124th Annual Meeting
of the
Texas Academy of Science

February 26th – 27th, 2021

Official Program

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Abbreviated Program Schedule:

FRIDAY February 26

8:00 am - 8:45 am	Section Chairs Pre-Session

9:00 am - 3:15 pm	Oral Paper Sessions I	Oral Paper Sessions 2
	• *Cell & Molecular Biology*	• *Biomedical Sciences*
	• *Chemistry & Biochemistry*	• *Neuroscience*
		• *Anthropology*
4:00 pm - 6:30 pm	Poster Session & Judging	

SATURDAY, February 27

8:30 am – 2:15 pm	Oral Paper Sessions 3	Oral Paper Sessions 4
	• *Mathematics & Computer Science*	• *STEM Education*
	• *Physics & Engineering*	• *Freshwater Science*
	• *Terrestrial Ecology & Management*	• *Marine Science*
	• *Geosciences*	• *Conservation Ecology*
		• *Systematics & Evolutionary Biology*
		• *Plant Biology*

2:30 pm - 4:30 pm	Graduate Student Oral Presentation Competition
5:00 pm - 5:45 pm	Outstanding Texas Educator Lecture
5:45 pm - 6:30 pm	Distinguished Texas Scientist Lecture

6:30 pm – 8:30 pm   Awards Ceremony
- Welcome (Dr. Shannon Hill, *President*)
- Outstanding Texas Educator Award (Dr. Francisco Gonzalez-Lima, *VP*)
- Distinguished Texas Scientist Award (Dr. Francisco Gonzalez-Lima, *VP*)
- Undergraduate Poster Section Awards (Dr. Cathy Early, *TAS Collegiate Academy*)
- Undergraduate Oral Presentation Awards (Dr. Cathy Early, *TAS Collegiate Academy*)
- Sammy Ray Marine Science Award (Joe Kowalski, *Marine Science Section Chair*)
- Amir-Moez Award for Excellence in Mathematics (Dr. Scott Cook, *Mathematics Section Chair*)
- Graduate Student Presentation Competition Awards (Dr. Travis Laduc, *TAS Graduate Academy*)
- Student Research Grants (Dr. Travis Laduc, *TAS Graduate Academy*)
- Outgoing Board Members (Dr. Shannon Hill, *President*)
- New Board Members (Dr. Shannon Hill, *President*)
- Introducing the New President of TAS (Dr. Shannon Hill, *President*)
- Next Year's Annual Conference & Final Comments (Dr. Kathleen Wood, *new President*)

Welcome and Acknowledgments
from the Academy President

Welcome to the 2021 annual meeting of the Texas Academy of Science! This year marks the 124th annual meeting of the Academy and our first virtual meeting. While this year's meeting will look different from those in the past, as always, we are looking forward to learning about the exciting research happening in the state of Texas and surrounding regions. Despite the novel virtual format, you will recognize many events that we have previously enjoyed, such as the Distinguished Texas Scientist and Outstanding Texas Educator keynote speakers, the Graduate Student Competition and the Awards Ceremony. And we are proud to continue supporting our graduate and undergraduate students with over $13,000 in research awards. There are some new features as well, including invited guest speakers in the Biomedical Sciences, Mathematics and Computer Science and Neuroscience sections as well as a virtual Geoscience field trip.

During the scheduled time of the research presentation, the author will be available to answer questions via chat. Once open, presentations and posters will be available online for the next year. This allows us to go back and view concurrent presentations, a nice benefit of a virtual platform.

There are many Academy members who deserve a special word of thanks for their tremendous efforts in ensuring this meeting's success. It is no small task to convert a meeting from face-to-face to a virtual format. Dr. Kathleen Wood, the 2021 Program Chair, and Dr. Ricardo Bernal, the Coordinator of Information Technology, have been the driving force behind every step of progress. Many thanks to the section Chairs and Vice Chairs, who have skillfully reviewed abstracts while learning new procedures and software pertaining to abstract and section management. I would like to give a special thanks to those who are presenting at this year's meeting -- from budget cuts to canceled travel, the last several months have presented unparalleled challenges in performing research, so I applaud your tenacity and dedication.

Please welcome and congratulate the incoming board members. And many thanks to our outgoing board members for their sage advice and august leadership. If you are interested in expanding your role with the Academy, please contact me, or any member of the board, as there are several board positions that open annually.

It has been my honor to serve as the president of the Texas Academy of Science and I look forward to seeing the Academy continue to grow and prosper in the years to come.

Shannon K. Hill, Ph.D.
President, Texas Academy of Science 2020 – 2021

About The Texas Academy of Science

History
First founded by teachers as the Academy of Science in Texas in 1880, the organization as we know it now emerged around 1929 and included a physicist, a botanist, a mathematician and two biologists as its founding members. Since 1949, TAS has published a peer-reviewed journal (The Texas Journal of Science), conducts an annual meeting that highlights research across 15 sections representing various science disciplines, provides substantial funding opportunities for students (~$25,000 awarded annually) and facilitates expert testimony on policy issues related to STEM or science education. TAS membership approaches 600 individuals, with a large portion of the membership being students.

Mission
As part of its overall mission, the Texas Academy of Science promotes scientific research in Texas colleges and universities, encourages research as a part of student learning and enhances the professional development of its professional and student members. TAS possesses a complex, intriguing and long-standing educational mission that continues to evolve.

Strategic Planning
The Texas Academy of Science (TAS) Board of Directors has approved a vision for a 5-year Strategic Plan: "to increase the visibility and effectiveness of TAS in promoting strong science in Texas." As part of that initiative, the Academy seeks to reach out to foundations and organizations that support and benefit the Texas science community. We believe that a number of opportunities exist for strategic partnerships that could bolster the impact of organizations that raise the profile of science in Texas. Our ultimate goal will be to make TAS the premier state academy in the United States; however, this cannot be accomplished without funding from both individuals and corporations. It should also be noted that 100% of the contributions given to TAS for student awards goes directly to those awards.

Welcome and Acknowledgements
from the Program Chair

Welcome to the 124th meeting of the Texas Academy of Science! This will be the first annual meeting that we have ever had in a virtual setting but we are looking forward to having many of the same high quality presentations and meeting events as we always do.

As always, putting together a meeting like this requires a lot of teamwork and indeed, we have had an excellent team of people working toward the success of this meeting. Our TAS president, Dr. Shannon Hill, continually provided encouragement to everyone involved in putting this together – and she is very good at that! Our Section Chairs and Vice Section Chairs spent a good deal of their Christmas break reviewing abstracts and getting ready for the parts they will be playing during this conference that are little different than the norm. And I frankly would not have been able to put this program together without the help of the TAS Coordinator of Information Technology, Dr. Ricardo Bernal. He took on many of the tasks that I normally would have had to shoulder myself, so I am extremely grateful for all that he did.

Although not exactly like previous meetings, we have done our best to provide meeting events that our membership has grown accustomed to – student oral and poster presentations, the Graduate Student Oral Presentation Competition, and presentations from this year's Distinguished Texas Scientist and Outstanding Texas Educator. We won't have a banquet this year BUT we will have an Awards Ceremony! Perhaps you can watch it as you eat dinner at home on Saturday night!

Mary Kathleen Wood

Kathleen Wood, President-Elect of the Texas Academy of Science

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THE TEXAS JOURNAL OF SCIENCE

Call for Manuscripts

The *Texas Journal of Science* is an open access 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. The Journal is received by TAS members, educational institutions throughout the USA, and international institutional subscribers. Scholarly papers reporting original research results in any field of science, technology or science education will be considered for publication.

The Journal is available online where accepted papers are published immediately and an annual print volume is mailed to TAS members at the end of the year. Old issues (1949-2010) are also available online for free from the Biodiversity Heritage Library. A link to old issues is available on www.texasjournalofscience.org

We are actively seeking quality manuscripts. Please visit www.texasjournalofscience.org to submit your manuscript for consideration.

Hannah Cotten
2021 Outstanding Texas Educator

Hannah Cotten graduated from the University of Texas at Austin in 2011 with High Honors, receiving a Bachelor of Science in Applied Learning and Development. She is currently a fifth grade Science Teacher at Hill Elementary in Austin, Texas and has taught for 8 years in Austin ISD. She currently also writes and develops STEM activities and lesson plans for JASON Learning and Feld Entertainment. Hannah has also started science after school clubs, such as the Water Bear Club and Animal Lovers Club. Additionally, she is a professional harpist and harp teacher in the Austin area.

Hannah has received numerous awards and recognition. Most recently, in December of 2020, she received the Presidential Awards for Excellence in Mathematics and Science Teaching (PAEMST). This award is the highest honor bestowed by the United States government specifically for K-12 science and math teachers. The Awards were established by Congress in 1983. Only three science teachers are selected from each State, and she was selected for the state of Texas.

Additionally, in June of 2018 she received a travel grant through Fund for Teachers, where she conducted research and brought science education and outreach to indigenous students in Las Lajas, Chirqui, Panama.

In April of 2018, she also received the Texas Medical Association Educator Award and grant, providing science materials and equipment for her classroom and school. Lastly, additional awards and recognition include: CoSN Conference Awarded Educator and Guest Speaker, JASON Learning Teacher Argonaut, Austin ISD Teacher of the Year and Profiled Alumni for the University of Texas College of Education.

She currently is in the review process of publishing her first manuscript with the Texas Journal of Science.

Dr. Donna Shaver
2021 Distinguished Texas Scientist

"Find the nest" is the signal that sends Donna's Cairn Terrier, Ridley, into action sniffing out the Kemp's Ridley sea turtle nests hidden on the beaches of Padre Island. This is just one of many ways she is involved in sea turtle conservation efforts in South Texas.

Even as a child, she knew that she wanted to work with endangered animals and conservation research. In 1979, she was a student at Cornell University when a brochure describing wildlife research opportunities on South Texas beaches caught her attention. She packed her bags and quickly found the place she wanted to spend the rest of her life. By 1985, she was a full-time employee with the National Park Service and was also completing a PhD in zoology from Texas A&M University.

Dr. Shaver has worked with sea turtles since 1980. She oversees a variety of sea turtle research and conservation projects conducted in Texas, collaborates with other researchers in the U.S. and Mexico, and provides training and leadership to hundreds of biologists and volunteers working with sea turtles in Texas. Dr. Shaver is the Texas Coordinator of the U.S. Sea Turtle Stranding and Salvage Network. In this capacity she maintains records of stranded sea turtles, nesting sea turtles, and sea turtle nests found in Texas, and helps lead detection and documentation efforts for them. Her largest and most long-term effort has been the Kemp's Ridley Sea Turtle Restoration and Enhancement Project at Padre Island National Seashore.

Since 2003, Dr. Shaver has been Chief of the Division of Sea Turtle Science and Recovery for the National Park Service at Padre Island National Seashore. To date, she has authored or co-authored more than 100 publications and reports dealing with sea turtles. The government of the Canary Islands invited Dr. Shaver to travel there to advise them on forming a nesting colony of loggerhead turtles, patterned after the work that Dr. Shaver led to re-establish nesting by Kemp's Ridley sea turtles at Padre Island National Seashore. Dr. Shaver has been interviewed by New York Times, Washington Post, Sea Rescue, Texas Country Reporter, Texas Bucket List, Dateline, Discovery News, Texas Monthly, and numerous other media outlets and has received several awards for her work.

Dr. Matthew Barnes
2021 Vice President

As a child, Dr. Matthew Barnes enjoyed flipping over rocks to catch bugs in the creeks of his hometown in Plano, Texas. He later discovered a more scholarly approach to aquatic ecology and studying human interactions with their environment as an undergraduate at Southwestern University, earning a B.A. in biology with a minor in sociology.

He attended his first TAS Meeting and delivered an oral presentation based on his undergraduate thesis in 2006, receiving his first external grant—a TAS Student Research Award—at the same meeting. Barnes earned his PhD from The University of Notre Dame, then he returned to Texas in 2014 to begin a position within the Department of Natural Resources Management at Texas Tech University.

Now an Associate Professor at Texas Tech, Barnes' research program focuses on forecasting biological invasions and conducting research that advances methodologies for the study and management of invasive species and the communities they impact. Research projects in his lab utilize a broad set of tools to address many different types of ecological questions, and past and current research approaches include predicting species occurrence with species distribution models, detecting rare species through environmental DNA (eDNA) surveillance, and investigating species impacts through field observations and laboratory experiments.

Dr. Barnes enjoys sharing these topics with students in the classroom, and his recently taught courses include Introduction to Freshwater Ecology, Quantitative Methods in Natural Resources Management, Natural Resources Policy for both undergraduate and graduate students, and the "Food, Agriculture, Natural Resources, and Human Sciences" cohort of the Texas Tech Program in Inquiry & Investigation. Barnes has served as Chair of the TAS Freshwater Science Section since 2018.

Dr. Alyx Frantzen
2021 – 2024 Academic Director

I am a born and bred Texan. I am from Fredericksburg, with deep roots in the Hill Country. I attended Texas Lutheran College (now University) and received my BS in mathematics/chemistry. New Mexico State University was home for my graduate work, starting in mathematics and eventually (joining the dark side) finishing in physical chemistry.

When I was starting my job search, I specifically looked for a position where teaching was the main focus and research was a tool used in teaching. I was lucky enough to find a position at Stephen F. Austin State University in 1998. I have been here ever since. I am currently an associate professor in the department of chemistry and biochemistry.

I participate in the Local East Texas Section of the ACS. I am active in the STEM research center at SFASU. I have been very active in research. The majority of the students we work with are undergraduate students. We have a very small graduate program. Over the years I have been at SFASU, I have probably had over 100 students participate in research projects. Many of the projects are set up to evaluate the inclination of the student to do research and evaluate their skills in the laboratory. I have taken students to conferences over the years and encourage all of them to present their work. My students have presented locally at the SFASU Undergraduate Research Conference, regionally at the ACS/SWRM and TAS meetings, nationally at the ACS meetings and internationally at the CMS meetings. The work that I do in lab tends to be very interdisciplinary, pulling in geology, forestry, agriculture and environmental fields. I have received the Teaching Excellence Award at SFASU; been the Spotlight Speaker at the SFASU Bright Ideas conference; and received the Faculty Mentor Award at the SFASU Undergraduate Research Conference.

I have participated in the TAS for many years now; giving presentations myself, having my students give presentations, serving as section chair, and serving as President. I now want to focus on serving the TAS as and Academic Advisor. I want to make sure we continue to be an organization that focuses on the advancement of students to achieve their potential in their chosen scientific goals.

Caleb Shackelford

2021 – 2023 Student Director

My name is Caleb Shackelford, I am a 20-year-old student in my third year at the University of Mary Hardin-Baylor (UMHB). I am pursuing a degree in biology and a minor in sociology. I grew up in the countryside of Durango, Texas where my love for science began. I graduated from Belton High School with a STEM endorsement and was the president of the Environmental Science Club while there. I continued my education into the collegiate atmosphere where I found an interest in biology, specifically environmental and urban ecology. Consequently, my strong interest in urban ecology has inspired me to write a proposal to implement green infrastructure on UMHB's campus.

In addition to my education, extracurricular opportunities have allowed me to enrich my experience at UMHB greatly. Some of these opportunities include biological research, University Ambassadors (serving the office of the president at university events), sociology club, and mission trips. Regarding biological research, I am in the process of discovering what species of rhizobia form symbiotic relationships with huisache inhabiting Belton, Texas. Additionally, my trip to India provided a great opportunity to understand cultural differences in a different part of the world and to provide for those in need.

My academic goals are to complete my undergraduate work at the University of Mary Hardin-Baylor and work towards gaining a master's degree from UT or A&M. Currently, I will be working as a rangeland management specialist intern with the USDA in hopes of becoming a wildlife biologist or obtaining a position in the biological and environmental sciences. A long-term goal is to work with students in a university or college setting where I can share my love of ecology and science in general.

2021 Texas Academy of Science Fellow

Dr. Kathryn Perez
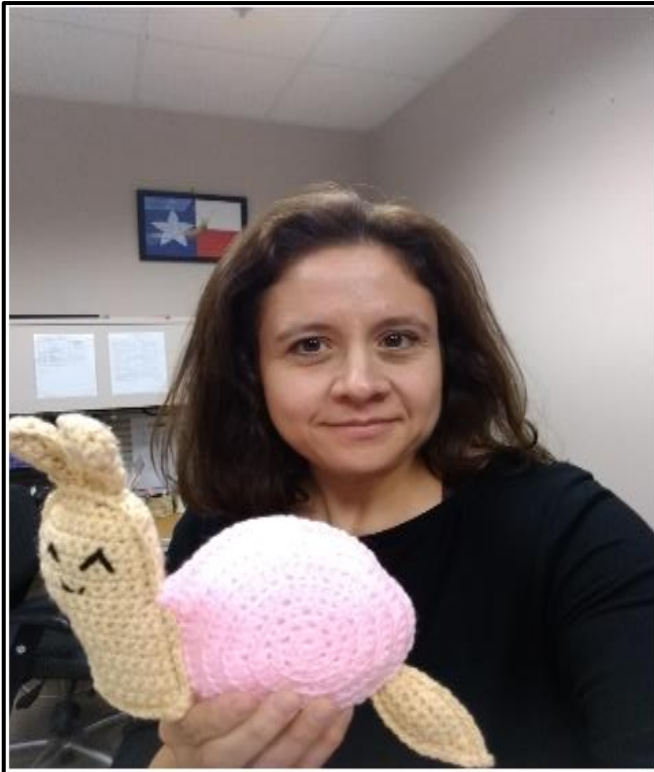
Dr. Kathryn Perez is an Associate Professor in the Department of Biology at the University of Texas Rio Grande Valley. She received her Bachelor's and Master's degrees from Angelo State University, and her PhD from the University of Alabama where she was an NSF-IGERT fellow in Interdisciplinary Freshwater Sciences.

She followed this with an NIH-IRACDA postdoctoral training fellowship which combined pedagogical training at the University of North Carolina, teaching at North Carolina Central, an HBCU, and conducting research at Duke University. She was a faculty member at the University of Wisconsin La Crosse before moving to UTPA/ UTRGV six years ago.

At UTRGV, Dr. Perez teaches General Biology, Invertebrate Zoology, Evolution, and Biology Capstone. She serves as the Undergraduate Program Director for Biology. Dr. Perez works in two research areas: the evolution and ecology of snails and student learning of evolution. She has over 40 publications on her snail research and 10 in biology education research.

Dr. Perez has been supported by the Texas Academy of Science since the start of her academic career, giving her first presentation at TAS in 1997 and receiving undergraduate and graduate student research awards. She has served TAS as a past section co-chair and chair for the Systematics & Evolutionary Biology section, student grant reviewer, student presentation and poster judge, Academic Director, and Texas Journal of Science Manuscript Editor and Associate Editor.

2021 Texas Academy of Science Fellow

Dr. Keith Pannell
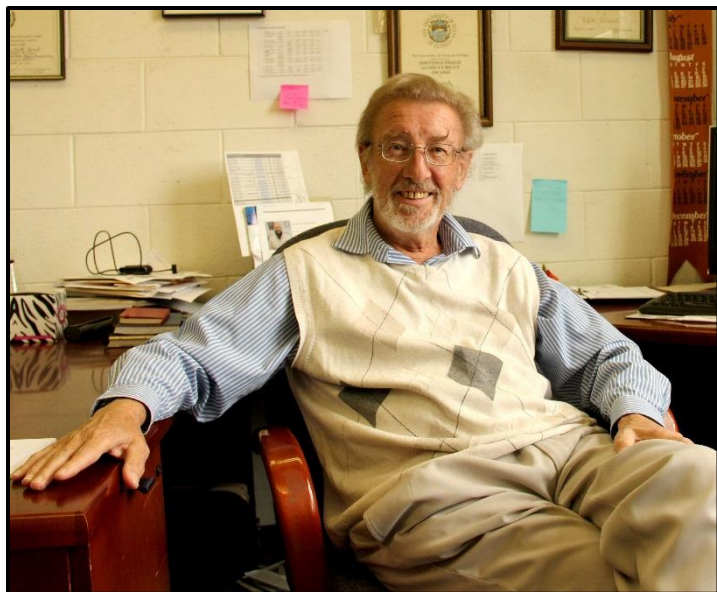
Dr. Pannell took B.Sc. and M.Sc. degrees from Durham University, England, and a Ph.D. degree from Toronto University, Canada. He held a postdoctoral fellowship at the University of Georgia (R. Bruce King) and an independent Research Fellowship at the University of Sussex.

In 1971 he joined U. T. El Paso. He is a member of the American Chemical Society, having served as Local Section chairman, National Councilor and a member of the International Affairs Committee and the Committee on Public Relations and Communications. He was co-general Chairman of the SW/Rocky Mountain Regional ACS meetings in 1999 and 2009, was on the editorial board of the ACS journal *Organometallics*, 1992-4, and the *Journal of the Mexican Chemical Society.*

Supported by NSF, NIH, PRF, NATO, DOE, and the Welch Foundation, he has published ~250 articles in international journals and in 2004 was recipient the ACS National Award for research involving undergraduate students, sponsored by the Research Corporation. In 2012 he received the SWACS Stanley Israel award for increasing diversity in Chemistry. At the U. T. El Paso he has received the Distinguished Achievement Award for Teaching (1989) and Research (1986), Excellence. In 2006 Professor Pannell was appointed a Welch Lecturer by the Welch Foundation.

Dr. Pannell devised and hosts a public radio program *Science Studio* which received the Texas Public Health Association Media Award in 1992, https://www.ktep.org/programs/science-studio. He recently served as President of the Texas Academy of Science.

Graduate Student Oral Presentation Competition

A single session will be held, Saturday February 27th, 2:30 – 4:30 p.m., without any conflicting sessions, thereby enabling maximum participation. The participants are listed below in the order in which they will present. Each presenter will have 15 minutes for their presentation and any questions. (GSOPC director: Dr. Travis Laduc, University of Texas at Austin.)

Quantifying bilateral prefrontal photoneuromodulation via broadband near-infrared spectroscopy. **Patrick O'Connor**, *University of Texas at Austin*.

> Transcranial infrared laser stimulation (TILS) is a novel, non-invasive intervention to neuromodulate metabolic and hemodynamic responses that enhance cognitive function via photobiomodulation of cortical tissue. TILS to the prefrontal cortex also augments memory, attention, executive function, and learning among healthy adults. The primary molecular mechanism by which TILS is hypothesized to act is the photo-oxidation of cytochrome c oxidase (CCO), the terminal and rate-limiting enzyme in the mitochondrial electron transport chain. By increasing oxidized CCO, TILS results in increased oxygen consumption and production of metabolic energy. Studies utilizing broadband near-infrared spectroscopy (bbNIRS) have demonstrated dose-dependent increases in oxidized CCO, oxygenated hemoglobin (HbO), total hemoglobin (HbT), and differential hemoglobin (HbD) as well as a dose-dependent decrease in deoxygenated hemoglobin (HHb) in the TILS-treated (ipsilateral) anterior prefrontal cortex. However, the spatial specificity of these effects remains understudied. Here we show that TILS caused significant ($p<0.05$) dose-dependent increases in HbO, HbD, and HbT in the ipsilateral prefrontal cortex, which continued to increase through the post-stimulation period. No significant hemodynamic or metabolic effects of TILS were found in the contralateral prefrontal cortex. These findings support the hypothesized neuromodulation mechanism by which TILS results in cognitive enhancement: dose-dependent photo-oxidation of cytochrome c oxidase that induces a robust hemodynamic oxygenation response, thereby promoting cognitive functioning in the prefrontal cortex. Furthermore, there was ipsilateral vs. contralateral specificity for the metabolic and hemodynamic effects. This study may advance bbNIRS as a novel brain mapping modality and guide research into future neuromodulation applications of TILS.

