillin and streptomycin. Then we measured how resistant the bacteria had become to these antibiotics by observing bacterial growth. Our results showed that the bacteria developed higher resistance to streptomycin, but not to ampicillin. This indicates that spontaneous mutations tend to generate more resistance-related changes for streptomycin. These findings improve our understanding into how different antibiotics may influence the supply of resistance mutations. They also explain how mutations and environmental factors interact to shape microbial evolution and antibiotic resistance over time.

P143-U Fungal Genotyping and Phylogenetic Categorization of Lower Attine Ants Cyphomyrmex wheelri and Mycetosoritis hartmanni *Lunden Hahn*[1], *Erin McFarland*[1], *Jon Seal*[1], *Katrin Kellner*[1] *(1. University of Texas at Tyler)* Lower attine (fungus-growing) ants cultivate a diverse group of fungal symbionts. The evolutionary relationships and biogeographic distributions of these fungi, however, remain incompletely understood. In particular, the lower-attine fungal lineages are grouped into major clades 1 and 2, with clade 2 being quite rare in the Americas and represented by only a single documented record. To investigate the diversity of fungal cultivars *Cyphomyrmex* wheeleri (CW) and *Mycetosoritis* hartmanni (MH), we sequenced fungal internal transcribed spacer (ITS) regions from colonies collected in the field and compared them to other published sequences. Current phylogenetic analysis indicates that these samples may be present in both major clades, suggesting previously unrecognized diversity among these lower attine mutualisms. To refine our phylogenic diagram and overall understanding, we aim to utilize alternative primer sets due to limitations with the current ITS markers. Ongoing analyses will clarify the placement of CW and MH fungal cultivars within the lower attine fungal tree and contribute to a more complete understanding of cultivar evolution and distribution across the lower attines.

P144-U The Effects of Historical Adaptation of Microbes in New Stressful Environments *Ivan Mendez*[1], *Kingsley Amoateng*[1], *Sora Kim*[1], *Julian Ramirez*[1], *Natalie Zarate*[1], *Wei-Chin Ho*[1] *(1. The University of Texas at Tyler)* Adaptation is a fundamental principle in evolutionary biology, as it allows organisms to develop traits that may affect their survival and reproduction in specific environments. Adaptive mutations often improve an organism's fitness in one environment, but when changing environments, the effects of the mutations may change. The historical effects of adaptive mutations are largely unknown, but they substantially determine the evolutionary dynamics in the early adaptation to complex environments. Moreover, if previously acquired mutations retain their advantages, organisms may transition more easily into new environments. However, if these mutations are detrimental in different environments, they may inhibit survival and adaptation. To explore this question, we examined three distinct bacterial populations evolved in (LB) medium for 900-days. The populations accumulated mutations that improved their fitness within this specific environment. To determine whether these acquired mutations were beneficial, neutral, or harmful in new environments, we transferred the adapted microbes into four new stressful environments: LB broth with alcohol, LB broth with $MgSO_4$, LB broth with HCl, and Glucose minimal medium. The results showed an idiosyncratic nature of historical adaptation, an unpredictable pattern of fitness effects. In three of the 12 cases studied, historical mutations provided significant fitness advantages in new environments, suggesting some mutations are useful. However, in five cases, beneficial mutations became stressful, indicating that microbes thriving in LB broth struggled in the new environment. Moving forward, we plan to examine the mutations in more detail to determine the genetic basis of these population-specific differences.

P145-G Resolving the Sphaerodactylus macrolepis species complex in the Puerto Rican bank Lilly Nguyen [1], *Juan Daza [1], Alexandra Herrera Martinez [1] (1. Sam Houston State University)*

Island groups offer unique insights on evolutionary processes. The Puerto Rican bank (including the islands of Mona, Monito, Desecheo, and the Spanish, United States, and British Virgin Islands) boasts great diversity of dwarf geckos. The *Sphaerodactylus macrolepis* complex is found only in Puerto Rico and the Virgin Islands, but recently, a combined analysis of molecular and morphological data resolved the relationships within this complex, elevating two subspecies, *S. grandisquamis* from the main island of Puerto Rico and *S. inigoi* from Vieques and West Culebra to the species level, and restricting *S. macrolepis* to all populations in East Culebra, and the rest of the Virgin Islands. *S. macrolepis* is a cryptic species complex that displays geographic order; however, coloration and pigmentation pattern seems to be consistent in all clusters identified with molecular data. Using morphological and morphometric data, combined with geographical analysis, we hope to clearly redefine the *S. macrolepis* complex. We will use external characters, measurements of the skeleton using digital X-rays and computed tomographies to explore additional variation within the Virgin Islands populations.