Archaeological remains of the thick-billed parrot (*Rhynchopsitta pachyrhyncha*) in the American Southwest: comparative morphology, cultural context, and Holocene biogeography. **John Moretti**, *University of Texas at Austin*.

> Archaeological samples of vertebrate remains offer a past perspective with unique capacity to document the response of extant organisms to past abiotic changes and inform on potential impacts of future climate change. A review of faunal remains collected from 1950's excavations of the Bonnell archaeological site (A.D. 1200-1400) in New Mexico recognized a single isolated tarsometatarsus of a mid-sized parrot. Detailed comparisons with 21 species demonstrate that the Bonnell specimen represents *Rhynchopsitta pachyrhyncha*, the Thick-billed Parrot. *Rhynchopsitta pachyrhyncha* is an endangered pinecone specialist that inhabits mountain forests in the Sierra Madre Occidental of Mexico. Archaeological occurrences of *R. pachyrhyncha* in the American Southwest are typically interpreted as trade items from Mexico despite early 20th century occurrences of the species in Arizona and New Mexico. I reviewed archaeological

occurrences of *R. pachyrhyncha* to test the hypothesis of extra-regional origin. A total of 10 occurrences are documented in Arizona and New Mexico, including Bonnell. Five sites are located within or nearby pine forest habitats suitable for *R. pachyrhyncha*. Another three sites are situated within arid environments, but contain clear evidence of prehistoric cultural utilization of forest resources. This distribution, combined with evidence from extant ecology, historic occurrences, and reintroductions, demonstrates an association between the sites and viable *R. pachyrhyncha* habitats. The combined lines of evidence indicate that forests in Arizona and New Mexico are part of the natural range of *R. pachyrhyncha* across deep time. As such, the American Southwest may be vital to the species long-term survival.

How to get high: positive selection on mitochondrial genes in high-elevation species. **Erik Iverson**, *University of Texas at Austin*.

Similar species replace each other both with latitude and elevation across Earth, presumably by adapting to differing climatic niches. The thirteen mitochondrial protein-coding genes, which play a key role in energy production and metabolism, have been suggested to play a role in adaptation to climate and elevation. However, it is not clear whether this is a general pattern that is consistent across animals with differing energetic requirements. We analyzed the mitogenomes of over 350 terrestrial vertebrates, insects, and freshwater fishes to test for selection at elevation, comparing "high" species to "low" sister taxa. We fit different evolutionary models to these cases in PAML and calculated the strength of selection on different branches. We also analyzed 6 families representing different classes, grouping branches by elevation and using RELAX to distinguish positive from relaxed selection. We detected a weak but significant signature of stronger selection across "high" species, which was driven by birds, mammals, and insects. The effect was not significant in reptiles, amphibians, or fishes. Selection increased with the magnitude of the upslope shift in a species' range and decreased with increasing genetic divergence between species. Family analyses suggested a stronger effect in endotherms, with evidence of positive rather than relaxed selection. The groups with the greatest signature of positive selection appear to be those with higher energetic requirements including the birds and mammals (endotherms) and insects (almost all of which represented flying species). This study lends support to the idea that mitochondrial genes, long thought to evolve exclusively under purifying selection, can also be adapted to environmental conditions. Adaptive trade-offs in mitochondrial function may represent specializations that help explain the ecological pattern of elevational, and by extension latitudinal, replacements.

Electrophysiological effects of transcranial infrared laser stimulation. **Dariella Fernandez**, *University of Texas at Austin*.

Transcranial Infrared Laser Stimulation (TILS) is a novel non-invasive brain intervention that has been found to modulate mitochondrial respiration and cellular functions in cortical neurons. In healthy adults, eight minutes of TILS to the right prefrontal cortex has been shown to improve memory and attention. However, little is known about what electrophysiological effect TILS has on the human brain. Thus, our objective was to map and image the electrophysiological effects in the cerebral cortex during and after TILS to the right prefrontal cortex. To investigate this question, we used electroencephalographic (EEG) recordings from the entire human scalp before, during and after the administration of a 1064 nm wavelength laser with a power density of 0.25 W per cm2 delivered to the right forehead using a randomized between-subjects, sham-

controlled design with subjects unaware of sham or active laser. Here we show that 8 minutes of TILS significantly increased the EEG power density of alpha and beta waves as compared to sham controls, with the largest increases seen in the alpha waves. These electrophysiological changes were dose-dependent and did not continue after the TILS intervention ended. The results from this study are important because they help us to further understand the mechanistic link between cerebral electrophysiological effects and the cognitive enhancing benefits from TILS and can help guide future applications of TILS.

Orexin receptor antagonists reverse aberrant dopamine neuron activity and related behaviors in a rodent model of stress-induced psychosis. **Hannah Elam**, *University of Texas HSC at San Antonio*.

Post-traumatic stress disorder (PTSD) is a prevalent condition affecting approximately 8% of the United States population and 20% of United States combat veterans. In addition to core symptoms of the disorder, up to 64% of individuals diagnosed with PTSD experience comorbid psychosis. Previous research has demonstrated a positive correlation between symptoms of psychosis and increases in dopamine transmission. We have recently demonstrated projections from the paraventricular nucleus of the thalamus (PVT) to the nucleus accumbens (NAc) can regulate dopamine neuron activity in the ventral tegmental area (VTA). Specifically, inactivation of the PVT leads to a reversal of aberrant dopamine system function and psychosis-like behavior. The PVT receives dense innervation from orexin containing neurons, therefore, targeting orexin receptors may be a novel approach to restore dopamine neuron activity and alleviate PTSD-associated psychosis. In this study, we induced stress-related pathophysiology in male Sprague Dawley rats using an inescapable foot-shock procedure. We observed a significant increase in VTA dopamine neuron population activity, deficits in sensorimotor gating, and hyperresponsivity to psychomotor stimulants. Administration of selective orexin 1 receptor (OX1R) and orexin 2 receptor (OX2R) antagonists (SB334867 and EMPA, respectively) or the FDA-approved, dual-orexin receptor antagonist, Suvorexant, were found to reverse stress-induced increases in dopamine neuron population activity. However, only Suvorexant and SB334867 were able to reverse deficits in behavioral corelates of psychosis. These results suggest that the orexin system may be a novel pharmacological target for the treatment of comorbid psychosis related to PTSD.

A road most traveled: utilizing the concept of transit-time to measure compactness. **Shawn Brody**, *Tarleton State University*.

School districts, voting precincts, utility service regions, and taxation zones — we are frequently tasked with dividing geographic regions into pieces that are connected and compact. Whereas connectedness is clear and binary, compactness is often a more nebulous concept. In fact, many state laws dictate that a political district must be compact, but what does compact mean? Historically, metrics like Polsby-Popper, Reock, or the convex hull method aim to define compactness based solely on a district's geographic shape. This project proposes a new definition of compactness. Transit-Time Compactness (TTC) scores a district using average travel-times between pairs of citizens living in the same district. The idea is that pairs of people separated by geographic barriers, like a river, bay, or mountain, are unlikely to interact or form a cohesive unit. Traditional geography-only measures would not take this into account, but TTC does. The advantage of TTC over traditional compactness measures will be demonstrated using several congressional district maps that have been struck down by the courts.

Geology and Fossils of Central Texas (Fort Worth to Mineral Wells)
2021 TAS Geosciences Virtual Fieldtrip

The Texas Academy of Science will visit Fossil Park west of Mineral Wells to collect a variety of Pennsylvanian fossils from the Mineral Wells Formation. This is a very well-known collecting location near Mineral Wells, Texas.

Mosque Point Park on Lake Worth Reservoir in west Fort Worth contains fossil beds at the top of the cliff seen in the photo below. Beautiful fossils beds can be seen at the top of the cliff and overlay an excellent exposure of the Paluxy Sandstone that forms the lower part of the cliff.

(The link to this field trip will be posted on the Annual Conference virtual website for you to enjoy any time during the conference. The fieldtrip has 2 components: the 1st component is a guidebook showing the locations of the stops and a discussion of each stop; the 2nd component is a video of each stop. Many thanks to LaRell Nielson, Michael Read, and Jenny Rashall for the work they did to put this together for us.)

Frank Wayne Judd
1939-2020

Dr. Frank Wayne Judd, distinguished emeritus professor at the University of Texas Rio Grande Valley (UTRGV), passed away on December 11, 2020 at his residence. Frank was born in Wichita Falls, Texas, 1939, to Ruby Dot and Frank Judd, where he spent most of his childhood. His parents preceded him in death. He went into the US Navy in 1957 until 1960. He was the first person in his family to attend college, and earned an undergraduate degree from Midwestern University (1965). He attained an MS degree at Texas Tech University in Zoology and a PhD degree in 1973. He first joined the faculty of the Biology Department at what was then called Pan American University, where he remained until his retirement from UTRGV in 2020. During his long and storied career he served as the director of the UTRGV Coastal Studies Lab (1984-1994) and chaired the Biology department (1996 to 1999).

Frank married Jane Okamura in 1969 and they had two daughters Amy Spangler (husband David) and Naomi Williams (husband Billy), two grandsons (Mitchell and Andrew Spangler) and two granddaughters (Kaylah and Jasmine Williams). While developing and maintaining an outstanding professional program, his love and devotion to his family never wavered. He and Jane were married 51 years.

Frank's career included stints as president of the Southwestern Association of Naturalists, Editor of the Texas Journal of Science, a member of the editorial board of Herpetologica, and the editor of SWANNEWS. He received numerous honors and awards, including the Distinguished Scientist Award from the Texas Academy of Sciences, the University Distinguished Faculty Award (research), and the Annual Conservation Award from the Frontera Audubon Society. He obtained 34 contracts or awards supporting his research and education duties and published 140 research publications, including three books, starting in 1967 and ending in 2020. His research reflects his interest in natural history and includes efforts associated with local fauna and flora. In addition to his research, he wrote a weekly column for a local newspaper from 1984 to 1994. Frank co-authored the book *The Texas Tortoise - A Natural History* with Francis L. Rose and was co-editor of *The Laguna Madre of Texas and Tamaulipas*.

Frank was a member of an elite series of naturalists who had deep and abiding interests in students, education, and research. He reminded us all that research unpublished was research unfinished. He was not only a guiding light to 13 MS students, but illuminated the lives of student and faculty peers through his intellect, dedication to purpose, willingness to work with and help others, and his dry wit. Once while collecting and hauling fossil matrix from a cave in Jamaica, he fell and broke his shoulder. His statement was that he fell out of a cave. When asked how a person could fall out of a cave, he lamented, "I cannot make it any simpler than that." His Christmas letters were gems of humor, and are already missed by his numerous acquaintances and friends. Unfortunately, the void for the environmental community only grows larger with the loss of such a dedicated and broad-based scientist and educator as Frank Wayne Judd.

~Written by Francis Rose

FRIDAY, FEBRUARY 26

All meetings during the Texas Academy of Science Annual Conference will be done by Zoom.

001. Section Chairs Pre-Session Meeting
8:00 to 8:45 a.m.

ORAL SESSION #1

002. Cell & Molecular Biology Oral Session
9:00 a.m. to 12:15 p.m.
Chair: Jeremy Bechelli, *Sam Houston State University.*
Vice-Chair: Mardelle Atkins, *Sam Houston State University.*
Participants:

9:00   002-01 U. **A screen for regulators of organ growth identifies crosstalk between mitochondrial ATP synthesis and the HIPPO pathway.** *Peyton Brent; Mardelle Atkins; Harris Obioma; Felix Oppong, Sam Houston State University.*

9:15   002-02 U. **Examining the inhibitory activity of the anti-CRISPR protein, AcrIIA7.** *Negar Koupaei, University of Texas at Austin.*

9:30   002-03 U. **Developing a model system to screen for human cachexia with analysis of skeletal muscle in *Drosophila melanogaster.*** *Logan Robert McDowell, Ellen Thompson, Mardelle Atkins, Sam Houston State University*.

9:45   002-04 U. **Redefining the threshold for tRNA gene cluster arrays in bacteria genomes using an in-house computational gene spacing algorithm and Java Script Programs.** *Jared Rodriguez, Dr. Robert Moore, Wayland Baptist University*.

10:00   002-05 U. **Engineering mycobacterial tuberculosis RecA for expression In an *E.coli* host.** *DJ Daugherty, Matthew Dyson, Wayland Baptist University*.

10:15   002-06 U. **Discovering new inhibitors of papain-like protease (PLpro) structure of SARS-CoV-2 using high-throughput virtual screening.** *Sandy Bakheet, Josh Beckham, Walter Fast, University of Texas at Austin*

10:30   002-07 U. **Using deep learning convolutional neural network models for exome mutation calling.** *Alejandra Flores, Tobias Coombs, Sarah Blatt, Arjun Bhutkar, Tyler Jacks, University of Texas at El Paso*.

10:45   002-08 G. **Characterization of *Salmonella enterica* serotypes Heidelberg and *Typhimurium* plasmids from human clinical isolates.** *Veronica Elena Rodriguez, Aaron Matthew Lynne, Sam Houston State University*.

11:00   002-09 G. **Development of a SYBR green-based RT-qPCR for the detection and quantification of Lone Star Virus.** *Megan Burch, Jeremy Bechelli, Sam Houston State University.*

11:15   002-10 G. **Analysis of five *Amblyomma americanum* putative immune genes reveals differential expression patterns during gram-positive and gram-negative bacterial infections.** *Jacklyn Thompson, Lindsay Porter, Kathy Li, Jacquelyn May, Stephen F. Austin State University.*

11:30   002-11 G. **Characterization of an immune-related gene in the lone star tick.** *Zach Elser, Stephen F. Austin State University*.

11:45   002-12 G. **Characterization of TRAF in *Amblyomma americanum* immune response to bacterial infection.** *Jacquelyn May, Lindsay Porter, Stephen F. Austin State University.*

12:00   002-13 G. **Sequence resolution and bioinformatic analysis of δ-LIT from widow spiders.** *Kaleth Salazar, Stephen F. Austin State University.*

003. Chemistry & Biochemistry Oral Session
12:30 p.m. to 2:30 p.m.
Chair: Aleksandra Zapata, *Schreiner University.*
Vice-Chair: Xiaozhen Han, *Stephen F. Austin State University.*
Participants:

12:30   003-01 G. **Toward the synthesis of Dragonamide E and its analogs as potential treatments for leishmaniasis.** *Nathaniel M. Smith, Sean C. Butler, University of Texas at Tyler.*

12:45   003-02 G. **Rhizosphere microbiome and potential of range expansion of exotic invasive guinea grass,** *Panicum maximum* **in the Lower Rio Grande Valley.** *Vanessa Thomas, Dr. Pushpa Soti, University of Texas Rio Grande Valley.*

1:00   003-03 G. **Molded capillary suppressor for open tubular ion chromatography based on a new ion exchange polymer.** *Fereshteh Maleki, Bikash Chouhan, Charles Phillip Shelor, Purnendu Dasgupta, University of Texas at Austin.*

1:15   003-04 G. **Progress toward the design, synthesis, and analysis of paired coiled-coil peptidic molecular building blocks.** *Jason E. DiStefano, Sean C. Butler, Dustin P. Patterson, University of Texas at Tyler.*

1:30   003-05 G. **Mesoporous aluminum oxide: synthesis methods for regulating textural properties for heterogeneous catalysis.** *Seyed Amir Jafari Ghoreshi, Frederick MacDonnell, University of Texas at Arlington.*

1:45   003-06 G. **Phosphorylation regulated chaperoning abilities of heat shock protein 27 are influenced by individual point mutations and molecular weight of model substrates.** *Bianka A. Holguin, Maria I. Grajeda, Alejandro Rodriguez, Janelly Villalobos, Anna Karen Orta, Supriyo Ray, Andres Orta, Ricardo A. Bernal, University of Texas at El Paso.*

2:00   003-07 G. **Continuously renewed copper electrode for amperometric measurement of carbohydrates.** *Shane R. Wilson, Philip Shelor, Purnendu Dasgupta, University of Texas at Arlington.*

2:15   003-08 G. **Assessing particulate matter (PM2.5 and PM10) using low cost sensors at various locations in the Rio Grande Valley (RGV) of South Texas.** *Esmeralda Mendez ,August Luna, Amit U. Raysoni, University of Texas at the Rio Grande Valley.*

ORAL SESSION #2

004. Biomedical Sciences Oral Session
9:00 a.m. to 12:45 p.m.
Chair: Joni H. Ylostalo, *University of Mary Hardin-Baylor.*
Vice-Chair: Brent Bill, *University of Texas at Tyler.*
Participants:

9:00   004-01 U. **Investigating if mitochondriopathies can be rescued by manipulating Hippo pathway signaling.** *Harris Obioma, Mardelle Atkins, Peyton Brent, Felix Oppong, Ellen Thompson, Sam Houston State University.*

9:15   004-02 U. **Cytotoxic effects of plant extracts on prostate cancer cell line PC-3.** *Tristan Galbreath, Kamri Knippa, Jolie Donaldson, Dr. Adam Reinhart, Wayland Baptist University.*

9:30   004-03 U. **Cytotoxic effects of various plant extracts on breast cancer cell line MB453.** *Kamri Knippa, Tristan Galbreath, Jolie Donaldson, Dr. Adam Reinhart, Wayland Baptist University.*

9:45   004-04 U. **Cytotoxic effects of medicinal plant extracts on the human breast cancer cell line MCF-7.** *Jolie Donaldson, Tristan Galbreath, Kamri Knippa, Dr. Adam Reinhart, Wayland Baptist University.*

10:00   004-05 U. **Combating cachexia using nanocarrier-facilitated targeted drug delivery.** *Shandis Fancher, Mercedes Delgado, Norma Perez-Garcia, Daisy Vargas, Brent R. Bill, Dustin Patterson, Ali Azghani, University of Texas at Tyler.*

10:15   004-06 U. **Hemocyte response to bacterial infection in** *Amblyomma americanum* **is dose dependent and peaks at 24 hours.** *Sylvia Schepps, Anna Scheuring, Jessica Villa, Grace*

Lopez, Lindsay M. Porter, Stephen F. Austin State University.

10:30   004-07 U. **Expression analysis and recombinant protein expression of lipocalin-like protein in the lone star tick.** *Kathy Li, Odotayo Odunuga, Lindsay M. Porter, Stephen F. Austin State University.*

10:45   004-08 U. **Analysis of perceptions of the 2019 novel coronavirus (SARA-CoV-2) in Central Texas.** *William Goodridge, Laura Weiser Erlandson, Texas A&M University - Central Texas.*

11:00   004-09 G. **The effects of plasticizer treatment on inflammation.** *Irma Zia, James M. Harper, Sam Houston State University.*

11:15   004-10 G. **Siphonapters associated with *Geomys arenarius* and its importance in public health in Samalayuca, Mexico.** *Natalia Guerra, Ana Gatica, Cuauhcihuatl Vital, Universidad Autonoma De Ciudad Juarez.*

11:30   004-11 G. **Activation of apoptosis in human endothelial cells infected with Colorado Tick Fever Virus.** *Sarah Owen, Luis Grado, Michelle Woodson, Jeremy Bechelli, Sam Houston State University.*

11:45   004-012 G. **Reversing the neurodegenerative disorder using carbon quantum dots.** *Jyoti Ahlawat, Mahesh Narayan, University of Texas at El Paso.*

12:00   004-013 G. **Infection of human endothelial cells with Colorado Tick Fever Virus stimulates cyclooxygenase 2 expression and vascular dysfunction.** *Stephanie Beane, Sam Houston State University.*

12:15   **Bench to bedside: scuPA for severe pleural infections.** *Distinguished invited speaker: Steven Idell, University of Texas Health Science Center at Tyler.*

005. Neuroscience Oral Session
1:00 p.m. to 1:45 p.m.
Chair: Danielle Grove, *Texas Lutheran University.*
Vice-Chair: Carlos Garcia, *University of the Incarnate Word.*
Participants:
1:00   005-01 U. **The use of concatemer subunit constructs to study the pharmacology of α4-**

and α4*- containing neuronal nicotinic acetylcholine receptor.** *Eloisa Peredia, Anna Sheraz, Omar El-Kishky, Gregory Sawyer, Farah Deba, Ayman K. Hamouda, University of Texas at Tyler.*

1:15   **Discovering a novel connection between contributors to Alzheimer's disease.** *Distinguished invited speaker: Kristi Dietert, University of Texas Health Science Center at San Antonio.*

006. Anthropology Oral Session
2:00 p.m. to 3:15 p.m.
Chair: Alexa Kelly, *University of North Texas HSC.*
Vice-Chair: Paloma Cuello Del Pozo, *Texas A&M University.*
Participants:
2:00   006-01 U. **Crowding and food quality significantly affect blowfly (*Lucilia sericata*) larval development and mPMI estimation.** *Samantha Hopper, Talia Freeman, Anamika Seth, Eva Thayer, Daniela Gutierrez, Mary Kay Johnston, Concordia University.*

2:15   006-02 U. **Preliminary analysis of sex-based differences in supratrochlear foramina prevalence.** *Ashlee Boyd, Sydney Anderson, Stephanie A. Baker, Alexa P. Kelly, Gisselle Garcia, Timothy L. Campbell, Baylor University.*

2:30   006-03 N. **The impact of remote sensing on Maya archaeology: using LiDAR to shed view on the Little Kingdoms among the Great Kingdoms. Understanding the Maya archaeology of northwestern Belize.** *Thomas Guderjan, University of Texas at Tyler.*

2:45   006-04 G. **Understanding energetic influences on Inuit nasal variation using 3D morphometrics.** *Alexa Kelly, Scott Maddux, University of North Texas Health Science Center.*

3:00   006-05 G. **Ancient human mobility of the Canary Islands: determining locality of Guanches via the use of radiogenic signatures of 87Sr/86Sr.** *Paloma Cuello del Pozo, Texas A&M University.*

Poster Presentations and Judging for All Sections
Friday, February 26, 4:00 to 6:30 p.m.

Anthropology Poster Session
Participants:

ANT-01 P G. **A mCT comb-based approach to standardize sampling locations of the coronal suture.** *Stephanie A. Baker, Timothy L. Campbell, Patrick J. Lewis, Sam Houston State University.*

Biomedical Sciences Poster Session
Participants:

BM-01 P U. **Gene expression changes in mesenchymal stem cells due to different pathologies: potential implications of an increased FLRT3 expression.** *Sara King, Dr. Joni Ylostalo, University of Mary Hardin-Baylor.*

BM-02 P U. **Therapeutic response of intrasplenically and intracaecally implanted HT-29 human colon cancer cells.** *Emmanuel Sanchez, Ivan Sosa, Jose Lopez, Karla Parra, Paloma Valenzuela, Diana Gonzalez Garcia, Joel Martinez, Karen Chavez, Shan Man, Urban Emmenegger, Anthony Mutsaers, Robert S. Kerbel, Giulio Francia, University of Texas at El Paso.*

BM-03 P U. **The design of artificial epidermal growth receptor dimers that mimic endogenous ligand-Induced activation.** *Allison Sunderhaus, Amanda Goudelock, Ramsha Imran, Dustin Patterson, May H. Abdel Aziz, University of Texas at Tyler.*

BM-04 P U. **Discovering novel inhibitors of main protease in SARS-CoV-2 by virtual screening.** *Jadelynn Aki, Josh Beckham (RE), Walter Fast (PI), University of Texas at Austin.*

BM-05 P U. **Discovery of inhibitory biomolecules of D-alanine: D-alanine ligase of *Staphylococcus aureus* using high-throughput virtual screening.** *Kaleigh Copenhaver, Dr. Josh Beckham, Dr. Walter Fast, University of Texas at Austin.*

BM-06 P U. **Bacteriophage purification and propagation for *Pseudomonas aeruginosa*.** *Jesus Garcia, Zacariah Hildenbrand, Ricardo Bernal, University of Texas at El Paso.*

BM-07 P G. **Understanding distribution of hantaviruses in the region of New Mexico with no known hantavirus pulmonary syndrome cases.** *Jaecy K. Banther, Samuel M. Goodfellow, Thanchira Suriyamongkol, Robert A. Nofchissey, Steven B. Bradfute, Ivana Mali, Eastern New Mexico University.*

BM-08 P G. **Modulation of VraS sensor histidine kinase activity and inhibition in presence of its response regulator VraR.** *Lane Marsh, Shrijan Bhattarai, Allison Sunderhaus, Paul Epie, May H. Abdel Aziz, University of Texas at Tyler.*

Cell & Molecular Biology Poster Session
Participants:

CELL-01 P U. **Characterization of mouse Schlafen 14 upon viral infection.** *Lilia Olmstead, Carlos Valenzuela, Manuel Llano, University of Texas at El Paso.*

CELL-02 P U. **Characterization of a chaperonin mutant.** *Samantha Garcia, Daniel von Salzen, Ricardo Bernal, University of Texas at El Paso.*

CELL-03 P U. **Functional significance of point mutations in Hsp27 that lead to neurodegenerative disease.** *Andres Orta, Bianka Holguin, Ricardo Bernal, University of Texas at El Paso.*

CELL-04 P U. **Exploration of N-thiocarbamoyl-7-nitroindolines for the generation of a photocleavable crosslinker.** *Philip T. Baily, Patricio Del Castillo, Aurelio Paez, Matthew R. Weaver, Roberto P. Iturralde, Carl W. Dirk, Chunqiang Li, Katja Michael, University of Texas at El Paso.*

CELL-05 P U. **Comparative expression analysis of brown and black widow toxins.** *Sebastian Torres, Abraham Landeros, Kaleth Salazar, Lindsay M. Porter, Stephen F. Austin State University.*

CELL-06 P NS. **Aptamer-DNA scaffolded silver nanocluster: A tool to prevent the biofilm of *Pseudomonas aeruginosa*.** Bidisha Sengupta, Prakash Adhikari, Prabhakar Pradhan, Stephen F. Austin State University.

Chemistry & Biochemistry Poster Session
Participants:

CHEM/B-01 P U. **Analysis of metals in Rio Grande River Basin of Texas by inductively coupled plasma-mass spectroscopy (ICP-MS).** Sara Ibarra, Victoria Doan, Gabriela Zuniga, Jaime Castro, Patricia Gonzalez, Edward Gonzalez, Alakananda Ray Chaudhuri, University of the Incarnate Word.

CHEM/B-02 P U. **Finding novel inhibitors of SARS-CoV-2 main protease.** Jeff Huynh, Ji Min Chon, Josh Becham, University of Texas at Austin.

CHEM/B-03 P U. **Expression and purification of human circadian protein hRORÎ³ for structural and functional studies.** Sebastian Sanchez, Alexander Madej, Brenda Moreno, Yuejiao Xian, Seung-Hee Yoo, Zheng Chen, Chuan Xiao, University of Texas at El Paso.

CHEM/B-04 P U. **A method for the determination of pesticides in soils by using liquid chromatography with photodiode-array detection (PDA) and fluorescence detectors.** Joshua S. Hamilton, Kefa K. Onchoke, Stephen F. Austin State University.

CHEM/B-05 P U. **Kaempferol: a potent ligand for unusual DNA motifs.** Matthew Beasley, Debarshi Roy, John Piletz, Bidisha Senguptat, Stephen F. Austin State University.

CHEM/B-06 P U. **A structure-activity study on the binding of quercetin with DNA-bound protein.** Taylor Grays, Bidisha Senguptat, Stephen F. Austin State University.

CHEM/B-07 P U. **A novel cellular and molecular study on curcumin in ovarian cancer cells.** Khang Nguyen, Brenita Jenkins, Praise Ola, Sofia Ievleva, Debarshi Roy, Bidisha Senguptat, Stephen F. Austin State University.

CHEM/B-08 P U. **The impact of microalgal extracts on *Stenotrophomonas maltophilia* biofilms.**

Keith V. Kern, Arlene Salazar, Justin M. Parkhill, BD Leverett, University of the Incarnate Word.

CHEM/B-09 P U. **Characterization of BTEX species at various TCEQ CAMS sites in Houston city in 2018.** August Luna, Amit U. Raysoni, University of Texas Rio Grande Valley.

CHEM/B-10 P U. **Zinc oxide nanotechnology expenditures in the production of agricultural provisions.** Mikayla Rodriguez, Dr. Milka Montes, PhD, University of Texas of the Permian Basin.

CHEM/B-11 P G. **Inhibitory role of F15 Fullerene in HIV-1 maturation.** Alejandro Rodriguez, Zachary S. Martinez, Edison Castro, Luis Echegoyen, Manuel Llano, Ricardo A. Bernall, University of Texas at El Paso.

Conservation Ecology Poster Session
Participants:

CONS-01 P G. **Freshwater turtle species richness in the Lower Pecos River in New Mexico and Texas.** Laramie B. Mahan, Lawrence G. Bassett, Thanchira Suriyamongkol, Michael R. J. Forstner, Ivana Mali, Eastern New Mexico University.

CONS-02 P G. **Presence of the amphibian pathogen *Batrachochytrium dendrobatidis* in a hot desert environment that exceeds its physiological tolerances.** Sadie Roth, Matthew Barnes, Kerry Griffis-Kyle, Texas Tech University.

Freshwater Science Poster Session
Participants:

FW-01 P U. **Zebra mussel size distributions in two recently-invaded central Texas reservoirs.** Jessica M. Konkler, Jason L. Locklin, Josiah Moore, Sam Poster, Laura Weiser Erlandson, Temple College.

FW-02 P U. **ZnO and TiO_2 embedded in photocatalytic styrene and acrylate resin for biofilm degradation studies.** Fernando Montalvillo, Dr. Milka Montes, Dr. Athenia Oldham, University of Texas of the Permian Basin.

FW-03 P G. **Phylogenetics and morphometrics of *Pyrgulopsis* populations in Texas.** Rebecca

Chastain, Kathryn Perez, University of Texas Rio Grande Valley.

FW-04 P G. **Maverick Creek woody species composition in San Antonio, Texas.** *Felipe Villanueva, Brain Laub, University of Texas at San Antonio.*

Geosciences Poster Session
Participants:

GS-01 P U. **Study on the chemical composition of the salt deposits of the Appalachian Basin within North Eastern Ohio.** *Chance Robinson, Stephen F. Austin State University.*

GS-02 P U. **Magnetite study in the Lake Nacogdoches area.** *Luke Whitenburg, James McDaniel, R. LaRell Nielson, Stephen F. Austin State University.*

GS-03 P G. **Stratigraphic analysis of the Capps Limestone in the Norton Oil Field in Runnels County, Texas.** *William J. Thompson, R. LaRell NIelson, Stephen F. Austin State University.*

Mathematics & Computer Science Poster Session
Participants:

MATH/CS-01 P U. **Using Python to question sincerity in Doodle polls.** *Miryam L. Galvez, Barbara M. Anthony, Chris Ojonta,* Southwestern University.

Neuroscience Poster Session
Participants:

NS-01 P U. **Zebrafish used as a nicotine screening tool to identify potential drugs to inhibit smoking in humans.** Amy Joffrion, Joseph Lively, Amy Montelongo, Vanessa Rosado, Kristel Ledesma, Brent R. Bill, University of Texas at Tyler.

NS-02 P G. **The role of xenobiotics in neurodegenerative diseases.** *Gabriela Henriquez, Mahesh Narayan, Eddie Castañeda, University of Texas at El Paso.*

Plant Biology Poster Session
Participants:

PLTBIO-01 P U. **Comparing molecular and morphological variation among enigmatic populations of *Mentzelia* section Trachyphytum (Loasaceae) from western California, USA.** *Kylie E. Davis, Mariana Castillo, Tyler B. Sanchez, Joshua M. Brokaw, Abilene Christian University.*

PLTBIO-02 P U. **Molecular comparisons among morphologically cryptic species in *Mentzelia albicaulis* complex (Loasaceae).** *Katelynn E. Shupe, Shelbi P. Stephenson, Hongjian Chang, Joshua M. Brokaw, Abilene Christian University.*

PLTBIO-03 P U. **Molecular investigation of biogeographic origins among populations of *Mentzelia dispersa* (Loasaceae) from western North America.** *Brianna N. Douglas, Kaylee M. Dahl, Katie E. Howe, Joshua M. Brokaw, Abilene Christian University.*

STEM Education Poster Session
Participants:

STM-01 P U. **PURSUE: undergraduate research journal, increases publishing opportunities for minority undergraduate STEM majors.** *Ineceia Carter, Ayanna Montegut, Tia Villeral, Yolander Youngblood, Prairie View A & M University.*

STM-02 P G. **A comparison of online and in-person graduate gross anatomy courses with an implementation of active learning.** *Libby Bradley, Emma Handler, Rustin Reeves, University of North Texas Health Science Center at Fort Worth.*

Systematics & Evolutionary Biology Poster Session
Participants:

SYST-01 P G. **Faunal comparison of Pleistocene localities at McFaddin Beach, Ingleside, and Moore Pit, Texas.** *Deanna Flores, William Godwin, Christopher J. Bell, Patrick J. Lewis, Sam Houston State University.*

SYST-02 P G. **Quadrate variation in the genus *Zygaspis*.** *Antonio Meza, Christopher J Bell, Patrick J Lewis, Sam Houston State University.*

SYST-03 P G. **Species delimitation in the domed cavesnail (*Phreatodrobia nugax*) using integrative taxonomy.** *Taylor Villanueva, Kathryn Perez, University of Texas-Rio Grande Valley.*

SYST-04 P G. **Investigating *Tryonia* springsnails through phylogeny and morphometrics.** *Houston Glover, University of Texas Rio Grande Valley.*

SYST-05 P HS. **Orthologs for pigmentation genes in *Schistocerca gregaria* are candidates for body color change during locust phase**

transition. *Sreeram Satish, Sai Prasada Manikonda, Baylor College of Medicine.*

Terrestrial Ecology & Management Poster Session
Participants:

TERR-01 P U. **Activity patterns of gray fox (*Urocyon cinereoargentius*) in an urban system.** *Saira Sitgreaves, Troy A. Ladine, East Texas Baptist University.*

TERR-02 P U. **Interaction between co-occurring populations of raccoons (*Procyon lotor*) and Virginia opossums (*Didelphis virginiana*) in an urban system.** *Cameron Castles, Troy A. Ladine, East Texas Baptist University.*

TERR-03 P U. **A survey of mesopredators in East Texas using scent lures.** *Maria Hendrickson, Diane Neudorf, Sam Houston State University.*

TERR-04 P U. **How stand age can affect carbon storage in a subtropical, deciduous forest.** *Amanda Scamardo, Tamara Basham, Collin College.*

TERR-05 P G. **A preliminary analysis of variation in shell morphology of the land snail *Haplocion pasonis* (Gastropoda: Urocoptidae) from west Texas.** *Cody Patterson, Ned Strenth, Nicholas Negovetich, Angelo State University.*

TERR-06 P G. **Nest box microclimate influences incubation behavior: a suburban and rural comparison.** *David Farris, Diane Neudorf, Sam Houston State University.*

TERR-07 P G. **Genetic analysis of beaver reintroductions in Texas.** *Drew Neyland, Monte Thies, Sam Houston State University.*

TERR-08 P G. **Metacommunity dynamics of medium- and large-bodied mammals in the LBJ National Grasslands.** *W. Craig McCain, David J. Hoeinghaus, Jaime E. Jiménez, University of North Texas.*

TERR-09 P NS. **Host by geographical distances across the Gracillariidae.** *Richard James Wilson Patrock, Texas A & M University Kingsville.*

SATURDAY, FEBRUARY 27

ORAL SESSION #3

007. Mathematics & Computer Science Oral Session
8:30 a.m. to 10:15 a.m.
Chair: Scott Cook, *Tarleton State University.*
Vice-Chair: Chris Mitchell, *Tarleton State University.*
Participants:

8:30   007-01 U. **Chemical espionage: modeling the relationship between the *Pieris brassicae* butterfly and *Trichogramma* wasps.** *Dashon Mitchell, Dr. Christopher Mitchell,* Tarleton State University

8:45   007-02 U. **Increase in exposure rates of the Eastern Equine Encephalitis Virus from the black-tailed mosquito to avian species: a mathematical approach.** *Aurod Ounsinegad, Dr. Christopher Mitchell, Tarleton State University.*

9:00   007-03 U. **The development of an in-house algorithm and Java scripts to define and identify gene clustering arrays in annotated genomes.** *Jared Rodriguez, Dr. Robert Moore, Wayland Baptist University.*

9:15   007-04 G. **Convolutional neural network for salamander classification.** *Preston Ward, Tarleton State University.*

9:30   007-05 N. **An examination of Latinx bilingual preservice elementary teachers' mathematical proficiency and language use when solving mathematical tasks.** *Maria E. Diaz, Jair J. Aguilar, Victor M. Vizcaino, University of Texas-Rio Grande Valley.*

9:45   **What is undergraduate research in math and who gets to do it?** *Distinguished invited speaker: Alicia Prieto-Langarica, Youngstown State University.*

008. Physics & Engineering Oral Session
10:30 a.m. to 10:45 a.m.
Chair: Gerald Mulvey, *University of the Incarnate Word.*
Vice-Chair: Kim Arvidsson, *Schreiner University.*
Participants:

10:30 008-01 U. **Experimental investigation of soiling losses on photovoltaic modules with artificially deposited dust of different particle sizes.** *German Rodriguez Ortiz, Thomas E. Gill, Deidra R. Hodges, Malynda Cappelle, University of Texas at El Paso.*

009. Terrestrial Ecology & Management Oral Session
11:00 a.m. to 12:45 p.m.
Chair: Richard Patrock, *Texas A&M Kingsville.*
Vice-Chair: Sara van der Leek, *University of North Texas.*
Participants:
11:00 009-01 U. **Conservation potential of symbolic state herpetofauna in the United States.** Erin McGilvray, Travis LaDuc, University of Texas at Austin.

11:15 009-02 U. **Shifts in seasonal activity pattern of male white-tailed deer (*Odocoileus virginianus*) in an urban system.** *Dakota Courtney, East Texas Baptist University.*

11:30 009-03 U. **Home range and spatial movement of Texas horned lizards (*Phrynosoma cornutum*) in the Southern High Plains of Texas.** *Sarah Macha, Dr. Andrew Kasner, Wayland Baptist University.*

11:45 009-04 G. **Choose the right side: staying on underside of leaves negatively affects the growth of tobacco hornworm caterpillars.** *Sakshi Watts, Rupesh Kariyat, University of Texas-Rio Grande Valley.*

12:00 009-05 G. **Can purple corn extract be a potential bio insecticide against insect herbivores?** *Sukhman Singh, Rupesh Kariyat, University of Texas-Rio Grande Valley.*

12:15 009-06 G. **Home range, habitat and microhabitat selection of the three-toed box turtle (*Terrapene carolina triunguis*) on a habitat island in North Texas.** *Sara van der Leek, Scott Kiester, Kenneth Steigman, Andrew Gregory, Jaime E. Jimene, University of North Texas.*

12:30 009-07 G. **Foul smelling terpene-rich trichomes mediate herbivore plant interactions.** *Ishveen Kaur, Rupesh Kariyat, University of Texas-Rio Grande Valley.*

010. Geosciences Oral Session
1:00 p.m. to 2:00 p.m.

Chair: LaRell Nielson, *Stephen F. Austin State University.*
Vice-Chair: James Westgate*, Lamar University.*
Participants:
1:00 010-01 G. **Deposition and diagenesis of the Blossom Sand, Panola County, Texas.** *Hannah Chambers, Stephen F. Austin State University.*

1:15 010-02 G. **Geochemical characterization of Utica shale play using XRF-based chemostratigraphy in Ohio.** *Barbara M. Kemeh, Julie M. Bloxson,* Stephen F. Austin State University.

1:30 010-03 G. **Inferences on basin thermal maturity and source rock potential within the Midland Basin through evaluation of clay mineral diagenesis and organic maturity.** *Hunter Green, Texas Tech University.*

1:45 010-04 N. **Development of rill marks on the beach face at Bryan Beach, Freeport, Texas.** *R. LaRell Nielson, Stephen F. Austin State University.*

ORAL SESSION #4

011. STEM Education Oral Session
8:30 a.m. to 10:15 a.m.
Chair: Phillip Greco, *Temple College.*
Vice-Chair: Julian Davis, *University of the Incarnate Word.*
Participants:
8:30 011-01 U. **PLTL Ambassador Program: expanding peer leading to early college students.** *Alissa G. Saenz, Jonathan A. Tipo, Geoffrey B. Saupe, James E. Becvar, University of Texas at El Paso.*

8:45 011-02 U. **Video editing: a valuable tool to enhance peer-led team learning for remote learning.** *Enid Martinez, Dania de la Hoya, Lester Ibarra, Jacob Najera, Adam Boyea, Mahesh Narayan, Geoffrey B. Saupe, and James E. Becvar, University of Texas at El Paso.*

9:00 011-03 U. **Changing the learning facilitation workbook each semester.** *Carolina Melendez, Raymundo Aragonez, Korina Avitia, Sofia Delgado, Jonathan Tipo, Madeline Olivas,*

Geoffrey B. Saupe, James E. Becvar, University of Texas at El Paso.

9:15   011-04 U. **Quality control in on-line peer-led workshops.** *Edna Tepezano, Paulina Torres, Brittney Baca, Lester Ibarra, Raymundo Aragonez, Jeremiah Davis Bell, Diego Maldonado, Carolina Melendez, Geoffrey Saupe, James E. Becvar, University of Texas at El Paso.*

9:30   011-05 N. **Teaching during the pandemic: HyFlexing.** *Joni H. Ylostalo, University of Mary Hardin-Baylor.*

9:45   011-06 N. **Academic community supports undergraduate success, especially during the isolation of a pandemic.** *Julian Davis, University of the Incarnate Word.*

012. Freshwater Oral Session
10:30 a.m. to 11:30 a.m.
Chair: Mathew Barnes, *Texas Tech University.*
Vice-Chair: Jeff Hutchinson, *University of Texas San Antonio.*
Participants:

10:30   012-01 U. **Population density differences of the invasive zebra mussel in two Central Texas lakes.** *Josiah S. Moore, Samuel E. Poster, Jason L. Locklin, Robert F. McMahon, Jessica M. Konkler, Alex J. Flory, Temple College.*

10:45   012-02 G. **Mercury contamination characterized by microbial Hg methylation genes in Martin Lake, East Texas.** *Sharon Schmidt, Javid McLawrence, Anil Somenahally, Ri-Qing Yu, University of Texas at Tyler.*

11:00   012-03 G. **Seasonal dynamics of food resources downstream of different tributaries in Cibolo Creek, Texas.** *Namrata Giri, Brian G. Laub, University of Texas at San Antonio.*

11:15   012-04 N. **Seasonal patterns of spring discharge at Silver Falls, Crosby County, Texas.** *John E. Stout, United States Department of Agriculture.*

013. Marine Science Oral Session
11:45 a.m. to 12:00 p.m.
Chair: Joseph Kowalski, *University of Texas–Rio Grande Valley.*
Vice-Chair: Ivy Jones, *Texas A&M Corpus Christi.*
Participants:

11:45   013-01 U. **eDNA metabarcoding analysis** of **anthropogenic effects on shark (Selachimorpha) diversity along the Texas Gulf coast.** *Madelyn Knauss, Stephanie Lockwood, Texas Tech University.*

014. Conservation Ecology Oral Session
12:15 p.m. to 12:30 p.m.
Chair: Troy Ladine, *East Texas Baptist University.*
co-Vice-Chair: Hannah Stouffer, *Texas Commission on Environmental Quality.* **co-Vice-Chair**: Houston Glover, *Brazosport College.*
Participants:

12:15   014-01 U. **A comparison of Carolina Wren nestling begging behavior and growth in urban and rural environments.** *Sara Moore, Dr. Diane Neudorf, Sam Houston State University.*

016. Plant Biology Oral Session
1:15 p.m. to 2:15 p.m.
Chair: Matthew Allen, *Wayland Baptist University.*
Participants:

1:15   016-01 U. **DNA barcoding in the species of *Chlorococcum* algae.** *Emily Martinez, University of Mary Hardin-Baylor.*

1:30   016-02 G. **Phylogenetic analysis of New World cypresses (Hesperocyparis; Cupressaceae): comparative sequencing of two newly developed chloroplast intergenic spacers.** *Alexander Sholl, Randall Terry, Lamar University.*

1:45   016-03 G. **Morphology and anatomy of the seed coat in the Texas species of *Argemone* (Papaveraceae).** *Shelby Conway, David E. Lemke, Texas State University.*

2:00   016-04 G. **Preliminary observations on the structure of extrafloral nectaries in Cactaceae.** *Jackson F. Burkholder, David E. Lemke, Texas State University.*

Abstracts for Oral and Poster Presentations

FRIDAY, FEBRUARY 26

ORAL SESSION #1

002. Cell & Molecular Biology
Participants:

9:00   002-01 U. **A screen for regulators of organ growth identifies crosstalk between mitochondrial ATP synthesis and the HIPPO pathway.** *Peyton Brent; Mardelle Atkins; Harris Obioma; Felix Oppong, Sam Houston State University.*

The Hippo signaling pathway has been regarded as the main influencer for organ size and development in Drosophila for years; however, recent genetic assays showed that while the Hippo pathway is a modulator of organ growth, completely removing Hippo signaling during development still allowed in normal organ growth. This means that additional regulators of growth need to be still identified. We have identified that knockdown of the ATP synthase Complex V subunit bellwether (blw) coupled with knockdown of Hippo pathway components produced smaller, misshapen eyes. This suggests that complex V is a modulator of organ growth and reveals a previously unknown interaction between mitochondrial ATP production and the Hippo pathway. Underscoring an interaction between the pathways, we have also observed that blw knockdown tissues upregulate transcriptional reporters of the Hippo pathway. We have also identified that blw knockdown phenotypes can be rescued by blocking oxidative stress. This result provides a possible link to the function of the Hippo pathway in moderating complex V phenotypes, as antioxidant genes are known targets of the pathway. I will present the results of our initial investigations into understanding how these two cellular components interact to regulate organ growth.