P146-U The role of Trachymyrmex smithii ants in structuring bacterial communities in their symbiotic fungus gardens *Sorrel Estrada [1], Erin McFarland [1], Katrin Kellner [1], Jon Seal [1] (1. University of Texas at Tyler)* This project examines the bacterial communities associated with the fungus gardens grown by Trachymyrmex smithii ants. The goal was to explore the role of structuring bacterial communities in fungus garden strains. In particular, we were interested in whether bacterial communities in T. smithii ant fungus gardens were different when ants were forced to grow a novel fungus, compared to ants growing a native fungus. Twenty queens were roughly split into two groups, each containing ten queens, which were obtained in July 2022 from a population near El Paso, Texas. The queens were forced to grow either a native or novel fungus. The novel fungus was obtained from a distantly related species, Acromyrmex versicolor, the desert leaf-cutting ant. Ants appeared to struggle in growing the novel fungus, as growth was poor over several months compared to the more productive queens growing native fungi. Likewise, their ability to produce offspring from the novel fungus was low. Using bioinformatic tools, we describe the differences between the bacterial communities of the two types of fungal species grown by the queens of T. smithii.

P147-U Quantitative Trait Locus mapping and functional validation of genes regulating circadian controlled locomotion in Drosophila species *Delwin Sunil [1], Yuan Yuan Kang [1], Benjamin Soibam [1], Pedro Rodriguez Navarro [1], Isabela Rodriguez Avila [1] (1. University of Houston-Downtown)* Circadian rhythms regulate many physiological and behavioral processes, including daily patterns of locomotion, but the genetic factors controlling these rhythms are not fully understood. Our lab has conducted a quantitative trait locus (QTL) mapping between two sister *Drosophila* species, *D. simulans* and *D. sechellia*, which display different 24-locomotive activities, as measured by the *Drosophila* Activity Monitoring (DAM) assay. Any candidate genes identified to be associated with the phenotype are further explored in D. melanogaster, a model system that is more widely studied and with more genetic tools available. Our QTL analysis identified significant peaks with high logarithm of odds (LOD) scores for morning and evening anticipation, but not for day and night activity. Further examination of the highest peaks identified candidate genes in neural pathways previously known to be involved in circadian rhythm regulation. Their proximity to the QTL peaks and their potential relationship to core circadian pathways make them especially promising candidates for further study. To validate their roles, we adopted mutant and RNA interference (RNAi) to knock down gene expression and examine how the loss of the genes might affect circadian locomotion. If validated, this unbiased screen approach can discover genes that have not been previously identified in regulating circadian controlled activities and further advance our understanding of the mechanisms underlying circadian rhythm.

P148-G Comparing cranial telescoping in select squamate groups

Paige Donkers [1], Juan Daza [1] (1. Sam Houston State University) Telescoping is a phenomenon in which cranial bones develop an extensive sutural overlap and proximity, especially in bones of the anterior part of the skull. This is widely known among cetaceans but has been observed to occur in some extant squamate groups, such as sphaerodactylid geckos, pygopods, and varanids. Telescoping in squamates has been understudied, as we do not know for certain why this event occurs only in some groups and what function it serves. However, telescoping has also been observed to occur in some mosasaurids, and some parallels have been proposed with whales. By comparing this ancient lineage to living squamate groups, we may be able to establish some parallels between telescoping in squamates. By using computerized tomography (CT) scans to create 3D models and calculate the extent of overlapping for specimens in each group, we expect to quantify the degree of telescoping between species with telescoped skulls. From there we can determine if there is a common factor that determines the convergent evolution of telescoping. By understanding what telescoping looks like in squamates we will gain a better understanding as to why this phenomenon occurred within multiple independent lineages.