9:15   002-02 U. **Examining the inhibitory activity of the anti-CRISPR protein, AcrIIA7.** *Negar Koupaei, University of Texas at Austin.*

Bacteria are constantly exposed to microbes and bacteriophages. The race between bacteria and phages resulted in the development of evolutionary mechanisms to prevent infections in bacteria including the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR-Cas) system. In return, phages have developed anti-CRISPR activities to reduce CRISPR-Cas proteins' effects. The CRISPR technology can be used to edit DNA/RNA sequences. However, this editing might cause accidental changes in the genome as a result of off-targeting. Therefore, developing a method to allow precise editing of DNA/RNA sequences is critical. ACRs are used as a method to precisely control the DNA/RNA editing activity of CRISPR enzymes that can minimize the side-effects of off-targeting. There are several genes that have anti-CRISPR proteins (ACRs) activity. Among those, AcrIIA7 was shown to exhibit a strong inhibitory effect on Cas9 in vitro. The overall goal of this project is to examine the biochemical activity of the AcrIIA7 on inhibiting the DNA/RNA processing activities of the CRISPR Cas nucleases. The experimental aims of this project are: 1. To clone the genes coding for the AcrlI7 anti-CRISPR proteins into the 6XHis-TwinStrep-SUMO-pET19b E.coli expression vector via Gibson Assembly, 2. To optimize the expression and purification condition of the recombinant AcrIIA7 protein, 3. To examine the inhibitory effect of AcrIIA7 on the DNA/RNA processing activities of Cas nucleases. The results of this project could be used to study the effect of anti-CRISPR in inhibiting/removing off-targeting of Cas nuclease and potentially become an applicable method to treat genetic disorders.

9:30   002-03 U. **Developing a model system to screen for human cachexia with analysis of skeletal muscle in *Drosophila melanogaster.*** *Logan Robert McDowell, Ellen Thompson, Mardelle Atkins, Sam Houston State University.*

Human cachexia and its homologous disease in fruit flies, is characterized as an intense and unstoppable wasting of the body's tissues, marked by extreme weight loss and loss of muscle function. In the medical field it is often viewed as a death sentence and usually accompanies end stage cancer pathologies. The life expectancy for a patient with extreme cachexia is often less than 3 months, and individuals are often unable to meet nutritional needs despite intravenous intervention. Our work at SHSU is focused on using *Drosophila melanogaster* in the developing of a model, to recapitulate human cachexia. To assess muscle function, we assayed the ability of larva to maintain adequate feeding and locomotive functions over multiple time points. To investigate the cause of the behavior change we examined larval muscle morphology using immunohistochemistry against key sarcomere

components: actin, alpha-actinin, and myosin heavy chain. There is a marked progressive loss of sarcomere structure which serves to recapitulate features of human cachexia muscle breakdown. The purpose of this study is to find a representative model in *Drosophila melanogaster* and work towards rescuing the phenotype in humans one day.

9:45   002-04 U. **Redefining the threshold for tRNA gene cluster arrays in bacteria genomes using an in-house computational gene spacing algorithm and Java Script Programs.** *Jared Rodriguez, Dr. Robert Moore, Wayland Baptist University.*

During the past 10 years it has been found that tRNA genes in certain bacteria exhibit clustering array regions defined as 20 or more tRNA genes with a density of at least 2 tRNA genes per thousand base pairs. However, this tRNA array definition was formulated from research on tRNA arrays in Eukaryotic organisms. Due to the difference in eukaryotic genomes and prokaryotic genomes, coupled with previous observations by Dr. Robert Moore and Gracia Sebastiao finding multiple tRNA genes being grouped as close as 10 base pairs from each other, we hypothesized that a more accurate definition of tRNA array thresholds could be defined. Using an in-house java program and a computational gene spacing algorithm we were able to sort through 15,000 complete genomes from the NCBI database and define tRNA cluster array thresholds based on trends seen in prokaryotic genomes. With the cluster thresholds defined by our algorithm and programs we can get a more precise idea of what is classified as a cluster array of tRNA genes in bacterial genomes. With the new cluster threshold definitions, further research can be applied to understanding the functionality and evolutionary history of these tRNA array clusters in bacterial genomes.

10:00   002-05 U. **Engineering mycobacterial tuberculosis RecA for expression In an *E.coli* host.** *DJ Daugherty, Matthew Dyson, Wayland Baptist University.*

RecA is critical for DNA repair in bacteria, and research links RecA function to the acquisition of drug resistance in Mycobacterium tuberculosis (Mtb). Studies addressing this mechanism are hampered by the challenges of cultivating pathogenic bacteria. Also, unlike in most species, the Mtb RecA gene contains an intein: an intervening sequence that autoproteolytically cleaves itself post-translationally. Our main goal was to engineer the RecA gene from Mtb for expression in E.coli. To accomplish this we consolidated Mtb sequences for RecA from NCBI databases and previous work on RecA intein cleavage sites. Two codon-optimized Mtb RecA sequences were prepared for E.coli expression: a longer gene expressing RecA with the intein, and a shorter gene expressing the mature form of RecA. Once optimized, the RecA flanking sequences were each similarly modified. Briefly, T7 promoters and Shine-Delgarno sequences were added to direct RNA polymerase and ribosome binding, respectively. Also, stop codons were removed and replaced with a NotI linker sequence in frame with a 6x histidine-STOP tag needed for downstream purification and detection. To verify the protein products from our constructs, plasmids bearing each form of RecA were used to transform KRX E. coli cells containing an inducible T7 polymerase gene. Proteins were induced with rhamnose, affinity purified, resolved by SDS-PAGE, and visualized using Coomassie staining. The induction of both the full length and the mature constructs yielded detectable protein bands with an apparent molecular weight of ~40 kda. This suggests that the self-splicing activity of the Mtb RecA is intact. One immediate objective is to demonstrate the scalability of this process and to develop approaches to study the mature and full length proteins in vitro. Our more long term goals are to further study intein splicing mechanisms. Our future studies will examine how Mtb RecA binds and coordinates DNA repair.

10:15   002-06 U. **Discovering new inhibitors of papain-like protease (PLpro) structure of SARS-CoV-2 using high-throughput virtual screening.** *Sandy Bakheet, Josh Beckham, Walter Fast, University of Texas at Austin*

Severe Acute Respiratory Syndrome is a respiratory illness. The SARS-CoV-2 virus is the causative agent of the most recent SARS outbreak: coronavirus disease 2019 (COVID-19). Its symptoms range from mild to severe illnesses including fever, cough, and shortness of breath. There are some known drugs being tested at the moment for a COVID-19 vaccine, however, long term effects or side effects are unknown. Therefore, alternatives are needed to reduce the risk of dangerous outcomes. One of the coronaviral proteases, the papain-like protease (PLpro), is an essential protein for viral replication. Inhibiting this protease will inhibit the replication of the genomic RNA, and it is, therefore, an attractive target for therapeutic intervention. In this project, Virtual Screening programs such as GOLD, VINA, and ICM were used to identify potential inhibitors

for the papain-like protease. Overall, the scores generated from the virtual screening programs were not as good as expected. The GOLD scores of a ligand originally placed in the active site of the protein structure generated a score of 69.19 which is lower than the optimum number, 100. However, some ligands docked using the virtual screening programs may be potential inhibitors with further testing in vitro.

10:30   002-07 U. **Using deep learning convolutional neural network models for exome mutation calling.** *Alejandra Flores, Tobias Coombs, Sarah Blatt, Arjun Bhutkar, Tyler Jacks, University of Texas at El Paso.*

Pancreatic cancer is a deadly disease with a very low five-year relative survival rate. Elucidating the molecular alterations driving the genesis and progression of pancreatic cancer is crucial for the development of targeted therapies. Although mutation calling is widely used to identify single nucleotide variants from next-generation sequencing data, the identification of somatic mutations is challenging due to inconsistent sample purity and tumor heterogeneity. Here, we perform mutation calling in exome sequencing datasets utilizing NeuSomatic, a convolutional neural network (CNN)-based approach that attempts to overcome challenges associated with low tumor purities and low allelic frequencies. We utilized 71 advanced human pancreatic ductal adenocarcinoma (PDAC) tumor exome samples with matched blood normal, originally published in Aguirre et al., which used the Broad Institute's Firehose Pipeline. We employed three pre-trained models of the CNN-based caller and compared our results to published findings. The three differently trained NeuSomatic models called varying numbers of mutations, and results from the exome-trained model suggest that contextual training might play a key role in model performance. We found the whole-exome trained NeuSomatic model to perform most similarly to the Firehose pipeline. The top four significant mutations (KRAS, TP53, CDKN2A, and SMAD4) were the same for both, with the number of calls exceeding those previously published for this patient cohort. This study raises the prospect of potentially novel somatic mutations in PDAC detected by CNN-based models in the presence of tumor purity and heterogeneity challenges. We identify a 3bp in-frame deletion in the EDC4 gene as one such variant not previously associated with metastatic pancreatic cancer.

10:45   002-08 G. **Characterization of *Salmonella enterica* serotypes Heidelberg and *Typhimurium* plasmids from human clinical isolates.** *Veronica Elena Rodriguez, Aaron Matthew Lynne, Sam Houston State University.*

Human salmonellosis is major health issue as it is the most common bacterial food-borne illness in the United States. Salmonella enterica serovars Heidelberg and Typhimurium are amongst the top causative agents detected and could cause invasive infections, which requires antimicrobial treatment. To make matters worse, antimicrobials such as cephalosporins, fluoroquinolones, and tetracycline, which are common antibiotics used to treat salmonellosis, may not successfully treat patients since many strains have become resistant to numerous antimicrobials. The spread of multidrug resistance has been due in large part to the transfer of large multidrug resistance (MDR) plasmids across various species of bacteria. The goal of this study is to characterize the plasmid replicon types of 96 S. enterica Typhimurium and 50 S. enterica Heidelberg human clinical isolates obtained from the Texas Department of State Health Services using multiplex PCR. Results show that replicon types A/C, Y, FIIA, FIB, Frep, N, L/M, HI1, and HI2 were detected, with IncA/C types being the most prevalent. These results are significant since MDR IncA/C plasmids are commonly found in Salmonella isolates from cattle, swine, poultry, and in studies observing human clinical isolates. Future research aims to further characterize these plasmids to understand how these plasmids are transferred to other bacteria.

11:00   002-09 G. **Development of a SYBR green based RT-qPCR for the detection and quantification of Lone Star Virus.** *Megan Burch, Jeremy Bechelli, Sam Houston State University.*

Lone Star Virus (LSV) is a newly characterized virus isolated from the Lone Star Tick, Ambylomma americanum. Genome sequencing data indicated LSV is related to members of the Bhanja group viruses including Heartland virus and Severe Fever with Thrombocytopenia Syndrome virus. LSV is a three-segmented single-stranded RNA virus with the potential to cause infection and cytopathic effect in humans and nonhuman primates as evidenced by infection in human (HeLa) and monkey (Vero) cell lines. RT-qPCR assays are beneficial for the prompt diagnosis of disease, monitoring of viral load, and biosurveillance. LSV does not currently have a diagnostic assay available. SYBR green-based methods are advantageous over probe-based RT-qPCR assays due to their ease of use and cost efficiency. Primers were developed for specific and

sensitive detection of LSV for the M segment of the genome. The amplified gene segment was cloned into a TOPO TA cloning vector and sequenced; alignment data showed a complete match to the M segment of LSV. The development of a SYBR green-based RT-qPCR assay for LSV will provide a rapid, sensitive, and specific detection method for diagnostic and research purposes.

11:15   002-10 G. Analysis of five *Amblyomma americanum* putative immune genes reveals differential expression patterns during gram-positive and gram-negative bacterial infections. *Jacklyn Thompson, Lindsay Porter, Kathy Li, Jacquelyn May, Stephen F. Austin State University.*

Amblyomma americanum, commonly known as the lone star tick, is known to be highly aggressive in seeking out a host and is a vector of many disease-causing pathogens, making them of high medical importance. However, although A. americanum has been heavily researched with respect to host interactions, much less is known about its immune system and how it responds to bacterial infections. In this study, we identified five putatively immune-related genes in A. americanum and qualitatively assessed their expression before and throughout the first 48 hours of infection with Escherichia coli (gram -) and Staphylococcus capitis (gram +) infection. Specifically, we investigated expression profiles of leucine-rich repeat (LRR), uridine diphosphate (UDP), tick alpha 2 macroglobulin (TA2M), lipopolysaccharide-induced CXC chemokine (LIX), and calmodulin-ubiquitin (CUB) genes. We found that expression patterns for each gene differed during the time periods investigated with some being expressed ubiquitously and others more selectively. Additionally, expression patterns between gram - and gram + infections differed. Characterizing genes involved in gram - versus gram + infection could lead to a greater understanding of why only gram - bacteria are transmitted as pathogens. In the future, it could be possible to manipulate the A. americanum immune response to lower infection rates among humans and animals.

11:30   002-11 G. Characterization of an immune-related gene in the lone star tick. *Zach Elser, Stephen F. Austin State University.*

An unresolved question in invertebrate immunology is how specificity in response is generated. Prior studies of the malaria mosquito, Anopheles gambiae, have identified a gene, Dscam, that is alternatively spliced to generate a vast repertoire of membrane receptors for identifying pathogens. Some of these proteins exhibited pathogen specificity, targeting malaria ookinetes, a specific stage of the pathogen's life cycle. In this study, we investigated a Dscam gene in the lone star tick, Amblyomma americanum (AamDscam). AamDscam was previously identified by our lab after sequencing transcripts of LPS-exposed ticks. Our goal was to investigate Dscam's involvement in the tick immune response. Using RNAi methodology, we were able to silence the Dscam transcript in A. Americanum ticks. Silencing occurred within 24 hours after injection of AamDscam double-stranded RNA. Ticks were then challenged with Escherichia coli. After 24 hours of infection, tick hemolymph samples were assessed by counting colony growth on hemolymph-smeared agar plates. We then compared colony counts of experimental plates with the colonies of identically treated but unsilenced controls injected with double-stranded green fluorescence protein (dsGFP) instead of dsDscam. Upon comparison between experimental and control plates, colony growth of experimental plates exhibited a significantly lower colony maturation time, with more total colonies. Our findings suggest that Dscam is important for the control of bacterial infection in ticks. Future studies will investigate whether Dscam in A. americanum is transcriptionally diverse, as found in other arthropods.

11:45   002-12 G. Characterization of TRAF in *Amblyomma americanum* immune response to bacterial infection. *Jacquelyn May, Lindsay Porter, Stephen F. Austin State University.*

Amblyomma americanum, also known as the lone star tick, is an aggressive tick species that readily bites humans. During their feeding process, the lone star tick often passes on disease-causing pathogens that are of public health importance. Current research is limited on how the lone star tick responds immunologically to bacteria, despite being a major vector for six different pathogens. To gain a better understanding of the relationship between bacterial infections and lone star ticks' immunological response, this study investigated Tumor Necrosis Factor Receptor Associated Factor (TRAF). TRAF has been identified as an immune-related gene in some arthropods. In this study, expression of this gene was determined via qualitative PCR analysis to be ubiquitous in gram + (Staphylococcus capitis) and gram - (Escherichia coli) bacteria throughout 24 hours of infection. Using RNAi silencing techniques, it was determined that 11 days was required for silencing of this gene to be achieved. The effects of this silencing on

hemocyte response and infection load will be discussed. By understanding how lone star ticks respond to non-pathogenic bacteria, a more complete knowledge of their immune system can be obtained. This could eventually lead to a deeper understanding of how ticks respond to human pathogens as well as the possible manipulation of their immune system to control their vector potential.

12:00   002-13 G. **Sequence resolution and bioinformatic analysis of δ-LIT from widow spiders.** *Kaleth Salazar, Stephen F. Austin State University.*

Widow spiders are well known for their potent venom toxins. Previous studies have begun characterization of the classes of toxins in these spiders, finding that some toxins are vertebrate-specific while others are insect-specific, raising the possibility of pursuing the insect-specific toxins as biopesticides. To this end, the first step is the sequencing, bioinformatic characterization, and recombinant expression of these toxins. In this study, the δ-latroinsectotoxin (δ-LIT) sequence of Latrodectus geometricus and of Latrodectus mactans were fully and partially resolved, respectively, using homology-based in silico probing of transcriptome libraries for PCR primer design paired with stepwise Sanger sequencing. The corresponding region for another widow species, Latrodectus tredecimguttatus, that have publicly available sequence data were compared to our resolved δ-LITs. Despite size similarity, these δ-LITs are variable in ankyrin domain number and arrangement as well as distribution throughout the protein. Recombinant protein expression construct design and expression in bacteria is discussed. The nucleotide similarities between the three Latrodectus spp. displayed an identity similarity ranging from 87% to 98% and, at the protein level, an identity similarity ranging from 83% to 99%. Information in this study contributes to the understanding of δ-LIT evolution throughout the widow spider genus, and the sequence resolution of the brown widow spider allows for follow-up studies that can empirically characterize the toxicity and biopesticide potential of this toxin.

003. Chemistry & Biochemistry
Participants:
12:30   003-01 U. **Toward the synthesis of Dragonamide E and its analogs as potential treatments for leishmaniasis.** *Nathaniel M. Smith, Sean C. Butler, University of Texas at Tyler.*

Modern science and technology have encountered an innovative and thrilling area of interest revolving the

manipulation and use of molecules at a nanoscale level; this original concept known as Nanotechnology. Further, nanotechnology is a prime model of the advancement of science since the times of pioneers such as John Dalton, Niels Bohr, and Ernest Rutherford. Nanoparticles, tiny in size have immense potential in their applications. In agriculture, nanoparticles have been found useful in functioning as nanocarriers that help deliver nutrients essential to plant growth and production. The upcoming research project being discussed aims to evaluate the passage of zinc oxide nanoparticles at various concentrations in the growth and development of multiple Oscium basilicium L. (commonly known as Basil) plant species. The use of nanotechnology in agriculture can more readily produce crops worldwide with higher nutritional value and quality. However, it is essential to note that the tiny nanoparticles can potentially cause toxicity amongst the environments in which they reside; therefore, it is imperative and necessary to investigate the use of nanotechnology in agriculture further. In this research project, we aspire to establish an appropriate zinc oxide nanoparticle concentration that can help facilitate plants' growth without causing toxic effects for future use in Nano fertilizers and industrial agriculture worldwide. Research of nanotechnology applications in agriculture is particularly relevant to the sustainment of human life worldwide, especially in poverty-ridden parts of the world where food is scarce or unavailable. Additionally, nanotechnology applications in agriculture have immense potential to increase crops' production and nutritional content while decreasing biowaste production-an ongoing Environmental concern. Hence, it is with reasonable cause and reason that this meaningful proposal sustains support from the Texas Academy of Science.

12:45   003-02 G. **Rhizosphere microbiome and potential of range expansion of exotic invasive guinea grass, *Panicum maximum* in the Lower Rio Grande Valley.** *Vanessa Thomas, Dr. Pushpa Soti, University of Texas Rio Grande Valley.*

Rhizosphere microorganisms are a key component of healthy soils. They play an important role in plant growth through nutrient cycling and increased stress tolerance. They directly influence the functioning of plant communities in both agricultural and natural ecosystems. A group of free-living beneficial bacteria generally known as plant growth promoting rhizobacteria (PGPR) have been reported to enhance plant growth and have been

widely used as biostimulants in agriculture. The goal of this study is to explore the plant soil feedback in an exotic invasive grass, Guinea grass (Pancium maximum) across different habitat types in the Lower Rio Grande Valley (LRGV). Guinea grass is an invasive bunch grass species native to western Africa, introduced to South Texas as a forage grass. In south Texas, guinea grass has escaped from the planted areas and has rapidly invaded native prairies, roadsides, old fields, and urban landscapes. My preliminary results indicate that the plant has some drought tolerance, moderate salt tolerance, prefers alkaline soils, and can grow in deep shade giving it a competitive advantage over native plant species. Currently there is very limited information on the ecology of guinea grass in south Texas. To determine the plant soil feedback in Guinea grass, I will collect and analyze the roots and rhizosphere soil samples from guinea grass and coexisting plants from 5 selected locations representing different environmental conditions in LRGV. I will analyze the physical and chemical characteristics of the collected soil samples. All samples will also undergo DNA extraction, then analysis of qPCR using 16S genes to understand the possible PGPR population and distribution in the LRGV. Further community evaluation will be through the use of next generation sequencing to identify the endosymbiotic bacteria associated with invasive and native grasses.

1:00 003-03 G. **Molded capillary suppressor for open tubular ion chromatography based on a new ion exchange polymer.** *Fereshteh Maleki, Bikash Chouhan, Charles Phillip Shelor, Purnendu Dasgupta, University of Texas at Austin.*

Ion (exchange) chromatography (IC) intrinsically requires highly conductive ionic eluents. Detecting trace ionic analytes conductometrically on such a background would be impossible. IC owes its success to the suppressor. The suppressor is an ion exchanger device that is placed between the column and the detector to reduce the conductivity background and simultaneously enhance the analyte signal. For anion chromatography (as an example), the suppressor is a cation-exchanger that exchanges eluent cations (typically Na+ or K+) in a KOH or NaOH eluent with H+. This results in a background of poorly conductive H2O while analytes like Cl-, NO$_3$-, SO$_4$$_2$- etc. enter the detector as highly conducting corresponding acids. Taking IC to the microscale is a challenge, particularly in fabricating a small enough membrane suppressor. We report on a ~ 50 Î¼m diameter capillary suppressor made with a new

cation exchange polymer by casting prepolymer solution around the 35 Î¼m tungsten wire mandrel permitting better sensitivity and lower limits of detection compared to commercial equipment. Mass spectrometric studies did not indicate any leaching from the polymer, unlike its macroscale commercial counterparts.

1:15 003-04 G. **Progress toward the design, synthesis, and analysis of paired coiled-coil peptidic molecular building blocks.** *Jason E. DiStefano, Sean C. Butler, Dustin P. Patterson, University of Texas at Tyler.*

Initial progress toward the design, synthesis, and characterization of paired coiled-coil peptidic molecular building blocks are presented. Molecular building blocks have been used for the manufacturing of advanced materials, the formulation of new drugs and drug delivery systems, the advancement of technology, and are fundamentally at the core to biological synthesis and processes. Six unique 32-residue peptides were designed and successfully synthesized with one modified residue to covalently crosslink two peptides via a 1,3-dipolar cycloaddition click reaction. Respective peptide pairs were also designed to exhibit controlled self-assembly of coiled-coil heterodimer peptide pairs. HPLC and size exclusion chromatography (SEC) results show successful synthesis and purification of individual peptides. Additional SEC data shows successful heterodimer association of synthesized peptide pairs along with covalent linkage via click reaction and self-assembly of paired coiled-coil peptide complexes.

1:30 003-05 G. **Mesoporous aluminum oxide: synthesis methods for regulating textural properties for heterogeneous catalysis.** *Seyed Amir Jafari Ghoreshi, Frederick MacDonnell, University of Texas at Arlington.*

A systematic study on the preparation of mesoporous alumina powders with pore diameters between 100 and 300 Ã…, surface areas in excess of 300 m2/g, and large pore volumes (larger than 1 cm3/g) were conducted using different solvent, non-ionic polymer templates, calcination, and peptization. This combination is proposed to be near optimum for cobalt on alumina Fischer-Tropsch catalysts in which pore diameter must be large enough for rapid mass transfer kinetics but not so large as to destabilize the solid support. A study of how the effect of different synthesizing parameters on the textural properties of the mesoporous aluminum oxide was investigated. Taking advantage of toluene as a solvent lead to the largest pore diameter of 211 Ã……

while using tert-Butyl alcohol resulted in the smallest pore 50 Å…. Furthermore, by combining some specific parameters we can maximize the efficiency of using pore-forming agents and consequently can regulate textural parameters to the desired property and finally showing how we can get the same properties with a non-templated synthesis method.