P149-G The Fungal Microbiome of Pheidole adrianoi, an ant that associates with mycorrhizae *Erin McFarland [1], Jon Seal [1], Katrin Kellner [1] (1. University of Texas at Tyler) Pheidole adrianoi* is a small ant found in the sandy pine forests in the southeastern US. This ant is unrelated to the true fungus-gardening ants, yet it appears to form a symbiosis with fungi. These ants have been observed to collect and line their nest chambers with the sclerotia of a mycorrhiza associated with the roots of pine trees. The ants create a structure that consists of a solid, connected layer of fungus inside the nest chamber that stays intact when excavated. Ants will rebuild this after it is disturbed. As very little is known about this potential symbiosis, we conducted an initial study describing the fungal and bacterial microbiome of these species using ITS and 16S Illumina-based sequencing, respectively. The overarching goal is to describe fungal and bacterial microbiomes to ultimately understand more about the basis of the interaction between *P. adrianoi* and its fungus. We found that the fungal and bacterial microbiomes of the mycorrhizal chamber lining are significantly distinct from the microbiomes of the non-chamber soil. This non-random structure suggests that the ants are structuring a bacterial and fungal microbiome that surrounds their nest chambers.

P150-U Assessing Male Mating Success Across Proto-Y Genotypes in Musca domestica *Juan Fuentes [1], Alexis Hernandez [1], Lotus Ha [1], Landon Sanz [1], Tania Barcenast [1] (1. University of Houston-Downtown)* Variation in sex chromosomes can drive behavioral and physiological adaptations across environments. In the house fly *(Musca domestica*), males possess a genetic system in which the male determining gene, *Mdmd*, can be located on any of several chromosomes, although in nature it is most commonly found on the ancestral Y (Y^M genotype) or a previously autosomal chromosome III (III^M), thereby converting it into a proto-Y chromosome. This provides a model for testing how sex chromosome variation influences reproductive success and behavior. Previous studies found that III^M males outcompete Y^M males for access to female mates, but those assays were performed in strains of nearly isogenic flies from a primarily III^M genetic background. To address this limitation, we performed competitive mating assays using males derived from a Y^M genetic background to determine whether genetic background influences this observed mating outcome difference. In addition, we also examined whether female genotype affects male competitive outcomes. Using a controlled mating assay, one Y^M male and one III^M male were placed with a single virgin female in individual containers. For each trial, we recorded copulation latency (time taken to initiate mating) and which male the female mated with. This poster presents whether male proto-Y chromosome genotype affects male competitive performance, how outcomes compare with previous studies conducted in III^M derived strains, and how these results may relate to sexual selection and gene environment interactions. Overall, this research highlights how small genomic differences shape reproductive behavior and support the persistence of sex chromosome polymorphisms across populations.

P152-G Diet and parasites of newly documented Hemidactylus from south Texas, USA *Kevin Green [1], Drew Davis [1] (1. Eastern New Mexico University)* Invasive species have the potential to disrupt native communities and ecosystem function by altering species interactions through many different processes. Direct and/or indirect competition, predation, and pathogen spillover are all ways in which invasive species can negatively affect native communities. There are four non-native species of *Hemidactylus* (Squamata: Gekkonidae) recognized to occur in south Texas, USA: *H. turcicus* (Mediterranean Gecko), *H. mabouia* (Wood Slave), *H.* aff. *malcolmsmithi*, and *H. garnotii* (Indo-Pacific House Gecko), with the latter three only being recently reported. Limited data exist surrounding these three recently reported species of *Hemidactylus* in the region, and efforts to investigate the potential consequences of their presence and the threat they pose to native communities are needed. Here, we investigated the diet and parasite load of these three recently established species. Three sampling trips were conducted in Cameron and Hidalgo counties to collect *Hemidactylus* specimens. Over the course of the three sampling trips, 5 *H. mabouia* and 210 *H.* aff. *malcolmsmithi* were collected; no *H. garnotii* were detected. Individuals were euthanized, and stomachs (from all individuals, N = 215) and lung pairs (from N = 128) were removed for later examination to determine diet and the presence of parasites, respectively. Stomach contents were sorted and identified to order using a dissecting microscope, and parasites were identified using both morphological and molecular techniques. Here, we present preliminary results from these studies and discuss ecological implications. These findings will provide information to inform future assessments of these introduced *Hemidactylus* on native species.

P153-U Investigating Post-Prandial Thermophily in a Fossorial Snake Species *Julian Villanueva [1], William I. Lutterschmidt [1] (1. Sam Houston State University)* Many reptile species exhibit post-prandial thermophily, increasing body temperature (T_b) to enhance digestive efficiency. Reptiles commonly achieve this increased T_b through basking and active behavioral thermoregulation.

However, are such thermophilic responses to prey ingestion, observed in reptiles that are fossorial and/or nocturnal in activity? The Sunbeam snake (*Xenopeltis unicolor*) is distributed widely throughout Southeast Asia but understudied and rarely observed in the wild due to its secretive fossorial and nocturnal behavior. We investigated the thermoregulatory responses of *X. unicolor* to prey ingestion and early digestion to determine if this species demonstrates post-prandial thermophily similar to diurnally active snakes. Sunbeam snakes (n = 6) were obtained from the Ophidian Research Colony (ORC, directed by Dr. Neil B. Ford, University of Texas - Tyler) and placed in a laboratory thermal gradient to observe temperature preference under post-absorptive and the post-prandial digestive conditions. We discuss our findings with relation to the ecological or physiological constraints associated with fossorial and nocturnal behavior.

P154-U Seasonal occurrences of mammals in Natchitoches parish Louisiana *Blake Willey [1], Chad Cryer [1] (1. Temple College)*

Understanding seasonal dynamics of mammal communities is essential for wildlife management and conservation in bottomland hardwood and mixed-agricultural landscapes of the Lower Mississippi Alluvial Valley. We used remote camera-trap surveys to quantify seasonal occurrence and detection patterns of terrestrial mammals in a 400-acre property in Natchitoches Parish, Louisiana. Between May 2025 and February 2026, we deployed motion-triggered game cameras across two sites on the property which represent the dominant local habitats ranging from bottomland hardwood to agricultural edge. Cameras operated continuously through the data collection period, yielding numerous time-stamped images used to identify individual species, as well as detection rates. We documented a diverse assemblage of common regional mammals including white-tailed deer, raccoon, Virginia opossum, nine-banded armadillo, feral hog, coyote, and carnivores such as bobcat and gray fox with species-specific seasonal peaks. Herbivores showed higher detection in late fall–winter, coincident with mast and agricultural harvest periods, while omnivores and carnivores exhibited elevated activity in the summer months, likely reflecting reproductive cycles and prey availability. Overall, our results help to highlight the seasonal structure in mammal occurrence at landscape scales in Natchitoches Parish and demonstrate the utility of game cameras for long-term monitoring. These patterns can be useful to humans as the have implications for timing of management actions provide a baseline for tracking future changes driven by land-use or climate shifts.

P155-U Influence of ultraviolet light on the distribution of fluorescent lichen *Layla Salina [1], Jordan Whittaker [1], Caleb Smith [1], Chad Cryer [1] (1. Temple College)* Fluorescent lichens are symbiotic assemblages capable of emitting visible light under ultraviolet (UV) excitation. They offer a unique biological model for examining environmental adaptation to UV radiation. This study investigates broad-scale patterns in the distribution of florescent lichen species across the United States, spanning habitats from high-UV environments of Texas to low-UV, shaded forests of Oregon. Using a grid method, average lichen coverage data was collected on trees found in environments that range from high, medium, to low levels of UV radiation. Preliminary analyses indicate that the distribution of fluorescent lichen is positively correlated with moderate to high ambient UV exposure, suggesting that fluorescence may play a role in photoprotection or stress mitigation. Conversely, regions with persistently low UV levels exhibited reduced fluorescent lichen distribution. These findings highlight fluorescence as a potentially functional trait influenced by large-scale environmental gradients, and they underscore the importance of UV radiation as a driver of lichen biogeography. This work contributes to a growing understanding of how symbiotic organisms respond to atmospheric and climatic variables and provides a foundation for predicting future distributional shifts under changing UV regimes. Further studies should look at the chemicals produced by lichens that help protect their photosynthetic symbionts in high UV areas by acting as a sunscreen, reflecting excess energy as light in the UV spectrum. This could be of use to humans as an alternative to traditional sunscreens, which can be harmful for the environment.