1:45   003-06 G. **Phosphorylation regulated chaperoning abilities of heat shock protein 27 are influenced by individual point mutations and molecular weight of model substrates.** *Bianka A. Holguin, Maria I. Grajeda, Alejandro Rodriguez, Janelly Villalobos, Anna Karen Orta, Supriyo Ray, Andres Orta, Ricardo A. Bernal, University of Texas at El Paso.*

Molecular chaperones are proteins that aid in the refolding of denatured proteins; they are ubiquitously expressed and essential to life as they play various roles in health and disease. The family of small heat shock proteins are low molecular weight proteins that act in response to cellular stresses such as heat shock and oxidative stress. Small heat shock protein 27 (Hsp27) is an ATP-independent chaperone that functions by preventing aggregation and shuttling partially denatured proteins to larger ATP-dependent chaperonin complexes for refolding. A dynamic equilibrium is established between dimeric subunits of Hsp27 that organize into higher molecular weight species. It is not agreed which Hsp27 state is responsible for its chaperoning capabilities. Additionally, five missense mutations in the HspB1 gene independently cause the neuropathies Charcot-Marie-Tooth Disease Axonal Type 2F (CMT2F) and Distal Hereditary Motor Neuropathy II (dHMNII). These diseases are characterized by degeneration of the peripheral nerves leading to progressive muscle atrophy and sensory abnormalities that manifest in the distal limbs. The molecular mechanism by which these single point mutations lead to disease is still not understood. Here we show the molecular chaperone capacities of Hsp27 with respect to its two possible conformations. In addition, we reveal functional and biophysical differences the five disease-causing proteins have with respect to WT Hsp27.

2:00   003-07 G. **Continuously renewed copper electrode for amperometric measurement of carbohydrates.** *Shane R. Wilson, Philip Shelor, Purnendu Dasgupta, University of Texas at Arlington.*

Currently the benchmark method for carbohydrate analysis in a variety of application areas involves anion exchange chromatography followed by electrochemical detection. One aspect that needs improvement is limited electrode life or long-term reproducibility. The gold electrode surfaces foul from deposition of oxidation products over a period of time, even after electrochemical cleaning steps are used. Disposable gold electrodes are often used; but reinstallation also requires recalibration. We describe here a novel electrochemical amperometric detector using a copper electrode that is consumed during the measurement process and a new surface is continuously generated, without changing the electrode distance/placement geometry. A copper wire acts as the working electrode; a stainless-steel tube acts as the counter electrode. At the working potential, a thin layer of copper oxide exists at equilibrium on the electrode surface. As carbohydrates contact the working electrode, they are oxidized, and the oxidation products remove the copper oxide by complexation. The oxide layer reforms. The net result is oxidation of the carbohydrate and consumption of the copper electrode. The latter is in the form of a wire and is pushed by a constant pneumatic pressure against the face of the sample inlet tube, composed of an inert insulating polymer. Performance is equivalent to gold electrodes in present use.

2:15   003-08 G. **Assessing particulate matter (PM2.5 and PM10) using low cost sensors at various locations in the Rio Grande Valley (RGV) of South Texas.** *Esmeralda Mendez, August Luna, Amit U. Raysoni, University of Texas at the Rio Grande Valley.*

With advances in technological sciences, individuals are able to utilize low cost air monitoring sensors to record air quality at homes, schools, and businesses. TSI BlueSky Air Quality Monitors address air quality concerns by collecting accurate real - time data while conveniently displaying data online. These are cloud based low cost monitors that may be installed at indoor and outdoor facilities, while collecting data through network BlueSky monitors measure mass concentrations of PM2.5 and PM10 synchronously with temperature and relative humidity. Air quality data collected from these air monitors are publicly accessible, informing the community of the air quality around them. It is important to measure local and regional aerosol particles to keep the public involved, especially those with specific health concerns such as asthma, wheezing, and seasonal allergies. In this study, six sensors were installed at

multiple locations across the Rio Grande Valley to monitor and compare PM2.5 and PM10 concentrations for a one month period. The findings indicate spatial heterogeneity in the PM concentrations across the region. Findings from study such as these would help characterize the exposure burden of the local population to air pollution issues impacting South Texas.

ORAL SESSION #2

004. Biomedical Sciences
Participants:

9:00   004-01 U. **Investigating if mitochondriopathies can be rescued by manipulating Hippo pathway signaling.** *Harris Obioma, Mardelle Atkins, Peyton Brent, Felix Oppong, Ellen Thompson, Sam Houston State University.*

The Hippo signaling pathway is considered a vital regulator of organ size in the Drosophila Melanogaster fruit fly and humans. We identified that the Hippo pathway works in conjunction with the mitochondrial ATP synthase, Complex V, to regulate organ size. Specifically, in fly eyes, depletion of Complex V components has minimal effects on eye growth. However, if Hippo signaling is simultaneously lost then the eye has a severe growth defect. This interaction characterizes Complex V as another new regulator of organ growth, and a possible interactor of the Hippo pathway. We decided to test this in the wings to investigate if the Hippo pathway communicates with Complex V in different tissues of the organism, and the results were consistent with our observations in the eye, though complex V loss alone in the wing has stronger consequences than in the eye. From these results, we hypothesized there is an interaction whereby decreased expression of the Complex V subunits caused an increase in Yorkie activity, an effector of Hippo signaling that promotes cell survival and proliferation. We tested this hypothesis and observed that indeed Yki is more active in Complex V knockdown tissues. I will present my work to test if increasing Yorkie activity using genetic approaches can further rescue the growth and survival of Complex V depleted tissues. These results suggest that further research into the interactions of the Hippo pathway and Complex V may provide a possible solution for Mitochondrial diseases/defects which are among the most common human genetic diseases.

9:15   004-02 U. **Cytotoxic effects of plant extracts on prostate cancer cell line PC-3.** *Tristan Galbreath, Kamri Knippa, Jolie Donaldson, Dr. Adam Reinhart, Wayland Baptist University.*

Prostate cancer is the most commonly diagnosed cancer among men in the United States. Developing effective treatments for prostate cancer has the potential to make a big impact on many lives. The history of plant extracts being used to treat different cancers dates back centuries. In this study, we explored the effectiveness of potentially less invasive treatments using medicinal plant extracts on a human prostate adenocarcinoma cell line (PC-3). Previous studies testing numerous extracts on 4T1 murine breast cancer cells informed the selection of plant extracts utilized in this study. A total of 19 ethanolic extracts were chosen to examine their cytotoxic effects on PC-3 cells by treating cells with 100ug/ml of each extract. Extracts of Saw Palmetto, Witch Hazel, Turmeric, Red Sandalwood, Sage, Chaparral, and Ginger were found to reduce cell viability by at least 50%. Based on these data, the aforementioned extracts were chosen to be examined further by performing dose response experiments. Five different concentrations of each extract (10 µg/mL, 25 µg/mL, 50 µg/mL, 75 µg/mL, and 100 µg/mL) were used to treat the cells and record cell viability post-treatment. Studies are ongoing to examine if the extracts exert their cytotoxic affects through apoptosis.

9:30   004-03 U. **Cytotoxic effects of various plant extracts on breast cancer cell line MB453.** *Kamri Knippa, Tristan Galbreath, Jolie Donaldson, Dr. Adam Reinhart, Wayland Baptist University.*

Breast cancer is the second leading cause of cancer death in women (second only to lung cancer). There is a 1 in 38 chance that a woman will die from breast cancer, according to the American Cancer Society. Treatment for cancer often includes chemotherapy and radiation, though the side effects of these treatments tend to be strenuous on the patients. Previously, studies in our laboratory have focused on the mouse 4T1 breast cancer cell line, observing the cytotoxic effects of various plant extract treatments. In this study, human MB-453 breast cancer cells were treated with select extracts to observe whether these medicinal plants may be used as a less arduous treatment for breast cancer in humans. The MB-453 cells were cultivated using traditional cell passing and incubation techniques. These cells were then treated with plant extracts made with 95% ethanol at a final concentration of 100 ug/ml. After a 24-hour

culture period, cytotoxicity was measured using a Cell-Titer Glo luminescence assay, revealing which extracts were most effective in causing cell death and apoptosis in MB-453 cells. Cinnamon, red sandalwood, yellow dock root, turmeric, elecampane, witch hazel, sage, and chaparral extracts were found to decrease cell viability by at least 50% when treated with 100 ug/ml extract, and were used to conduct dose response experiments to determine which extracts were most effective. Through the dose response studies, it was determined that witch hazel, sage, and chaparral proved to be the three most effective extracts in reducing MB453 cell viability.

9:45   004-04 U. **Cytotoxic effects of medicinal plant extracts on the human breast cancer cell line MCF-7.** *Jolie Donaldson, Tristan Galbreath, Kamri Knippa, Dr. Adam Reinhart, Wayland Baptist University.*

Breast Cancer is the most common cancer in women, and 42,170 women are expected to die from it in 2020. Chemotherapeutic treatments are a treatment option using drugs that target and often kill fast-growing cells whether or not they are cancerous. Chemotherapy drugs may cause significant damage to the patient's mouth, reproductive system, digestive tract, and hair follicles where the cells are naturally required to rapidly divide. Herbal treatments have been used for thousands of years to treat a variety of medical conditions, including cancer. In a previous study done in our lab, the viability of the mouse breast cancer cell line, 4T1, was observed in its response to the cytotoxic effects of multiple plant extracts. In this study, the human breast cancer cell line MCF-7 was used to evaluate the 19 various plant extracts found to be cytotoxic to mouse 4T1 cells. Cell viability was measured using Cell Titer-glo Luminescence Assay. The extracts that reduced cell viability by 50% or more when treated with 100 ug/ml were further examined in a dose response. Chaparral, Witch Hazel, Sage, Yellow Dock Root, Saw Palmetto, Turmeric, Red Sandal Wood, Pygeum, Elecampane, and Wu Jai Pi were the extracts used in the dose response. The first four of those extracts were extremely effective in inhibiting cell viability, even in the lower concentrations. Studies are underway to understand whether or not if the extracts exert their cytotoxic affect through apoptosis.

10:00   004-05 U. **Combating cachexia using nanocarrier-facilitated targeted drug delivery.** *Shandis Fancher, Mercedes Delgado, Norma Perez-Garcia, Daisy Vargas, Brent R. Bill,* *Dustin Patterson, Ali Azghani, University of Texas at Tyler.*

Cachexia is a debilitating condition of muscle wasting which occurs in patients suffering from chronic illnesses such as multiple sclerosis, AIDS, and cancer. Not only does this condition limit mobility, but it also increases morbidity and mortality and accounts for 20% of all cancer-related deaths. Current treatment for cachexia centers around palliative care, but there is no effective method for halting or reversing muscle wasting. Inducing growth of skeletal muscle through nutrition and exercise is encouraging; however, systemic drug therapy is challenging due to lack of selective uptake of existing drugs by skeletal muscle tissues. Nanocarriers appear to be an advantageous means to accomplish targeted drug delivery to skeletal muscle without impacting neighboring tissues. We hypothesized that nanocarriers containing muscle cell receptor binding peptides would bind in a cell-specific manner. In order to investigate this, novel, non-pathogenic virus-like particles (VLP), which are uniquely suited for cellular entry and release of cargo, were genetically engineered to carry cell-binding peptides on their surfaces and 5-iodoacetamidefluorescein (5-IAF) inside. Five VLP variants were created, each equipped with a distinct external peptide displayed on the capsid, including two specific to skeletal muscle tissues, a negative, nonspecific scrambled sequence, positive RGD binding peptide, and vehicle-only control. We expect the cells exhibiting muscle targeting peptides will display the 5-IAF fluorescent probe, while other cell lines will fail to fluoresce. We will employ confocal (Zeiss) and ZOE (Bio-Rad) digital fluorescence microscopy to view fluorescence probes specific to cell membrane and organelles in order to differentiate plasma membrane adhered VLPs from internalized cargo. These findings may be used for selective targeting of skeletal muscle tissue for therapeutic delivery in animal models (zebrafish and mouse) of cachexia in pre-clinical trials.

10:15   004-06 U. **Hemocyte response to bacterial infection in *Amblyomma americanum* is dose dependent and peaks at 24 hours.** *Sylvia Schepps, Anna Scheuring, Jessica Villa, Grace Lopez, Lindsay M. Porter, Stephen F. Austin State University.*

Amblyomma americanum, the lone star tick, is a tick vector of various infectious bacterial agents such as Ehrlichia chaffeensis, E. ewingii, and Francisella tularensis. While it is known that the primary cell type involved in the tick immune response to bacteria is the

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hemocyte, research on these cells is limited and there have been no prior studies on A. americanum hemocytes specifically. In this study, we addressed whether male and females have a comparable hemocyte response to bacterial infection and whether varying infection loads resulted in quantifiably different hemocyte responses. We also assayed various time points during infection to quantify the point of peak hemocyte response. We found that peak hemocyte response occurs by 24 hours post-infection, while prior to that time the response is still building. Not surprisingly, we found a higher number of hemocytes respond as initial infection load increases. Males and females did not differ in hemocyte response. A clear understanding of the tick immune response sets the stage for follow-on studies that can investigate individual cell types and their role in the immune response. It is important to detail the tick-bacteria relationship to understand how the tick immune system is undermined in the transmission of human and animal pathogens.

10:30   004-07 U. **Expression analysis and recombinant protein expression of lipocalin-like protein in the lone star tick.** *Kathy Li, Odotayo Odunuga, Lindsay M. Porter, Stephen F. Austin State University.*

Amblyomma americanum is a medically important ectoparasite that is a vector for many pathogens. Despite this fact, the interactions between ticks and the pathogens they carry has been understudied. In particular, few tick immune genes have been characterized. Therefore, in this study, we characterized a putative immune gene, a lipocalin-like protein, that was initially discovered as responsive to LPS exposure. Lipocalin has been shown to play a role in immunity in other organisms as a transporter for hydrophobic molecules. Previous studies show that lipocalin in ticks is expressed in hemocytes and is upregulated in response to bacterial challenge. In expression analysis studies, we find that this gene is ubiquitously expressed, suggesting that if immune-related, this gene is important in early stages of infection. Definitive designation of a role in immune response requires empirical assessment, therefore we designed an expression construct for recombinant protein expression in pPROEX and p202/BL21 expression systems. we found that our recombinant lipocalin-like protein expresses as a ~24 kDa protein, in line with our predictions. Recombinant protein expression is the first step in pursuing functional validation of this protein as important in tick immune function.

10:45   004-08 U. **Analysis of perceptions of the 2019 novel coronavirus (SARA-CoV-2) in Central Texas.** *William Goodridge, Laura Weiser Erlandson, Texas A&M University - Central Texas.*

The 2019 novel coronavirus, SARS-CoV-2, quickly permeated globally, infecting 65.4 million people worldwide and 14.1 million people in the United States with a transmission rate (R0) of 2-4. This virus has a differential mortality rate among age classes and is exacerbated by the presence of comorbidities. Proper control of the spread of SARS-CoV-2 is essential through social distancing, behavior, and using Personal Protective Equipment (PPE). Access to proper knowledge, protocols, and testing is vital to mitigate any epidemic, especially one of this magnitude. In the current age of technology and the internet, people have a wealth of information at their fingertips through smart phones, computers, or televisions. Even with these tools at our disposal, some people may still struggle with access to up-to-date information on the COVID-19 pandemic and COVID-19 testing and to distinguish between accurate versus false information. Not having accurate knowledge to help cull the spread of COVID-19, can result in undo spread of this virus potentially causing harm towards themselves and others. The goal of this study was to survey a sample of adults in the Central Texas region to analyze the extent of the knowledge and perceptions of this virus, how to prevent spread, the implementation of protective measures, and access to COVID-19 testing. Our results showed a trend of distrust in many forms of media and their ability to provide factual information on the COVID-19 pandemic, causing mixed opinions on the severity of the virus and the efficacy of mitigation protocols such as PPE. Further analysis showed dissatisfaction in the availability and cost of COVID-19 testing, as many participants sought improvement in COVID-19 testing for the public.The results of this study will allow a better understanding of the knowledge and perceptions of people in Central Texas to the COVID-19 pandemic and what can be done to better educate people to slow the spread of this virus.

11:00   004-09 G. **The effects of plasticizer treatment on inflammation.** *Irma Zia, James M. Harper, Sam Houston State University.*

Plasticizers are man-made chemicals used in the manufacture of a variety of products to ensure flexibility and longevity. While these compounds allow for the formation of more durable products, they have proven to be detrimental to the health of living organisms. Dibutyl

phthalate (DBP) and bisphenol A (BPA) are two widely used plasticizers that are classified as endocrine-disrupting chemicals (EDC) due to their effects on developmental, endocrinological, reproductive, and metabolic function. We sought to investigate the effect of these compounds on the inflammatory response in vitro using a mouse macrophage cell line (RAW 264.7). These studies indicated that high doses of either DBP or BPA altered the total cell count with time with or without LPS exposure. When used in combination, an even greater effect was seen. We also found that 80 µM of DBP, alone or in conjunction with BPA, had a significant effect on the measurable level of the cytokines interleukin-6 (IL-6), tumor necrosis factor alpha (TNF-a), and interleukin 1 beta (IL-1b) after LPS-treatment. Overall, these data suggest that plasticizers can influence the inflammatory response which may have implications for human health.

11:15   004-10 G. Siphonapters associated with *Geomys arenarius* and its importance in public health in Samalayuca, Mexico. *Natalia Guerra, Ana Gatica, Cuauhcihuatl Vital, Universidad Autonoma De Ciudad Juarez.*

The study of life present in the desertic ecosystem offers a perspective of its general conservation status, the natural landscape is changing and the interaction between the host and parasites too. Besides, the epidemiological chain allows us to recognize which links intervene in case of detecting a pathogenic agent that affects human health. This study aimed to identify siphonaptera parasites in Geomys arenarius rodents settled in a walnut farm in Flora and Fauna Protection Area Medanos de Samalayuca in northern Chihuahua, Mexico. Using eight Gophinator traps during the post-humid season in 2019 and dry, humid and post-humid season in 2020 we collected 39 specimens of G. arenarius. Fleas specimens were collected from the hair and skin of the captured G arenarius. A total of 16 fleas were submitted to a clearing and desiccation technique (Martin,1994) to identify the morphological and biometric characteristics to determine the gender and the genus of the ectoparasite. This research contributes to the scientific world with the first report of the Foxella genus in the host Geomys arenarius in FFPA Medanos de Samalayuca in Chihuahua, Mexico. Likewise, this finding allows future studies to identify infectious agents of wich siphonaptera and rodents can be carrier.

11:30   004-11 G. Activation of apoptosis in human endothelial cells infected with Colorado Tick Fever Virus. *Sarah Owen, Luis Grado, Michelle Woodson, Jeremy Bechelli, Sam Houston State University*

Colorado tick fever virus (CTFV), the causative agent of Colorado tick fever, has a double-stranded segmented genome and is in the Family Reoviridae and genus Coltivirus. Symptoms of the infection are characterized by sudden diphasic fever, headache, myalgia, petechial rash, and photophobia, but severe forms of the disease can include meningoencephalitis, hemorrhagic fever, and death in children. Disease severity results in approximately 20% of patients requiring hospitalization, highlighting a need to better understand this neglected virus. However, the mechanisms underlying CTFV induced pathology and severe complications remain unknown. Because CTFV is spread by tick bite and disseminates systemically via hematogenous routes, we examined the interactions between endothelial cells (ECs) and CTFV in vitro. Our findings indicate that dermal microvascular ECs, HMEC-1, are susceptible and permissive to CTFV infection. To investigate the role of CTFV infection on endothelial barrier function, we assessed transendothelial electrical resistance by xCELLigence and observed a dose-dependent decrease in cell index indicative of increased vascular permeability. From this data, we hypothesized that CTFV induces apoptotic cell death. HMEC-1 cells infected with CTFV at 48 hours revealed significantly increased Annexin V staining and reduced viability in infected cells compared to uninfected controls suggesting CTFV induces apoptotic cell death in human ECs. Upon further investigation, we observed that HMEC-1 cells infected with CTFV at 24 and 48 hours had increased caspase-3/7 activation and that the addition of a pan-caspase inhibitor, Z-VAD(OMe)-FMK, reduces caspase-3/7 activation and cell death in the CTFV infected HMEC-1 cells. Overall, our data suggests that caspase-mediated apoptosis is a critical mechanism by which CTFV induces disease in the host. Future work includes characterizing the mechanisms of apoptosis in CTFV infected HMEC-1 cells.

11:45   004-012 G. Reversing the neurodegenerative disorder using carbon quantum dots. *Jyoti Ahlawat, Mahesh Narayan, University of Texas at El Paso.*

In recent years, carbon dots have become the center of interest owing to their high aqueous solubility, low cost, low toxicity, biocompatibility, and resistance to photobleaching. In our work, we have demonstrated a straightforward approach for synthesizing CQDs using the Hydrothermal method. CQDs with an average size of

8 nm were synthesized using phenylboronic acid as the carbon source. The as-synthesized CQDs were spherically shaped as observed using the Transmission Electron Microscopy. The prophylactic efficacy of as-synthesized CQDs was evaluated against the human SH-SY5Y neuroblastoma cell line. Hoechst 33342/ Propidium iodide dual staining results verified rescue of majority of cells under ROS stress caused by rotenone, a well-known pesticide, due to the free radical scavenging action of our CQDs. Further, Annexin V/PI dual staining showed anti-apoptotic activity of the as-synthesized CQDs. Moreover, CQDs acted as a bio-imaging agent. Thus, our study demonstrates the potential of carbon quantum dots as an effective prophylactic system to prevent oxidative stress caused by rotenone. Keywords: Neurodegenerative Disease, Rotenone, CQD, prophylactic system.

12:00 004-013 G. **Infection of human endothelial cells with Colorado Tick Fever Virus stimulates cyclooxygenase 2 expression and vascular dysfunction.** *Stephanie Beane, Sam Houston State University.*

Colorado tick fever virus (CTFV) is a tick-borne double-stranded RNA virus in the Reoviridae family that causes the potentially life-threatening illness, Colorado tick fever (CTF). Severe CTF symptoms include meningitis, bleeding disorders, and meningoencephalitis. The mechanism of CTFV mediated pathology is currently unknown. There are no detailed studies to define molecular mechanisms underlying CTFV infection-associated vascular damage. Cyclooxygenase-2 (COX-2) is a known mediator of inflammatory responses and various pathophysiological conditions. We demonstrate in this study that infection of HMEC-1, which are highly susceptible to infection, show induction of COX-2 but has no apparent effects on COX-1 isoforms using transcriptomics analysis and qPCR. Angiopoietin-1 (ANG-1) and angiopoietin-2 (ANG-2) are known biomarkers produced during the dysfunction of vascular endothelium in many infections. The ratio of ANG-2/ANG-1 is a biomarker of endothelial activation and vascular damage that could be used to identify severe infections. Additionally, Tie-2 is an endothelial receptor involved in inflammation and vascular leakage. Analysis of transcriptomics data and qPCR show an increased ANG-2/ANG-1 ratio and elevated Tie-2 expression at 12- and 24-hours post-infection. Furthermore, Interleukin-6 (IL-6), Interleukin-8 (IL-8), and monocyte chemoattractant protein-1 (MCP-1) are pro-inflammatory cytokines that are recognized markers of vascular inflammation. Our data show a significant elevation of soluble IL-6, IL-8, and MCP-1 48 hours post-infection. Our data suggests CTFV induces pathological characteristics of vascular activation and dysfunction as measured through enhanced COX-2 expression, skewed ANG-2/ANG-1 ratio, and increased levels of pro-inflammatory cytokines. We uncover specific biomarkers for CTFV-induced vascular dysfunction inflammation response, highlighting future therapeutic research for the control of this neglected tick-borne disease.