P156-U Arachnid Diversity at Firebase Libby and Callahan County *Jacob Wooten [1], T.J. Boyle [1] (1. McMurry University)*

The goal of this research is to determine the diversity of arachnids in Callahan County. Collections were made at 3 localities using pit-fall traps, flip traps and by hand. Based on literature searches, there are an estimated 70 different arachnid species in Callahan county. Thus far, we have collected and identified 57 species. A species accumulation curve based on our collection data suggests that future collections could still provide more new species.

P157-G The Impact of Social Isolation on Madagascar Hissing Cockroaches *Asmau Shiyanbade [1], Diane Neudorf [1], Sibyl Bucheli [1] (1. Sam Houston State University)* Social interactions play a vital role in shaping behavior and development across many animal groups, but the impact of social experience in advanced subsocial insects remains poorly understood. We investigated how social isolation alters exploratory behavior, avoidance responses, physical development, and social competence in the Madagascar hissing cockroach (*Gromphadorhina portentosa*). We tested individuals reared in groups and in complete isolation to quantify movement patterns. Growth and maturation were monitored biweekly, and we used a social reintegration test to assess how isolation influences later interactions with unfamiliar conspecifics. We predicted that isolated cockroaches would show increased avoidance, reduced exploratory activity, slower growth, and impaired social responses. We will discuss the findings from our study in the context of how social insects respond to social deprivation and the broader relevance to behavioral plasticity, sociality, and the ecological relevance of social experience.

P158-U Influence of tree bark pH on lichen distribution
Ruby Tapia [1], Jada Gosey [1], Cyah White [1], Alicia Hawkins [1], Chad Cryer [1] (1. Temple College) Lichens are composite organisms formed from a mutualistic relationship between a fungus and a photosynthetic partner, usually algae or cyanobacteria. They are found in diverse environments and are well known for their ability to colonize surfaces such as rocks, soil, and tree bark. Lichen communities are shaped by a complex interplay of microenvironmental conditions, among which bark pH plays a critical role. This study investigates how bark pH varies across common tree species in Central Texas and how these differences influence lichen distribution. Bark samples were collected from multiple tree species, and their pH levels were measured and compared to the average lichen coverage measured on each tree species. Preliminary analyses indicate that tree species with more alkaline bark, such as Ulmus crassifolia and Celtis laevigata, support higher lichen richness and greater abundance of foliose and fruticose forms. In contrast, species with acidic bark, including Quercus fusiformis and Quercus buckleyi, tended to host communities dominated by crustose lichens with lower overall diversity. These patterns suggest that bark pH acts as a key driver of lichen niche partitioning across Central Texas. Understanding these relationships enhances our ability to use lichens as bioindicators of environmental quality and provides insight into how shifts in tree community composition may alter regional lichen biodiversity.

P159-U Nest Density of Atta texana in a Temperate East Texas Forest *Megan Rhea [1], Erin McFarland [1], Jon Seal [1] (1. University of Texas at Tyler)* *Atta texana* are the Northernmost species of leafcutter ant, which are commonly found in the Southern United States and some parts of Northern Mexico. These ants are unique in their ability to thrive in temperate environments, unlike closely related leafcutter species such as *A. cephalotes* and *A. colombica*, which are native to tropical regions. Leafcutter ant research has primarily focused on these tropical species, leaving the more temperate species relatively understudied in the field. Leafcutter ants form large networks of tunnels and chambers underground, which can span several hundred meters in width and reach depths of up to 6 meters. Their large colony size requires adequate space, therefore, these colonies have lower abundance and wider territory than would be seen in smaller colonies, such as *Trachymyrmex septentrionalis* or *Pogonomyrmex badius*. This project aims to quantify the population density of *Atta Texana* and compare findings to related Atta species found in the tropics. *Atta texana* colonies in Lindsay Park, located in Tyler, Texas, were observed and mapped using GIS methods. The density was found to be 7.216 hectares per colony, suggesting that *Atta texana* colonies are less dense than their tropical relatives. These findings add to our understanding of the ecological role and impacts of these ants.

P160-U Are they Fools, or Will they Learn? Behavioral adaptation in Physarum polycephalum
Ella Johnson [1], Hannah Loya [1], Samuel De La Garza [1], Mary Kay Johnston [1] (1. Concordia University Texas)
Decision-making and learning are fundamental cognitive processes that shape how organisms interact with their environment. While cognition has traditionally been associated with neural taxa, modern research has demonstrated the capability of non-neural organisms to employ heuristics and learning to adapt their behavior and become more successful foragers. *Physarum polycephalum* (Myxomycota: Physaraceae), a common acellular slime mold, exhibits decision-making capabilities and habituation, a simple form of learning, which enable its foraging behavior to align with the predictions of optimal foraging theory. However, it has not been shown if *P. polycephalum* is capable of associative learning, or if repeated exposure to misleading environmental cues can alter its foraging heuristics. Our experiment sought to evaluate whether the heuristic processes of *Physarum polycephalum* can be influenced to make different nutritional trade-offs by the repeated application of cues. Our results suggest that slime molds acclimate quickly to the experimental environment, based on pseudopod body mass allocation and travel time to patch. We also show that individual slime molds, though genetically identical, have idiosyncratic responses. This may indicate that previous conditions have consequences for present behavior. While the mechanisms underlying

cognition and decision-making vary across taxa, the rules and strategies favored by decision-makers have commonalities which give insight into what heuristics tend to be favored by natural selection. The results of this experiment provide insight into adaptive decision-making in non-neuronal organisms which can be applied across fields of ecology, zoology, and neuroscience.

P161-U Nasal botfly prevalence in the 2025 hunting season of white-tailed deer Tyler Miller [1], *Chad Cryer [1] (1. Temple College; 2. Cryer Taxidermy Shop)* Nasal botflies (family *Oestridae*), are obligate parasites of white-tailed deer (*Odocoileus virginianus*), can influence host health, behavior, and population dynamics, yet regional prevalence varies widely and is often under documented. This study assessed the prevalence and intensity of nasal botfly larvae during the 2025 hunting season in central Texas, a region characterized by dense deer populations and highly variable climatic conditions. Nasal cavities from hunter-harvested deer were examined across multiple counties. For each deer, age, sex, antler score, harvest time and location were recorded when possible, and larvae were also identified to developmental stage when possible. Preliminary analysis revealed a measurable presence of nasal botflies across the surveyed area, with prevalence varying significantly by age class and geographic location, but not by sex or antler score. Adult deer exhibited higher infestation rates and greater larval loads than subadults, suggesting increased exposure duration or age-related susceptibility. Spatial patterns indicated localized hotspots potentially associated with microclimatic conditions favorable to botfly activity. These findings contribute new baseline data for central Texas and highlight the importance of continued monitoring to understand how environmental change, deer density, and seasonal climatic shifts influence parasitic dynamics in regional cervid populations.

P162-N Composting Polystyrene Using Superworms: Some Practical Applications Tara Hansler [1], *Richard Patrock [2] (1. Texas Southmost College, 2. Texas A&M University)* Polystyrene (PS) is a problem in local communities because it is widely used for food containers and the lack of recycling services available for it. But one species of meal worm, *Zophobas morio,* (informally called the superworm) has been shown to eat and digest PS. Combining the breakdown of PS by superworm larvae and beetles with growing plants in the same area may be key to developing a lifecycle for PS that is beneficial instead of deleterious to communities. There are three questions that have not been adequately addressed in the literature concerning the practical applications of using larvae and beetles in PS recycling programs. First, do the larvae and beetles prefer whole containers of PS or smaller shredded pieces of PS? This is important to know for the preparation of PS for optimal composting with superworm beetles and larvae. Second, do adult beetles consume as much PS as larvae? This is important to understand as superworm colonies are formed for composting use. Third, do sensitized larvae from multiple generations of beetles raised on PS encourage nonsensitized (those not parented by beetles fed PS diets) group members to feed on PS? This is an important factor in kickstarting bioremediation in superworm colonies. To explore these questions, we have 6 trials with beetles and larvae feeding on two different forms of PS. Results from this study will aid in developing plans for composting PS with superworms.

P163-U Distribution of UV+ lichens on various tree species in Central Texas Jacquelyn Rios [1], *Chad Cryer [1] (1. Temple College)*
Lichens are a fungal organism that forms a mutualistic relationship with algal cells or cyanobacteria. Lichens, in all areas, must protect their photosynthetic symbiotic partners from harmful biotic factors such as herbivory for animals, and abiotic factors such as excess UV ray exposure. When hit with sunlight, some lichen reflect excess energy as light in the UV spectrum with chemicals in the upper cortex of the lichen thallus. These chemicals help to protect the photosynthetic cells beneath by acting as sunscreen. However, the distribution of UV+ lichens across various native tree species in Texas remains unknown. Here we used a grid-method to measure the percent of coverage of UV+ lichen on five commonly found tree species in Texas. Our results demonstrate how the coverage of UV+ lichens vary within a species of tree as well as between tree species. We anticipate this model being a starting point for using lichen as a bioindicator of UV levels in an environment.