12:15 **Bench to bedside: scuPA for severe pleural infections.** *Distinguished invited speaker: Steven Idell, University of Texas Health Science Center at Tyler.*

005. Neurosciences
Participants:

1:00 005-01 U. **The use of concatemer subunit constructs to study the pharmacology of α4- and α4*- containing neuronal nicotinic acetylcholine receptor.** *Eloisa Peredia, Anna Sheraz, Omar El-Kishky, Gregory Sawyer, Farah Deba, Ayman K. Hamouda, University of Texas at Tyler.*

Pharmacological targeting of neuronal nicotinic acetylcholine receptors (nAChRs) holds promise in the development of drug to alleviate chronic pain, treat nicotine dependence, and slow cognitive decline associated with Alzheimer's disease. Research at Amgen Inc., and our laboratory have identified CMPI as a positive allosteric modulator (PAM) of the (α4)3(β2)2 nAChR subtype. Using mutational and computational analyses, we identified a set of amino acids within the α4 subunit extracellular domain that are required for CMPI potentiation of (α4)3(β2)2 nAChR and indicate that binding of CMPI at the α4:α4 subunit extracellular interface is critical for (α4)3(β2)2 nAChR potentiation. To study the contributions of other subunit extracellular interfaces (e.g. β2:α4), we used pcDNA3 plasmids encoding linked subunits (β2-α4-β2-α4-α4) to introduce amino acid substitution within a specific subunit interface.Then, a cRNA of this concatenated construct is prepared in vitro and injected into Xenopus laevis oocytes to express a nAChR that contains a single amino acid mutation in an individual subunit and enable us to study the effect of this mutation on CMPI effect. Our preliminary recordings show that CMPI potentiation of ACh-induced current was preserved in (α4)3(β2)2 nAChR containing point mutations at the β2-α4 interface (β2-α4-β2-α4-α4H142V, β2-α4-β2-α4-α4Q150F, and β2-

α4-β2-α4-α4E92I). Experiments to examine the effect of same point mutations at other interfaces are ongoing. These studies will define the structural features and molecular mechanism of CMPI interactions with the (α4)3(β2)2 nAChR and facilitate structure-based design of novel nAChR PAMs.

1:15 **Discovering a novel connection between contributors to Alzheimer's disease.** *Distinguished invited speaker: Kristi Dietert, University of Texas Health Science Center at San Antonio.*

006. Anthropology
Participants:

2:00 006-01 U. **Crowding and food quality significantly affect blowfly (*Lucilia sericata*) larval development and mPMI estimation.** *Samantha Hopper, Talia Freeman, Anamika Seth, Eva Thayer, Daniela Gutierrez, Mary Kay Johnston, Concordia University.*

Insects provide vital clues to help determine the post-mortem interval (PMI) during forensic investigations. Blowflies (Diptera: Calliphoridae) are conspicuous, early colonizers on carrion, and their larval development proceeds through a series of easily identifiable instars. Previous studies have shown that PMI estimation using blowfly larval development is affected principally by colonization rate and temperature. However, the national obesity epidemic may have another unintended consequence--it may affect PMI determination by altering larval food quality. Here, we propose that food source quality and larval density significantly affect developmental rates, and these factors should be considered in PMI estimation using blowflies. In our experiment, we reared wild-caught Lucilia sericata in the lab in a 3x2 full factorial design (N=6), controlling the protein:fat ratios of their food source along with larval densities. Larvae reared on a high protein diet showed significant increases in body size through all instars (potentially leading to underestimating PMI in obese individuals), and larvae reared in crowded environments showed rapid growth and high survival in the first instar relative to uncrowded environments. An additional outdoor experiment illustrates that flies are not always the first nor predominant colonizers in Central Texas, and we show evidence for resource monopolization at baits by the invasive fire ant, Solenopsis invicta. We do not find evidence that insects discriminate based on food quality, but different assemblages of species tend to

colonize baits in open meadow versus closed-canopy forest.

2:15 006-02 U. **Preliminary analysis of sex-based differences in supratrochlear foramina prevalence.** *Ashlee Boyd, Sydney Anderson, Stephanie A. Baker, Alexa P. Kelly, Gisselle Garcia, Timothy L. Campbell, Baylor University.*

Supratrochlear foramina are normally occurring septal defects on the distal aspect of humeri and have been suggested to occur at higher frequencies in females. A review of the literature suggests the presence of this feature is highly variable between populations. From a forensic standpoint, a better understanding of sex-based frequencies of this feature is needed if it is used as a line of evidence in determining sex of unknown individuals. In this study we test for sex-based differences in modern forensic specimens (n=402) housed at the Forensic Anthropology Center at Texas State, Texas State University and the Southeast Texas Applied Forensic Science Facility (STAFS), Sam Houston State University. Additionally, we also test archaeological samples represented by Archaic stage Native American sites of Indian Knoll and Windover (n=61), and an additional Egyptian/Nubian sample (n=42) from the site of el-Hesa Cemetery 2 dating to approximately the Late Roman era. Differences in frequencies were tested using Chi-square. Due to small sample sizes for some ancestral categories, forensic specimens were treated together as single population, as were the archaeological Native American specimens. Results showed that sex-based differences were present in both the forensic (Chi-square=16.78, p<0.01) and Native American samples (Chi-square=8.83, p<0.01) with females possessing STF at a higher rate. Alternately, no differences were detected in the el-Hesa sample (Chi-square=0.32, p>0.05). Overall percent incidence varied between samples, with approximately 15% of the forensic, 41% of the Native American, and 60% of the el-Hesa sample exhibiting this feature. These data support the high degree of variability of STF presence reported in the literature. Future research on this topic will include further sampling of forensic specimens from the STAFS collection in order to generate sample sizes needed to partition out the modern forensic sample.

2:30 006-03 N. **The impact of remote sensing on Maya archaeology: using LiDAR to shed view on the Little Kingdoms among the Great Kingdoms. Understanding the Maya archaeology of northwestern Belize.** *Thomas Guderjan, University of Texas at Tyler.*

Much of the recent public discussion about the ancient Maya has focused on the history of the great dynasties, such as the Kaan dynasty. This discussion will focus on the small kingdoms of northwestern Belize whose scale, population size and economic importance to the rest of the Maya world has yet to be fully understood. Since remote sensing has changed our view after 27 years of field research, this discussion will focus on the scale, complexity and economic underpinnings of the kingdoms of the region.

2:45   006-04 G. **Understanding energetic influences on Inuit nasal variation using 3D morphometrics.** *Alexa Kelly, Scott Maddux, University of North Texas Health Science Center.*

As the nasal complex is primarily responsible for heating, humidifying and filtering inspired air prior to entry into the lungs, geographically-patterned variation in nasal morphology has long been attributed to climatic adaptation. However, previous studies have also demonstrated sexual dimorphism in overall nasal size, with larger nasal passages in males hypothesized to reflect greater volumetric demands for oxygen intake due to higher metabolic requirements. Yet, to date, no study has attempted to study this dynamic using a comprehensive model of the internal nose encompassing height, width, and length dimensions in conjunction with actual individual-specific metabolic data. Here, we employ data collected from both the nasal and post-cranial skeletons of 84 (36 female/48 male) modern humans indigenous to Point Hope, Alaska. Twenty-seven 3D-coordinate landmarks were collected from CT scans of the nasal skeleton using 3D Slicer software. Associated postcranial data for each individual were obtained from an existing dataset (Auerbach & Ruff 2004) and used to calculate body mass and basal metabolic rate (BMR) using climate-specific formulae. Following theoretical expectations, multivariate regression results indicate that overall nasal passage size is significantly correlated with both body mass (r= 0.516, p<0.0001) and BMR (r=0.624, p<0.0001). Conversely, within this one sample (i.e., holding climate constant), overall nasal passage shape was not significantly correlated with either body mass (r=0.105, p=0.428) or BMR (r=0.152, p=0.068). These results support previous suggestions that, within geographically indigenous populations, males and females exhibit similar nasal shapes due to shared climatic conditions, while differing in nasal size due to sexual dimorphism in energetic demands.

3:00   006-05 G. **Ancient human mobility of the Canary Islands: determining locality of Guanches via the use of radiogenic signatures of 87Sr/86Sr.** *Paloma Cuello del Pozo, Texas A&M University.*

The use of stable isotopes of strontium has become a popular tool for archaeology to investigate past human migration. This method, borrowed from the field of geochemistry, proofs useful as mammals are continuously ingesting natural elements and their various isotopic species via food, water, and to a lesser degree through respiration. As a daughter isotope of rubidium 87, strontium 87 is found at various quantities depending on the antiquity and abundance of Rb in the geochemical substrate of a region. The ratio between strontium isotopes 87 and 86 (87Sr/86Sr) is measured to help determine local radiogenic signatures in the terrain and inhabitants. Humans obtain Sr mainly from vegetarian diets, a mineral that incorporates in the skeleton as a substitute for calcium during the formation of the hydroxyapatite crystal lattice, the mineral foundation of bone and teeth. The method in archaeology compares ancient human skeletal material to known local radiogenic 87Sr/86Sr present in the geological region of study. This tool has currently been applied widely including within oceanic islands, which are considered an optimal place for the use of 87Sr/86Sr as an identifier of foreign individuals. This study is the first showing ancient human results from the Canary Islands, a region that due to its natural abundance has attracted humans as early as the first millennia BCE. Data from this project confirms the locality of 14 skeletons from archaeological sites from Tenerife Island based on 87Sr/86Sr measurements obtained from teeth. These ratios are compared to previously obtained bioavailable baseline values and are proof that local parameters fall in line with those common among ancient populations living in oceanic-volcanic islands. This project is using a subset of samples from my doctoral dissertation, which is focused on understanding why such cultural diversity existed among the ancient aboriginals of the Canary Islands.

Poster Session Abstracts

Friday, 4:00 to 6:30

Anthropology Poster Session

Participants:

ANT-01 P G. **A mCT comb-based approach to standardize sampling locations of the coronal suture.** *Stephanie A. Baker, Timothy L. Campbell, Patrick J. Lewis, Sam Houston State University.*

In this study, we seek to establish a protocol for standardization of sampling sites along sutures using Avizo segmenting software and present a microcomputed tomography (mCT) comb-based approach to standardize sampling sites along the coronal suture. Computed tomography scans are often used to evaluate areas of complex structures, are non-destructive, and can provide additional methods to assess trauma. Cranial sutures are complex interdigitating synarthrotic joints that unite the bones of the cranium and can be used to assess age, trauma, and early sutural closure. Six human cranial trauma cases and three control specimens housed at the Southeast Texas Applied Forensic Science (STAFS) facility in Huntsville, Texas and the Forensic Anthropology Research Facility (FARF) in San Marcos, Texas were used in this study. All specimens are adult males >56 years of age. Specimens were mCT scanned at the University of Texas High-Resolution X-ray Computed Tomography (UTCT) and FARF facilities. For standardization of data collection, Type-1 landmarks were used with imaging of the coronal sutures beginning at their origin at the anterior margin of the sphenoparietal suture (sphenion) and terminating at the intersection with the sagittal suture (bregma). Avizo 9.7.0 imaging software was used to measure and define the chord distance between sphenion and bregma where twenty equidistant points were plotted along the chord. From these defined points, sampling sites at orthogonal angles from the chord line were placed along the coronal suture. Utilizing a cord bound by landmarks to define the spacing and placement of sampling sites along a three dimensional, curved, tortuous feature like the coronal suture, allows for both precision and replicability between studies. Moreover, this methodology is time efficient and can be applied to other complex features of the skull where sampling site standardization may be difficult.

Biomedical Sciences Poster Session

Participants:

BM-01 P U. **Gene expression changes in mesenchymal stem cells due to different pathologies: potential implications of an increased FLRT3 expression.** *Sara King, Dr. Joni Ylostalo, University of Mary Hardin-Baylor.*

Mesenchymal stem cells (MSCs) are multipotent stem cells that are currently under clinical exploration as an innovative therapeutic approach for tissue repair, regeneration, and even tumor suppression. Despite the inspiring potential of MSCs, their effectiveness remains limited and uncertain due to the risk of tumorigenicity, proinflammation, and fibrosis after transplantation. The aim of this bioinformatics study was to identify a common set of differentially expressed genes in mesenchymal stem cells from different pathologies that could shed light onto the reason for the ineffectiveness of MSCs in people with certain diseases. Raw gene expression data sets of control MSCs and MSCs from lung cancer, acute myeloid leukemia, and osteoporosis patients were obtained from a public data repository and analyzed with TAC software. Gene expressions were then organized by the top thirty largest and smallest linear fold changes. Numerical rank, linear fold change, and p-values were considered in the selection of significant up-regulated and down-regulated genes. From the 180 analyzed genes, five were commonly up-regulated and seventeen were commonly down-regulated across the different data sets. Four of the up-regulated genes were involved in cellular functions regarding growth processes and cell-to-cell adhesion. FLRT3 gene was the most significantly up-regulated in all three diseases, propagating increased receptor signaling, cell to cell adhesion, protein binding and bridging, and chemorepellent activity potentially contributing to the potential tumorigenic, inflammatory, and fibrotic nature of MSCs. These results provide information for a testable hypothesis as to why MSCs may not be effective in patients with some conditions.

BM-02 P U. **Therapeutic response of intrasplenically and intracaecally implanted HT-29 human colon cancer cells.** *Emmanuel Sanchez, Ivan Sosa, Jose Lopez, Karla Parra, Paloma Valenzuela, Diana Gonzalez Garcia, Joel*

Martinez, Karen Chavez, Shan Man, Urban Emmenegger, Anthony Mutsaers, Robert S. Kerbel, Giulio Francia, University of Texas at El Paso.

We tested schedules of metronomic chemotherapy regimens and cancer development in animal models. These regimens include combinations with bevacizumab. We generated orthotopic models of the human HT29 cancer cell line in SCID mice. HT29 cells were transfected to express EGFP (GFP), luciferase or human chorionic gonadotropin (hCG) and subsequently injected intracaecally or intrasplenically. Intrasplenic injections of one million cells resulted in a rapid generation of liver metastases, and in some cases ascites. Metronomic cyclophosphamide (CTX) administration, either alone or in combination with an upfront bolus CTX administration caused a modest increase in survival in the absence of overt host toxicity. Here we show therapeutic benefit was observed with the combination of the anti-VEGFR2 antibody (DC101) together with metronomic CTX, provided therapy was initiated at an early stage, and with a regimen of gemcitabine (160mg/kg, i.p.) given every three days. The development of HT29 orthotopic models that are readily monitorable should improve the preclinical evaluation of new therapeutic strategies. These studies will demonstrate translational aspects of chemotherapy type and distribution for clinical trials in late-stage metastatic colorectal cancer.

BM-03 P U. The design of artificial epidermal growth receptor dimers that mimic endogenous ligand-Induced activation. *Allison Sunderhaus, Amanda Goudelock, Ramsha Imran, Dustin Patterson, May H. Abdel Aziz, University of Texas at Tyler.*

Epidermal Growth Factor Receptor (EGFR) is a clinically validated target for a multitude of human cancers. The receptor is activated upon ligand binding through a critical dimerization step. Dimerization can be replicated in vitro by locally concentrating the receptor kinase domains on the surface of lipid-based vesicles. However, the process to produce the liposomal vesicles in a uniform size, achieve the same degree of localization, and maintain reproducibility is laborious, technically difficult, and not amenable to high throughput screening. Here we show the use of coiled coils to induce spontaneous receptor kinase domain dimerization in vitro to form non-membrane bound artificial receptor mimics in solution. Two engineered forms of EGFR kinase domain fused to coiled coil

complementary peptides P3 and P4 were designed to self-associate upon mixing. Two fusion protein species (P3-EGFR and P4-EGFR) independently showed the same activity known to exist with EGFR kinase domains. Upon mixing the two species, coiled coil heterodimers were formed that induced EGFR association that was accompanied by an 11.5-fold increase in the phosphorylation rate indicative of kinase domain activation. These levels of activation are equivalent to the one achieved using vesicle localization and mimicking in vivo ligand-induced activation. This would enable structural and functional studies by facilitating dimerization, avoiding the use of external reagents, and facilitating high throughput screening campaigns for drug discovery studies of this clinically important receptor class.

BM-04 P U. Discovering novel inhibitors of main protease in SARS-CoV-2 by virtual screening. *Jadelynn Aki, Josh Beckham (RE), Walter Fast (PI), University of Texas at Austin.*

Coronavirus disease 2019 (COVID-19) is a member of the coronavirus family and is caused by SARS-CoV 2. This virus is responsible for a global pandemic, and the elderly or individuals with underlying health conditions are most at risk for developing severe illness. However, the 64 million confirmed cases show that anyone is at risk for transmission, and the need for a therapeutic or drug for COVID-19 became a priority. Viral proteases are well-validated drug targets in general, so the main protease would be a good candidate. The main protease cleaves the polyprotein of the virus into individual, functional proteins, and the proteolytic release is a process that is essential to the replication cycle. The uniqueness of this enzyme compared to human proteases also contribute towards its potential as a drug target. Structure-based computational methods were utilized to identify potential inhibitors of the COVID-19 main protease (6LU7). Virtual screening with molecular docking programs GOLD and VINA was used to dock novel compounds into the target protein to examine their binding interactions. Of the positive controls docked, Ritonavir and Atazanavir scored 93.3 in GOLD and 303.1 in VINA respectively. Various compound libraries consisting of 233,652 ligands (NIH Clinical Collection, MayBridge HitFinder9, ZINC ChemBridge Library, In-house collection, CNS, Fragment Set) were screened in GOLD with scores ranging from 23.85-113.71. Additional library screenings will be performed to further discover promising novel ligands for biological assay testing.

BM-05 P U. **Discovery of inhibitory biomolecules of D-alanine: D-alanine ligase of *Staphylococcus aureus* using high-throughput virtual screening.** *Kaleigh Copenhaver, Dr. Josh Beckham, Dr. Walter Fast, University of Texas at Austin.*

New antibiotic-resistant strains of *Staphylococcus aureus* continue to emerge, creating additional challenges to not only treating symptoms of infections but also preventing the spread of bacteria. *S. aureus* is the leading cause of infections in U.S. healthcare facilities and exposure to the pathogen can lead to a variety of ailments including pneumonia, endocarditis, sepsis, and in severe cases, death. D-alanine: D-alanine Ligase (DDI) is an essential enzyme of *S. aureus* that assists in peptidoglycan cross-linkage formation. Peptidoglycan is vital to bacterial cell walls as it provides structural support for the cell to withstand the osmotic pressure gradient that exists between the cytoplasm and materials outside of the cell. Current antibiotics, such as Vancomycin, target and disrupt peptidoglycan synthesis, but antibiotic resistance limits the use of this treatment. The objective of this research is to discover novel ligands via virtual screening that can bind and potentially inhibit DDI from functioning. Computational ligand libraries of varying sizes and molecular scaffolds were docked against the Vancomycin-resistant DDI crystal structure, and each ligand was given an overall binding score derived from the intermolecular forces with the protein. Thus far, a total of 139,091 computational ligands have been virtually docked and rank-ordered. Positive controls scored between 40.29 and 71.20, negative controls scored between 25.80 and 64.31, and library docking scores ranged from 59.96 to 92.22. While these results do not prove ligands will inhibit the DDI enzyme in vivo, virtual screening has significantly narrowed the best potential ligands to be tested in the lab. High-scoring ligands have the potential to bind well to DDI and their inhibition abilities can be further investigated through biochemical assays to determine the ligand's viability as a potential pharmaceutical.

BM-06 P U. **Bacteriophage purification and propagation for *Pseudomonas aeruginosa*.** *Jesus Garcia, Zacariah Hildenbrand, Ricardo Bernal, University of Texas at El Paso.*

A series of recent published studies has revealed that various microbial species grow abundantly in carbonaceous wastewaters produced in the energy sector where they can form biofilms and deteriorate infrastructure. These bacteria, such as *Pseudomonas*

aeruginosa, can become resistant to UV, ozone, and other traditional forms of disinfection. The focus of this research is to identify bacteriophages that will eliminate the bacteria found in raw oilfield waste. A bacteriophage, or phage, is a virus that selectively eliminates bacteria by infecting it and reproducing inside it. Once it has finished replicating, the cell goes through a lytic or lysogenic cycle. After making several observations of multiple bacteria strains and corresponding phages, our study has identified SN bacteriophage of the Myoviridae family as a focus for our study. Our preliminary findings suggest that the SN phage was able to infect and kill *Pseudomonas aeruginosa* as indicated by the presences of phage plaques in the plague assay within 12 hours. We were able to obtain a higher phage titer of 10^9 PFU/ml by isolating the phages from the plate containing plaques. Purification of the phage was performed by infecting *Pseudomonas aeruginosa* in liquid medium and isolating the SN phage using ultracentrifugation. Successful future trails may lead to a combination of phages mixed into a cocktail to eradicate all microbes found in raw oilfield wastewater. Ultimately these finding may potentially serve as a cost-effective method to eradicate problematic microbes from compromising energy infrastructure without the use of harmful chemical additives.

BM-07 P G. **Understanding distribution of hantaviruses in the region of New Mexico with no known hantavirus pulmonary syndrome cases.** *Jaecy K. Banther, Samuel M. Goodfellow, Thanchira Suriyamongkol, Robert A. Nofchissey, Steven B. Bradfute, Ivana Mali, Eastern New Mexico University.*

Hantaviruses are zoonotic RNA viruses that cause Hemorrhagic Fever with Renal Syndrome (HFRS) and Hantavirus Pulmonary Syndrome (HPS) in humans. In the US, New Mexico is the leading state in number of HPS cases, with a total of 118 since the 1975 outbreak. Since the majority of reported cases are from northwestern NM, minimal research attention has been given to the eastern portion of the state. However, studies conducted in bordering Texas counties have indicated the presence of hantaviruses and have confirmed HPS cases. Literature suggests a potential overlap of the Sin Nombre (SNV), El Moro Canyon, and Muleshoe virus in eastern NM, and a recent study found six species positive for hantavirus specific antibodies in this region. Here, we aim to investigate hantavirus antibody seroprevalence, identify hosts, and genetically confirm hantaviruses across eight under surveyed counties in eastern NM. To date, we have surveyed 15

sites over 22,500 trap nights and captured 520 individuals belonging to two families: 31% Heteromyidae and 69% Cricetidae. Seven of those are known hantavirus hosts. Species richness ranged from two to eight species per site, while capture per unit effort varied from 1% to 5%. We have genetically confirmed the presence of SNV in a subset of lung samples through RT qPCR and identified additional seropositive individuals through enzyme-linked immunosorbent assays (ELISA). Laboratory work is ongoing, and we will resume trapping efforts in March 2021. This study significantly expands our understanding of hantavirus species distribution, hantavirus prevalence among their respective hosts, and has a potential to illuminate any spillover events and/or discovery of novel hantaviruses.

BM-08 P G. **Modulation of VraS sensor histidine kinase activity and inhibition in presence of its response regulator VraR.** *Lane Marsh, Shrijan Bhattarai, Allison Sunderhaus, Paul Epie, May H. Abdel Aziz, University of Texas at Tyler.*

Upregulation of cell wall synthesis in pathogenic Staphylococcus aureus is a prominent cause of increasing resistance to current antibiotics. VraS, a histidine sensor kinase of a two-component regulatory system utilized by the bacteria, has been identified as a key factor in the development of antibiotic resistance. Upon sensing bacterial cell wall stress signal, the kinase undergoes an autophosphorylation reaction then transfers the phosphate group to its cognate response regulator VraR causing its activation, DNA binding and stimulation of cell wall synthesis gene cluster. Inhibition of VraS was shown to reverse this trend and restore the sensitivity of S. aureus to commonly used antibiotics. The modulation of VraS activity and inhibition in presence of its VraR was not investigated. Here we show that VraS rate of phosphorylation increases in presence of VraR which could indicate either increased pool of the recycled kinase after the phosphotransfer reaction or a conformational activation induced by VraR binding. The results also show that VraR causes VraS to be less susceptible to inhibition by the histidine kinase inhibitor NH125. We anticipate our studies to spark more in-depth exploration into the effects of response regulators on modulation of activity and inhibition of target kinases and highlight the importance of including VraR during screening for VraS potential inhibitors to mimic the microbiological conditions.

Cell & Molecular Biology Poster Session
Participants:
CELL-01 P U. **Characterization of mouse Schlafen 14 upon viral infection.** *Lilia Olmstead, Carlos Valenzuela, Manuel Llano, University of Texas at El Paso.*

The Schlafen family of proteins have been suggested to have important functions in cell proliferation, immune cell development, and anti-viral response. A member of this family, Schlafen 11, has already been characterized as an interferon-stimulated gene that is able to control viral protein synthesis by regulating tRNA abundance. Through this mechanism, Schlafen 11 has been shown to impair HIV-1 infection and Flaviviruses. However, not much is known about other members of the Schlafen family and their potential as virus inhibitors. This presentation will aim to characterize the mouse homologue, Schlafen 14, to observe its anti-viral activity upon infection with HIV-1. Given this, we hypothesize that Schlafen 14 will display anti-viral activity and preferentially restrict the replication of HIV-1. Experiments were first carried out with gene cloning by creating a mouse Schlafen 14 expression plasmid. The resulting DNA was sequenced and analyzed for any mutations with Sanger Sequencing. Upon finding no mutations, human glioblastoma (A-172) cell lines were generated expressing mouse Schlafen 14 or a Schlafen11-specific shRNA (KD). HIV-1 infection was evaluated by measuring the level of the viral protein p24 in the cell supernatant by an ELISA and luciferase activity in cell lysates by using an enzymatic assay. Preliminary results revealed that the level of HIV-1 p24 expression was significantly lower in A-172 cells expressing mouse Schlafen 14 than in A-172 Schlafen 11 KD cells revealing that Schlafen 14 may exhibit anti-viral functions. We believe that Schlafen 14 may do this by ribosomal stalling, a mechanism proposed to explain the deleterious effect of the Schlafen proteins on viral protein expression. It is expected that this work will have the potential to expand our knowledge on viral functionality and the antiviral activity of the Schlafen protein family, an area poorly explored.

CELL-02 P U. **Characterization of a chaperonin mutant.** *Samantha Garcia, Daniel von Salzen, Ricardo Bernal, University of Texas at El Paso.*

In the cell, protein folding, and refolding is an essential mechanism that allows for vital biological interactions to occur. To aid proteins in conforming to their native structure, cells evolved a specialized protein complex termed a chaperonin. Chaperonins are multi-subunit

enzymes that self-assemble to create a hollow cylinder where unfolded protein substrates are folded in the internal chamber by the means of an ATP dependent pathway. A specialized chaperonin termed φEL is the first of two enzymes to be encoded by a bacteriophage and has been identified as an ortholog of Gro EL. φEL refolds a substrate through a mechanism that involves the separation of the φEL cylinder into two rings. This study proposes that ring separation is an important intermediate in refolding substrate within the φEL complex. In this investigation, we demonstrate that a point mutation (A91T) leads to the inhibition of ring separation in the φEL chaperonin. The chaperonin has been expressed in *E. coli* and purified to homogeneity using column chromatography. The effects of the mutation will be characterized with a kinetics assay to investigate if all protein folding activity has been abolished. Furthermore, electron micrographs reveal that the chaperonin mutant is unable to form single-ring intermediates and all complexes observed are intact double rings. We anticipate that no single-ring intermediates will be produced, and the mutant will not be able to refold substrate proteins. This unique protein folding dynamic could contribute to the classification of a new group of chaperonins. Research reported in this poster was supported by the Minority Access to Research Careers programs (Grant number: 2T34GM008048 sponsored by the NIH/ NIGMS). This content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health. The project is also supported by The Welch Foundation AH1649.

CELL-03 P U. **Functional significance of point mutations in Hsp27 that lead to neurodegenerative disease.** *Andres Orta, Bianka Holguin, Ricardo Bernal, University of Texas at El Paso.*

Protein folding into a native conformation can be interrupted by environmental and physiological factors. The process of protein folding is critical and misfolding can lead to multiple neurodegenerative diseases. Environmental and physiological factors that can lead to misfolding can include exposure to heavy metals, oxidative injury, and heat shock. Molecular chaperones, specifically heat shock proteins (Hsp), aid in the refolding and stabilizing of misfolded proteins as a response to heat stresses. This study focuses on the mitochondrion small heat shock protein 27 (hsp27) that prevents aggregation in substrates through their stabilization and transferring to ATP dependent chaperonins for refolding. It is speculated that the active form of hsp27 is a large oligomeric complex that is in equilibrium with dimeric subunits. However, in its phosphorylated form this equilibrium is shifted towards the small dimeric subunits. The hydrophobic region of the hsp27 dimer binds to the misfolded protein, stabilizing it until complete transfer to a chaperonin. Five single point mutations (S135F, R127W, R136W, T151I, and P182L) have shown to be associated with the neurodegenerative disease Charcot-Marie-Tooth (CMT). CMT affects the motor and sensory neurons of the peripheral nervous system which affects weakness and atrophy of distal muscles. Therefore, this study focuses on characterizing the activity of wild type Hsp27 and the single point mutations in both their chaperone active oligomeric and dimeric forms for comparison.

CELL-04 P U. **Exploration of N-thiocarbamoyl-7-nitroindolines for the generation of a photocleavable crosslinker.** *Philip T. Baily, Patricio Del Castillo, Aurelio Paez, Matthew R. Weaver, Roberto P. Iturralde, Carl W. Dirk, Chunqiang Li, Katja Michael, University of Texas at El Paso.*

The photolytic properties of N-acyl-7-nitroindolines make them attractive for the development of photocleavable crosslinkers when reversibility of the crosslinking by light illumination is desired. However, the acylation of 7-nitroindolines can be quite challenging. If other carbonyl-containing functional groups of 7-nitroindoline were more readily accessible while retaining photoreactivity, the development of such crosslinkers would be facilitated. Here we demonstrate the efficient syntheses of N-thiocarbamoyl nitroindolines, including a homobifunctional photocleavable crosslinker for amines, and compare their photolysis kinetics with that of an N-acyl-7-nitroindoline. We also show that these 7-nitroindoline derivatives can undergo one photon or two photon photolysis at 350 nm or 710 nm, respectively. N-Thiocarbamoyl-7-nitroindolines undergo a clean photochemical conversion to a product believed to be a dimer of 7-nitrosoindoline, which is different from the known predominant photolysis products of N-acyl-7-nitroindolines. Our quantum chemistry calculations have elucidated a likely photochemical reaction pathway of thiocarbamoyl-7-nitroindolines, which is in strong agreement with our experimental data. This study expands the scope of 7-nitroindoline-containing compounds and informs the development of novel photocleavable crosslinkers. PTB is grateful for a MARC scholarship. Research reported in this publication was supported by the National Institute of General Medical

CELL-05 P U. **Comparative expression analysis of brown and black widow toxins.** *Sebastian Torres, Abraham Landeros, Kaleth Salazar, Lindsay M. Porter, Stephen F. Austin State University.*

Texas is home to two species of widow spiders. One of them, the southern black widow or Latrodectus mactans, is native, while the second, the brown widow or Latrodectus geometricus, is invasive. Widow spiders are widely feared due to their potent venom toxins and thus the investigation of the molecular composition of widow venom has garnered much attention and research. Prior research has indicated that these spiders have a unique toxin expression profile including the expression of toxins throughout the spider's body. What is unclear, however, is whether all toxins are ubiquitously expressed or whether there is a more selective toxin expression throughout the widow tissues. In this study, we addressed whether brown and southern black widow spiders express both the vertebrate-specific δ±-latrotoxin and the insect-specific δ ±- and δ ´-latroinsectotoxins in only venom glands or also throughout the cephalothorax and abdomen. We also compared expression profiles in females and males and profiles throughout the life stages: eggs, spiderlings, and adults. Interestingly, both vertebrate-specific and insect-specific toxins are expressed throughout life stages and tissues, with the exception of the δ ´-latroinsectotoxin which appears to have a much more selective expression profile. This expression pattern suggests potential differential roles in defense and predation and will help to prioritize which toxins that will be further investigated by recombinant protein expression for functional assays.

CELL-06 P NS. **Aptamer-DNA scaffolded silver nanocluster: A tool to prevent the biofilm of *Pseudomonas aeruginosa.*** *Bidisha Sengupta, Prakash Adhikari, Prabhakar Pradhan, Stephen F. Austin State University.*

Biofilms are communities of bacteria on a surface, which are caged by the extracellularly secreted proteins, carbohydrates, and/or DNA. The phenotypes of these multicellular aggregates are distinct from those of planktonic cells. The biofilms are resistant to anti-microbial agents, which give rise to chronic bacterial infections and death in human beings. The present study is designed to explore the effect of silver nanolcusters (Ag-NC) on the biofilm formation by Pseudomonas aeruginosa (PA). Two DNA aptamers specific for PA and part of their sequences were chosen as templates for growing the Ag-NC. Circular dichroism (CD) studies determined the presence of secondary structures on the DNA templates. UV/Vis absorption, and fluorescence spectroscopic measurements confirmed the formation of the fluorescent Ag-NC. Mesoscopic physics-based partial wave spectroscopy (PWS) was used for the first time in Ag-NC based studies, to analyze the backscattered light signal that can detect the degree of nanoscale mass density/refractive index fluctuations for detecting the biofilm formation. A comparative analyses was performed among the different aptamers with respect to the control sample. The decrease in disorder strength (Ld) of the Ag-NC treated samples compared to the untreated PA cells was attributed to the decrease in the biofilm. We envision to create a new paradigm in using a powerful optical microscopic technique like PWS in detection, and aptamer enclosed silver nanoclusters to prevent biofilms, for notorious pathogen like Pseudomonas aeruginosa.

Chemistry & Biochemistry Poster Session
Participants:
CHEM/B-01 P U. **Analysis of metals in Rio Grande River Basin of Texas by inductively coupled plasma-mass spectroscopy (ICP-MS).** *Sara Ibarra, Victoria Doan, Gabriela Zuniga, Jaime Castro, Patricia Gonzalez, Edward Gonzalez, Alakananda Ray Chaudhuri, University of the Incarnate Word.*

This study was carried out to determine the concentration levels of metals in the water samples from seven different sites of the Rio Grande River Basin in Texas between Amistad Reservoir and Zapata that covers a region of two hundred and fifty miles in order to assess the metal distribution patterns of the river in this region. The seven sites selected for the study were Amistad Dam, Del Rio, Eagle Pass, Laredo-Colombia, El Cenizo, San Ignacio, and Zapata. The EPA has set federal standards for the amount of pollutants and metal ions allowed for safety in surface, potable and recreational waters. The metals were analyzed by Inductively Coupled Plasma-Mass Spectroscopy (ICP-MS) using the EPA method 200.8. The river water samples were collected and acidified with nitric acid (1+1) and hydrochloric acid (1+1), filtered in the lab through a 0.45 µm filter followed by digestion between 93-96°C, and analyzed for twenty-seven metals by ICP-MS using a Varian 820-MS model. The percent recovery values for these metals in the spiked control samples

varied between 96% and 110%. Only the Amistad Reservoir water sample showed the Pb concentration of 0.041 mg/L which was above the federally regulated EPA limit of 0.015 mg/L Pb content for surface water. The remaining metals analyzed in all the seven water samples were well within the permissible limits of the EPA and the State of Texas Commission on Environmental Quality standards. Further water quality studies will include analysis of metals in the remaining sites of the Rio Grande Basin of Texas from Falcon Reservoir to Brownsville in order to assess the risk to human health and the environment associated with the levels of these metal content in the Rio Grande River water.

CHEM/B-02 P U. **Finding novel inhibitors of SARS-CoV-2 main protease.** *Jeff Huynh, Ji Min Chon, Josh Becham, University of Texas at Austin.*

SARS-CoV-2, also known as the causative agent of the 2019 coronavirus disease, has caused a global health crisis and has been noted to be the most significant outbreak of the 21st century. The lack of therapeutic options and significant mortality rate make this disease a pressing candidate for drug discovery. One promising drug target is the main protease (denoted as Mpro or 3CLpro) due to its importance in viral replication in the early stages of infection. The enzyme cuts the polyproteins translated from viral RNA to produce functional and mature viral proteins. In addition to this target proteins essentiality, its highly conserved active site and dissimilarity to human proteases make Mpro a worthwhile target. Virtual screening was used to identify top compounds that may serve as potential hits for later biochemical assays. The molecular docking program GOLD was used to dock and give predicted binding via a GOLD score for several control compounds against the 6WTT crystal structure of Mpro to test the validity of this method. The positive control GC-376 was docked in a similar conformation to its x-ray crystallography pose and ranked high with a GOLD score of 87.53. Several compounds were selected from over 200,000 in various compound libraries such as: the NIH Clinical Collection, Maybridge HitFinder 9, and ZINC ChemBridge Library. Further screening was done on larger compound libraries from MayBridge and ZINC, which had high score ranges of 58.43-98.24 and 52.5-106.78, respectively. Another virtual screening program, ICM, was used in parallel on the same libraries to identify candidate compounds using an alternative scoring algorithm. From these collective results we are able to better visualize the binding interactions that are predicted to inhibit the functions of Mpro and compare the scoring algorithms of two virtual screening programs. We plan to screen more ligands to identify novel scaffolds that can contribute for further research against the Mpro.

CHEM/B-03 P U. **Expression and purification of human circadian protein hRORÎ³ for structural and functional studies.** *Sebastian Sanchez, Alexander Madej, Brenda Moreno, Yuejiao Xian, Seung-Hee Yoo, Zheng Chen, Chuan Xiao, University of Texas at El Paso.*

The circadian rhythm is an internal biological clock that runs in an abundance of organisms and regulates the sleep wake cycle among many other physiological functions. Long term disruption of this internal clock can cause sleep disorders, metabolic diseases, and high risks of cancer. The circadian rhythm is controlled at molecular level by the transcriptional-translational feedback loop (TTFL) that involve positive transcriptional activators CLOCK/BMAL1 and negative feedback suppressors PERs/CRYs. The Retinoic Acid Receptor-Related Orphan Receptors (RORs) function as ligand-dependent transcription factors which regulate BMAL1 production to improve circadian rhythm stability and robustness. It was shown that the naturally occurring flavonoid Nobiletin can bind to human ROR gamma (hRORγ) and increase its function through a yet unknown mechanism. Understanding the interaction between hRORγ and Nobiletin would provide insights in enhancing the circadian rhythm and ameliorating its related diseases. This project focuses on solving the three-dimensional structure of hRORγ/Nobiletin complex to establish the mechanism of their interaction. The hRORγ gene was cloned and expressed using E. coli BL21 cells. Expression protocols were optimized to produce large amounts of hRORγ recombinant proteins. The soluble portion of expressed protein was purified using affinity chromatography and size exclusion chromatography, and the purified recombinant hRORγ is properly folded indicating from circular dichroism data. Once the required concentration is reached, the purified hRORγ will be co-crystalized with Nobiletin. The crystals would be used for structural determination using X-ray crystallography. The structural information will shed light on Nobiletin's enhancement mechanism on circadian rhythm and provide guidance in related drug development.

CHEM/B-04 P U. **A method for the determination of pesticides in soils by using liquid chromatography with photodiode-array detection (PDA) and fluorescence detectors.**

Joshua S. Hamilton, Kefa K. Onchoke, Stephen F. Austin State University.

The development of a simple method for the determination of several commonly used pesticides in soil samples was investigated. Standard solutions of carbaryl, chlorothalonil, chlorpyrifos, and permethrin were prepared and analyzed by using High Performance Liquid Chromatography with Photodiode-Array Detection (PDA) and Fluorescence detectors (HPLC-PDA-FD). With PDA detection, the LOD and LOQ for carbaryl were 12.77 ppm and 38.71 ppm, respectively. The LOD and LOQ for chlorothalonil were 8.23 ppm and 24.94 ppm, respectively. With the more sensitive FD, the LOD and LOQ for carbaryl were lowered to 10.57 ppm and 32.04 ppm, respectively. Further investigation on the elution profiles of permethrin and chlorpyrifos was obtained. In addition, UV-Vis spectrophotometry was used to qualitatively determine the absorbance spectra for each target pesticide. Further method optimization, validation, and extraction development is under examination for application to soil samples collected from around Nacogdoches City, in East Texas.

CHEM/B-05 P U. **Kaempferol: a potent ligand for unusual DNA motifs.** *Matthew Beasley, Debarshi Roy, John Piletz, Bidisha Senguptat, Stephen F. Austin State University.*

The structure of the telomeric region is conserved in almost all eukaryotes. The DNA sequence at human telomeres consists of tandem guanine rich repeats of (TTAGGG). Literature data shows that the G strand is longer than the C strand, indicating a 3' -G overhang at telomeres. The G-and C- (in the complementary strand) rich sequences in telomeric DNA and promoter regions of human genome are associated with tumorigenesis. Stabilizing these unusual tetraplex structures in DNA can prevent tumor cell proliferation, which have been regarded as potential pathways for cancer therapy. Kaempferol (3,5,7,4′-tetrahydroxyflavone) is a bioactive plant flavonoid of immense importance as a potent anticancer agent. In the present study, we have prepared a juice of kale, and HPLC studies show the resemblance between the fluorescence chromatograms of kale juice and kaempferol. Kale juice exhibits a preferred binding for C-rich DNA sequence over G-rich and duplex DNA oligonucleotides. We have exploited the fluorescence property of kaempferol to examine its interactions with relevant macromolecular targets, namely double stranded (from calf thymus, CT), and quadruplex (QD, G4 and C4) DNA. In the presence of CT DNA dramatic changes are observed in the intrinsic fluorescence behavior of kaempferol. Spectroscopic data suggest that kaempferol binds intercalatively between the base pairs in CT DNA, whereas it is a loop binder in G4 and C4 DNA. Dramatic changes in differential absorbance spectra of G/C-quartet DNA with and without kaempferol were observed, suggesting the stability of quadruplex structures with the natural product. This study furthers the importance of kale as a potent therapeutic and would open the door to new avenues in medicinal chemistry.

CHEM/B-06 P U. **A structure-activity study on the binding of quercetin with DNA-bound protein.** *Taylor Grays, Bidisha Senguptat, Stephen F. Austin State University.*

Since Albert Szent-Gyorgyi's Nobel Prize winning research in 1937, synthetic and natural flavonoids have been extensively studied by researchers around the world. Quercetin (3,3',4',5-7-pentahydroxyflavone), is ubiquitous in plant of higher genera, and are widely studied for their high therapeutic potency and low systemic toxicity to treat a wide spectrum of diseases which include cancers, neurodegenerative disorders, and atherosclerosis. Here, an exploratory study on quercetin has been performed in protein-DNA microenvironment. Our previous studies have revealed that quercetin binds in the interdomain cleft region of serum albumin protein. However the behavior in protein-DNA environment is not studied yet. Usually flavonols with a 5-OH group show fluorescence emission only when they are bound with a rigid environment. Absorption, fluorescence, and circular dichroism (CD) spectroscopic measurements have been carried out at five different temperatures, 15, 20, 25, 30 and 37 °C to observe the influence of the structure of protein-DNA on the binding with quercetin. The dual fluorescence characteristics (excited state proton transfer, ESPT) of quercetin increased with increasing temperature, which indicated quercetin binds with the macromolecular conjugate more at the physiological temperature 37 °C. Studies of quercetin with HSA at multiple temperatures indicated that structure of the protein influences the thermodynamics of the binding process. The novel use of plant flavonoids as their own reporters, exploiting their intrinsic fluorescence properties, for probing their interactions with relevant targets is further exemplified in this study.

CHEM/B-07 P U. **A novel cellular and molecular study on curcumin in ovarian cancer cells.** *Khang Nguyen, Brenita Jenkins, Praise Ola,*

Sofia Ievleva, Debarshi Roy, Bidisha Senguptat, Stephen F. Austin State University.

Since the discovery of G-quartet (G4) by M. Gellert in 1962, much attention has been given on G4 and C4 (also called i-motif) as important drug design targets for the treatment of various human disorders. G4 forming sequences are prevalent in human genome, which includes many important regions of the eukaryotic genome, such as telomere ends, regulatory regions of many oncogenes c-kit, proto-oncogene c-myc, Kirsten rat sarcoma viral oncogene homolog (KRas). Curcumin (diferuloylmethane), an anti-inflammatory and antioxidant compound, is found in the rhizomes of the plant Curcuma longa. The phyto polyphenolic chemical curcumin has been in the prominence due to its diverse pharmacological activities. Here, we studied the binding of curcumin with G-quartet and duplex DNA as well as protein bound DNA. Curcumin showed inclination toward binding with G4 than C4 and duplex sequences. Furthermore, cellular studies have been initiated on HeyA8 ovarian cancer cells. Curcumin treatment inhibited the proliferation of HeyA8 cells in a dose responsive manner demonstrated by MTT and colony formation assay. Curcumin treatment also triggers degradation of lipid droplets in HeyA8 cells in an autophagic dependent manner. Finally, we showed that curcumin enhanced the sensitivity of carboplatin treatment in many folds in HeyA8 cells. Further studies on the binding of curcumin with HeyA8 DNA are underway.

CHEM/B-08 P U. **The impact of microalgal extracts on *Stenotrophomonas maltophilia* biofilms.** *Keith V. Kern, Arlene Salazar, Justin M. Parkhill, BD Leverett, University of the Incarnate Word.*

Stenotrophomonas maltophilia is an opportunistic Gram-negative pathogen that demonstrates increasing incidence in clinical settings and a high frequency of resistance to clinically relevant antibiotics. Biofilm formation by *S. maltophilia* has been widely studied as a central mechanism in its resistance development and has become a target for drug development, with anti-biofilm designs focused on altering behavioral and chemical features of the process rather than on bactericidal activity. Microalgae are part of microbial communities in every ecological niche on earth but little is known about how their interactions with bacterial pathogens impact biofilm dynamics. The present study examines the impact of sustainably-produced microalgal extracts on biofilm formation and biofilm viability in three strains of *S. maltophilia*, ATCCïƒ' 13637, ATCCïƒ'

51331, and ATCCïƒ' BAA-2423. Assays for bacterial biofilm formation and bacterial biofilm viability have been performed according to established methods to determine whether the extracts inhibit *S. maltophilia* film forming activities or increase sensitivity of *S. maltophilia* in established biofilms to common antibiotics. Semi-quantitative and qualitative analyses of the extracts has revealed detectable levels of several molecular classes of antibiofilm agents. Preliminary results demonstrate enhanced sensitivity of all three strains of *S. maltophilia* biofilms to aztreonam and ceftriaxone in the presence of microalgal extracts. With the exception of extracts from *Ochromonas danica* and *Nannochloropsis oculata*, no significant bactericidal impacts on these strains of *S. maltophilia* were observed with extracts alone. The present results obviate the need for a detailed chemical analysis of the extracts and are discussed with regard to potential applications.