P164-U Seed predation differs between native and exotic seed species, and across a latitudinal gradient Ana Caballero [1], *Sage Gruver [1], Charlotte Savage [1], Yahida Soto [2], Will Bieker [3], Lana Bolin [3] (1. Collin College, 2. Austin Community College, 3. University of New Mexico)* Species interactions like competition, predation, and mutualism are a key focus of ecology. Species interactions commonly differ in strength between invasive and native species, and The Enemy Release Hypothesis posits that invaders may be successful by escaping their co-evolved enemies during invasion. However, evidence for the Enemy Release Hypothesis is mixed. Furthermore, latitudinal gradients in species interactions have been detected globally, but such gradients also may exist on smaller geographical scales. Here, we investigated how a species interaction – seed predation – differs between invasive and native plant species, whether seed predation rates follow a latitudinal gradient, and whether this gradient is driven by insects, vertebrates, or both. As part of a summer research program designed to increase research access for community college students (Science CORPS: sciencecorpsprogram.org), we conducted a distributed study at sites across Texas and New Mexico. At each site,

we set out two trays (one of which restricted vertebrate access) containing seeds from four native and four exotic plant species, and counted the number of seeds of each species remaining after six days. We found that seed predation was greater on exotic species than native species, contradicting the Enemy Release Hypothesis. We also detected a latitudinal gradient across our two states, which was driven by invertebrates. These results suggest that the Enemy Release Hypothesis may not explain the success of these exotic plant species, at least in terms of release from seed predators, and that latitudinal gradients in species interactions can exist even on small geographical scales.

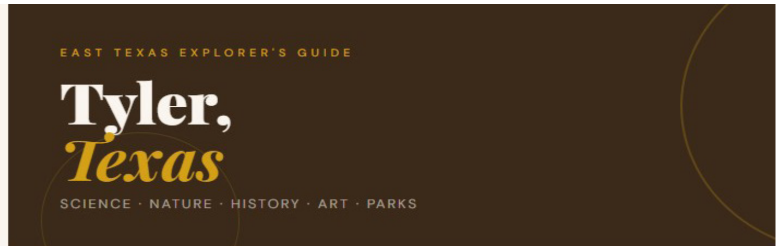
Things to Do

SFA Department of Earth Sciences and Geologic Resources will be leading a post-conference field trip on Sunday, March 1 to the John Bunker Sands Wetland Center near Seagoville, Texas. This field trip would be of interest to students and faculty from geoscience, environmental science, biology, and STEM education. The constructed wetlands are part of the East Fork Water Reuse Project, that receives effluent water from Lake Lavon and uses a 2,000-acre wetland to recycle this water to provide municipal water supplies to the city of Dallas and surrounding communities. It also acts as a refuge for over 300 bird species, including bald eagles, mammals, insects, and native and aquatic plants.

Logistics: We will depart from the UT Tyler campus at 8:00 a.m. on Sunday, March 1, and travel to Seagoville, arriving at our first stop at approximately 10:00 a.m., with a comfort stop along the way. We will have two stops outside the wetland center to view the sedimentation ponds and Trinity River terraces, and proceed to the visitor's center, arriving between 10:45 and 11:00 a.m. Participants will check in and pay the $15 entrance fee. Once all the paperwork has been completed, we will be led on a tour of the wetland center by the executive director, Kayleigh Bucur. The tour is expected to take between 1 and 1.5 hours, including questions, but participants can depart early as needed.

The walking tour will take place on an elevated boardwalk and levees. Please wear sturdy walking shoes and bring binoculars, water, hat, and sunscreen if needed. The wetland center requires all participants to sign a Liability Release; field trip leaders will have copies available before departure so we can streamline our check-in.

After the tour: Depart the wetland center. Participants may grab a quick lunch in Seagoville or destination of choice.



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