CHEM/B-09 P U. **Characterization of BTEX species at various TCEQ CAMS sites in Houston city in 2018.** *August Luna, Amit U. Raysoni, University of Texas Rio Grande Valley.*

Concentration of BTEX (Benzene, Toluene, Ethylbenzene, and m, p, and o-Xylenes) species were analyzed at 10 locations in the Houston area for 2018. . The study comprised of data from various Houston CAMS (Central Ambient Monitoring Sites) operated by TCEQ (Texas Commission on Environmental Quality). The Houston area was selected because the urban air quality in this city is greatly impacted by emissions from petroleum refineries, heavy traffic, and other industrial activities. Each of the CAMS site is located in different areas in the Houston area as this helps characterize the spatial variation in the BTEX concentrations within the urban airshed. Results indicated that benzene, toluene and ethylbenzene species are strongly correlated with each other ($0.611 < r < 1.00$, $p < 0.05$). m, p-Xylenes were moderately correlated with other BTE species, ($0.411 < r < 1.00$, $p < 0.05$). This is true with the exception of three CAM sites due to lack of data. Our results demonstrate that BTEX concentrations are highest at CAMS sites which are located in close proximity to industries processing petroleum and crude oil as well as areas impacted by heavy vehicular traffic such as major interstate highways and roadways.

CHEM/B-10 P U. **Zinc oxide nanotechnology expenditures in the production of agricultural provisions.** *Mikayla Rodriguez, Dr. Milka Montes, PhD, University of Texas of the Permian Basin.*

Modern science and technology have encountered an innovative and thrilling area of interest revolving the manipulation and use of molecules at a nanoscale level; this original concept known as Nanotechnology. Nanoparticles (NPs), tiny in size have immense potential in their innumerable applications. In agriculture, nanoparticles have been found useful in functioning as nanocarriers that help deliver nutrients essential to plant growth and production. The upcoming research project being discussed aims to evaluate the passage of zinc and silicon oxide (ZnO and SiO_2) nanoparticles at several concentrations, and to assess their role in the growth/development of multiple *Oscium basilicium* L. (commonly known as Basil) plant species. The nanoparticle application will be accomplished through two methodologies- application of NPs to soil fertilizer, and a NP foliar spray. Subsequent to the application of ZnO and SiO_2 NPs, the basil plants will be assessed for various aroma constituents as well plant quality. The preliminary data suggest that the use of SiO_2 NPs in addition to a heavy metal such as zinc, will provide increased plant strength, mass, and aroma constituent properties in comparison to those not treated with NPs. In this research project, we aspire to establish an appropriate zinc and silicon oxide nanoparticle concentration that can help facilitate plants' growth without causing toxicity to the plant. Research of nanotechnology applications in agriculture is particularly significant to the sustainment of human life worldwide, especially in poverty-ridden parts of the world where food is scarce or unavailable. Additionally, nanotechnology applications in agriculture have immense potential to increase crops' production and nutritional content while decreasing biowaste production- an ongoing Environmental concern.

CHEM/B-11 P G. **Inhibitory role of F15 Fullerene in HIV-1 maturation.** *Alejandro Rodriguez, Zachary S. Martinez, Edison Castro, Luis Echegoyen, Manuel Llano, Ricardo A. Bernall, University of Texas at El Paso.*

HIV-1 is the most prevalent of the major HIV strains currently affecting the human population. Several anti-HIV drugs exist, but drug resistant strains emerge rapidly, rendering treatments useless in many cases. For decades, it has been known that fullerene compounds inhibit the HIV-1 life cycle, but the mechanism of this has not been elucidated. Molecular docking simulations proposed that fullerene compounds interact with HIV-1 Protease, inactivating it and preventing the processing of the Gag polyprotein. Recent studies have invalidated this claim and have demonstrated that functionalized C60 and C70 fullerene compounds prevent the

maturation of HIV-1 in a protease-independent manner. In this work we attempt to elucidate the interaction between derivatized fullerene compounds and an HIV-1 target protein in-vitro. Key aspects of this work include the cloning, expression, purification, and visualization of the proteins using electron microscopy, along with the assays that will highlight the mechanism by which fullerene compounds inhibit the maturation of HIV-1. These findings can help pinpoint novel target sites in HIV-1 proteins, opening the way for the production of new drugs.

Conservation Ecology Poster Session
Participants:
CONS-01 P G. **Freshwater turtle species richness in the Lower Pecos River in New Mexico and Texas.** *Laramie B. Mahan, Lawrence G. Bassett, Thanchira Suriyamongkol, Michael R. J. Forstner, Ivana Mali, Eastern New Mexico University.*

Freshwater turtles represent vital components of aquatic and terrestrial ecosystems, providing many important ecological services (e.g., energy flow, seed dispersal, mineral cycling, etc.) Additionally, they serve as bioindicators of environmental health by accumulating chemicals that reside in their respective aquatic systems. The Pecos River is one of the most anthropogenically altered rivers in the US. Agricultural practices, dam construction, channelization, and petroleum production have significantly altered the river flow and overall water quality. These factors have long threatened the connectivity and viability of wildlife populations, including freshwater turtles. Yet, the Pecos River itself has not been properly surveyed for turtles in over a decade. In this study, we report preliminary results of freshwater turtle surveys across 16 sites in the Pecos River in New Mexico and Texas during the summer of 2020. Upon capture, turtles were individually marked, measured, and released. We recorded water quality parameters such as pH, conductivity (μ/s), temperature (°C), flow (m/s), water depth (m), and water turbidity (m) from all sites. We captured five species of turtles including Red-eared Slider (*Trachemys scripta*), Spiny Softshell turtle (*Apalone spinifera*), Yellow Mud turtle (*Kinosternon flavescens*), Common Snapping turtle (*Chelydra serpentina*), and the Rio Grande Cooter (*Pseudemys gorzugi*). The species richness of turtles ranged from 0 to 5 species, with number of captures ranging from 0 to 170 turtles per site. *Pseudemys gorzugi,* currently under review by the USFWS for potential federal protection, was captured at five locations, with individuals confirmed at a sixth site. This

work will continue, with an additional 16 sites set to be surveyed in the summer of 2021. Our work seeks to significantly contribute to our understanding of freshwater turtle distribution across this riverine system and aid in the assessment of conservation status of *Pseudemys gorzugi*.

CONS-02 P G. **Presence of the amphibian pathogen *Batrachochytrium dendrobatidis* in a hot desert environment that exceeds its physiological tolerances.** *Sadie Roth, Matthew Barnes, Kerry Griffis-Kyle, Texas Tech University.*

The pathogenic chytrid fungus *Batrachochytrium dendrobatidis (*Bd) is a prominent factor in declining amphibian populations worldwide. It was previously assumed that Bd, a fungus highly sensitive to heat, desiccation, and UV exposure, could not survive in isolated water systems of hot deserts. However, limited sampling in 2012 detected Bd in constructed wildlife water catchments in the Sonoran Desert. These catchments are designed to supplement naturally available water in isolated ephemeral rock pools (tinajas) and are constructed with underground or covered reservoirs to prolong their hydroperiod. We hypothesized that these reservoirs may buffer temperature extremes in water, such as those experienced in tinajas, and therefore provide a thermal refuge for Bd in a system where maximum water temperatures can exceed 40°C. Here we show that Bd is in fact present in an environment that regularly exceeds its known thermal tolerances. We found that constructed catchments do not provide thermal refugia for Bd, as they reach similar temperature extremes to those observed in tinajas. Despite these high temperatures, we detected Bd in environmental DNA (eDNA) samples from catchments and on the skin of amphibians in both catchments and tinajas. Therefore, it appears that the Bd found in these Sonoran Desert water sites can withstand higher temperatures than the currently known thermal tolerances of Bd. These findings provide evidence that some Bd may be more temperature resistant than previously understood and emphasize the importance of sampling for Bd even in regions previously excluded as inhospitable environments.

Freshwater Science Poster Session
Participants:
FW-01 P U. **Zebra mussel size distributions in two recently-invaded central Texas reservoirs.** *Jessica M. Konkler, Jason L. Locklin, Josiah Moore, Sam Poster, Laura Weiser Erlandson, Temple College.*

The zebra mussel (*Dreissena polymorpha*) is an invasive freshwater species that was first reported in Lake Texoma, Texas in 2009. They have since invaded Belton Lake (2013) and Stillhouse Hollow Lake (2016). As of October 2020, zebra mussels are established or have been detected in 30 Texas reservoirs across five river basins. Herein, we report mussel length distributions at various depths in Belton and Stillhouse Hollow Lakes. Mussel sampler plates were deployed in April 2020 and June 2020. Sixteen 20x20 cm plates were attached to a single nylon rope that was vertically suspended from the water surface to the lakebed. Four plates each were at depths of 1m, 4m, 8m, and 11m. Mussels were removed from the samplers in October 2020, scanned on a flatbed scanner, and measured to the nearest 0.1 mm. While the Stillhouse Hollow population had higher densities (n = 7,164 and 2,463 on April and June plates, respectively) than the Belton population (n = 142 and 349), the Belton mussels were larger (11.37 ± 3.14 and 9.87 ± 2.41 mm) than Stillhouse Hollow mussels (6.86 ± 3.18 and 6.08 ± 3.19 mm). This difference occurred at all depths in both systems, with the Belton population presenting larger mussels. When lengths were compared by depth within each reservoir, Stillhouse Hollow mussel lengths differed with depth on both the April/June samplers, but this was only found on the June samplers in the Belton population. These size differences are likely due to mussel densities and food resources as dissolved oxygen and temperature levels were similar.

FW-02 P U. **ZnO and TiO$_2$ embedded in photocatalytic styrene and acrylate resin for biofilm degradation studies.** *Fernando Montalvillo, Dr. Milka Montes, Dr. Athenia Oldham, University of Texas of the Permian Basin.*

ZnO and TiO$_2$ nanoparticles embedded in resin have already been proven to photocatalytically degrade organic pollutants due to the nanoparticles catalyzing the formation of Reactive Oxygen Species (ROS) such as OH· or O2·. ROS are very reactive and easily dismantle other molecules. For example, our immune system uses them to combat pathogens. Phagocytic leukocytes use them to kill the pathogen after being ingested by the white blood cell. However, it has not been determined if activated resin can kill microorganisms. Thus, our hypothesis was that ZnO and TiO$_2$ photocatalytic paints are antimicrobial. Before the antimicrobial properties

could be tested, the plates had to be made and characterized. In order to do that, instruments such as the UV-Crosslinker, Scanning Electron Microscope (SEM), Energy Dispersive X-Ray Analysis (EDS), and Rotary Magnetron Sputtering Coating Machine were used. Next, the project will focus on the study of antimicrobial properties. In this step, colony-forming units will be used to test the bactericidal properties of photocatalytic paint in the months of January and February. If TiO_2 and ZnO are able to inactivate or kill the bacteria in the water, this photocatalytic paint can be a cost-efficient tool to clean water. The paint can be applied to surfaces and it would just require sunlight to produce the reaction. If the paint can clean pollutants and kill plausible pathogens by just using sunlight, drinking water could be obtained at a very low cost.

FW-03 P G. **Phylogenetics and morphometrics of *Pyrgulopsis* populations in Texas.** *Rebecca Chastain, Kathryn Perez, University of Texas Rio Grande Valley.*

Pyrgulopsis (Gastropoda: Hydrobiidae) is a speciose genus of small snails found in freshwater springs throughout North America that exhibit high levels of endemism and are at an elevated risk of extinction. Four species are found within the state of Texas: *P. texana, P. ignota, P. metcalfi,* and *P. davisi,* all of which are considered to be endangered and are restricted to only a few localities in west Texas. They are understudied, and their relationships to each other as well other members of their genus are unresolved, posing obstacles to their conservation. They are of particular importance due to their inhabitance of Texas spring systems and ciénegas, which are declining due to groundwater withdrawal and pollution among other anthropogenic stressors; therefore, their protection would benefit efforts to conserve these unique ecological assemblages. Our project aims to collect and analyze morphometric and phylogenetic data concerning each population of these four species in order to establish conservation units which may be considered in future management and policymaking.

FW-04 P G. **Maverick Creek woody species composition in San Antonio, Texas.** *Felipe Villanueva, Brain Laub, University of Texas at San Antonio.*

Urbanization is increasing and poses a threat to riparian communities. The increased growth of cities like San Antonio is replacing upland vegetation with impervious surfaces. Such land cover transformation alters environmental filters like hydrologic patterns, forcing a shift in species composition of riparian communities that may lead to simplification, damaging ecosystem functions, such as flood mitigation and natural filtration systems. Once disturbed, municipal agencies may eventually try to restore lost ecosystem functions. For restoration projects to be successful, managers should understand local environmental filters, as this knowledge helps select species with traits matched to local environmental conditions. The primary aim of this study is to improve the understanding of relationships in urbanized ephemeral streams by collecting the woody composition of Maverick Creek. Maverick Creek was found to have 27 woody species overall, including 26 natives and one exotic. Transect 1 saw seven species totaling 69.2% of vegetated cover, with 43.6% of coverage being in the floodplain. A total of 44.4% of woody species were classified as a low canopy, compared to older established species comprising only 20.0% of the overall woody species. This suggests that most woody species in Transect 1 are relatively young. Therefore, this research is significant to restoration efforts, as projects need to incorporate locally based spatial and temporal environmental filters to be successful.

Geosciences Poster Session
Participants:
GS-01 P U. **Study on the chemical composition of the salt deposits of the Appalachian Basin within North Eastern Ohio.** *Chance Robinson, Stephen F. Austin State University.*

The Appalachian Basin Salt Deposits lies within the borders of Michigan, Ohio, Pennsylvania, New York, and West Virginia. The salt deposits were deposited during the Silurian. The deposits' thickness varies throughout its area, with the largest thickness being around Michigan and the smallest in Ohio. The salt deposits are mined for salt and other secondary resources that may have been deposited with the salt. The problem is that the last survey of the salt deposits was in 1978 by the United States Geological Survey. Here I show the Geochemistry of samples from geologic cores drilled in North Eastern Ohio, using X-ray Fluorescence. Results from my study show that the Geochemistry of the samples was near the concentrations expected. Chlorine concentrations ranging from 540000 to 600000 ppm, and Calcium concentrations ranging from 30000 to 100000 ppm. There were varying degrees in concentrations of trace elements as well that had concentrations ranging from 30 ppm to 84020 ppm, depending on the sample. My results show that the chemical makeup of the

samples met expected concentrations. I believe that my study on the chemical makeup of the salt samples from the section of the Application Basin in Ohio will be a starting point for future investigations into the overall composition of the basin. The knowledge of both the general and chemical makeup will allow for more effective surveying for useful resources.

GS-02 P U. **Magnetite study in the Lake Nacogdoches area.** *Luke Whitenburg, James McDaniel, R. LaRell Nielson, Stephen F. Austin State University.*

Magnetite was found in the lake, beach and fluvial deposits at Lake Nacogdoches, Texas. Following this discovery, a sample pattern was setup to determine the location and extent of the magnetite deposits in the lake and on tributaries to the lake. This resulted in six more deposits being located. One additional deposit was found in lake sediments, four deposits in beach bars and one deposit along Mill Branch, a tributary to the lake. In the lake deposits, the grain size of the sub-angular to rounded magnetite clasts ranged from fine-grained to course grained sand. The magnetite deposits in the lake water were found in water depths between 1 to 3 meters. Magnetite clasts found in beach sediments were sub-angular to sub-rounded and ranged in sizes from fine-grained sand to pebble sized clasts. Magnetite deposits were also collected from Mill Branch, which is a tributary that flows into Lake Nacogdoches and across outcrops of the Weches Formation. Sediments in Mill Branch contained magnetite clasts that were sub-angular to sub-rounded and ranged in size from medium sand to pebble sized clasts. This study suggests that the origin of the magnetite clasts is the iron oxide cemented units in the Weches Formation that outcrops around the lake. Magnetite and iron oxide were produced by diagenesis at the time of cementation following the deposition of the Weches Formation on a shallow marine shelf and before uplift and erosion of the current cycle. Uplift, weathering and erosion produced the magnetite clasts found in the study area.

GS-03 P G. **Stratigraphic analysis of the Capps Limestone in the Norton Oil Field in Runnels County, Texas.** *William J. Thompson, R. LaRell NIelson, Stephen F. Austin State University.*

A stratigraphic and depositional environmental analysis of the Capps Limestone Member of the Mineral Wells Formation was undertaken in the Norton Oil Field in Runnels County, Texas. The Capps Limestone is approximately 22 meters thick in the study area and contains interbedded limestone, sandstone and shale units. The limestone units range from laminated mudstone to fossiliferous packstone. Some wells contain minor amounts of sand in the limestone (mudstone) units and in places, the sandy limestone (mudstone) grades upward into thin bedded sandstone. Near the middle of the Capps Limestone a number of shale units are interbedded with the limestone (mudstone) units. Shale units present in the Capps Limestone range in thickness between 5 cm and 1 meter. The Capps Limestone in the Norton Oil Field in Runnels County was deposited on a shallow shelf as is indicated by the laminated mudstone and fossiliferous packstone. The sandstone units represent an influx of sand from a delta environment to the east. Shale units may represent deeper areas on the shallow shelf or a lagoonal setting. Deposition of the Capps Limestone occurred as part of a rapid oscillation between transgressive to regressive systems tracks during the Desmoinesian (Kasimovian-Moscovian) Age (Middle Pennsylvanian Period)

Mathematics & Computer Science Poster Session
Participants:
MATH/CS-01 P U. **Using Python to question sincerity in Doodle polls.** *Miryam L. Galvez, Barbara M. Anthony, Chris Ojonta,* Southwestern University.

Online tools such as Doodle polls are frequently used by organizations and individuals to find and coordinate times to meet with others. While the algorithm used to determine an optimal meeting in a Doodle poll is simple, computer-aided decentralized decision-making processes are expected to continue to increase in prevalence. With implications far beyond meeting scheduling, it is important to understand how participants' behavior and interactions with such systems align with theoretical assumptions. Since Doodle polls are a form of approval voting, theoretical results from voting theory often underpin work on Doodle polls. One common assumption is sincerity, where a voter never says yes to a less-preferred option without having said yes to all more preferable choices. In this faculty-student research project, we conduct a user study where college students at one institution complete Doodle-style polls. Specifically, students were provided with a hypothetical schedule and then asked to consider how they would report their availability in multiple scenarios, rating their availability from 1 to 5, responding with yes or no, and sometimes considering the availability of others with whom they are trying to coordinate for a class project. We analyze responses both quantitatively using Python and qualitatively through hand analysis, seeking to determine the extent to which users are sincere. While

few users met the definition of sincere, many tended towards sincerity, potentially suggesting that people intend to act sincerely but may have difficulty with consistent behavior over a large number of choices.

Neuroscience Poster Session
Participants:

NS-01 P U. **Zebrafish used as a nicotine screening tool to identify potential drugs to inhibit smoking in humans.** Amy Joffrion, Joseph Lively, Amy Montelongo, Vanessa Rosado, Kristel Ledesma, Brent R. Bill, University of Texas at Tyler.

The addictive nature of tobacco, and its addictive constituent nicotine, make the act of cessation extremely difficult. Unaided attempts succeed approximately 3% of the time and aided cessation succeeds 33% of the time; therefore, there is a considerable need for new cessation agents. The search for new cessation agents involves mouse experiments, and suffers from the high costs associated with the care and maintenance and statistical power. The goal of our work is to establish the zebrafish as a drug screening tool to reduce costs and increase the number of animals that can be assessed. Embryonic zebrafish assays have demonstrated significant behavioral outcomes for initial exposure to nicotine and sensitization. Assays that look at complex aspects of the addictive behavior, for example, alterations in anxiety due to acute or extended use of nicotine and seeking behavior, as demonstrated with the conditioned place preference (CPP) test, have not been as well characterized. We demonstrated that the 3-chamber CPP test was insufficient due to a high variability within responses; therefore, the focus of this project was to assess a two (light-dark)-chambered testing apparatus. We hypothesized a clear preference for the dark chamber would be displayed. Our initial aquarium setup demonstrated a preference for the dark chamber as expected; however, an unexpected chamber of entry affect was observed (p<0.0001). Technical issues led us to modify tank design leading to a much darker "dark chamber." A preference for the dark chamber was not observed; and an increased amount of freezing and fish jumping out of the testing apparatus occurred. Both behaviors suggest zebrafish have higher anxiety levels not seen in the previous setup. Further characterization of the behaviors following training are being assessed, but we propose that this system represents an improvement over our previous apparatus.

NS-02 P G. **The role of xenobiotics in neurodegenerative diseases.** *Gabriela Henriquez, Mahesh Narayan, Eddie Castañeda, University of Texas at El Paso.*

Two diseases, one tale. The self-assembly of protein aggregation is the molecular hallmark for many neurodegenerative diseases. The misfolded form of amyloidogenic proteins forms aggregates identified as oligomers and protofibrils. These toxic agents potentially increase redox states' level, changes the metal ions homeostasis, and provokes a cascade of DNA damage. As a result, this phenomenon causes cellular macromolecules disruption, neuronal viability dysfunction, and finally, neurodegeneration. This study focuses on better understanding the cross-toxicity between amyloids commonly found in Alzheimer's disease (AD) and Parkinson's disease (PD). Their common denominator is the associated accumulation and aggregation of specific protein biomarkers; these amyloids tend to form self-seeding and spread seeds into neurons. To investigate any possible relation between amyloid proteins, we examined the inoculation of AD-b-amyloid peptide into a non-native location, the Substantia Nigra pars compacta (SNPc) PD-Locus. Consequently, this exogenous inoculation will determine if b-amyloid peptide is indeed a risk factor for Parkinson's pathogenesis through its natural characteristic of cell-to-cell propagation while acting as a prion-like mechanism and sequestering other essential proteins for brain functioning. These diseases are age-associated with progressive deterioration of neuronal mechanisms. Therefore, this study seeks to demonstrate the toxicity induced by the peptide b- amyloid, in two different fragments (1-42, 25-35) over 6, 9, and 12 months on Lewis rat. Finally, this study seeks to determine the mechanism that links amyloidosis and synucleinopathy, when an amyloidogenic vector in heterotypic neurons elicits cross-pathology.

Plant Biology Poster Session
Participants:

PLTBIO-01 P U. **Comparing molecular and morphological variation among enigmatic populations of *Mentzelia* section Trachyphytum (Loasaceae) from western California, USA.** *Kylie E. Davis, Mariana Castillo, Tyler B. Sanchez, Joshua M. Brokaw, Abilene Christian University.*

Recent morphological analyses of populations of *Mentzelia* section Trachyphytum from sparsely vegetated vertic clays in the California Southern Coast Ranges have recovered previously unrecognized combinations of characters used to distinguish *Mentzelia*

gracilenta, Mentzelia lindleyi and *Mentzelia pectinata*. Previous molecular studies of section Trachyphytum have found evidence of homoploid hybridization and allopolyploid speciation. However, because these populations represent unusual substrate conditions, we investigate patterns of molecular genetic variation in order to test whether these morphological patterns are correlated with phylogenetic signal rather than unusual environmental stress. Preliminary results suggest that most of these populations share greatest genetic similarity with *Mentzelia pectinata*, as species with a much more southern distribution, whereas a minority can only be genetically linked to *Mentzelia lindleyi*, the species with geographic range closest to the unidentified populations.

PLTBIO-02 P U. **Molecular comparisons among morphologically cryptic species in *Mentzelia albicaulis* complex (Loasaceae).** *Katelynn E. Shupe, Shelbi P. Stephenson, Hongjian Chang, Joshua M. Brokaw, Abilene Christian University.*

Mentzelia albicaulis is a allo-octoploid species with the highest ploidy level and widest distribution among species within *Mentzelia* section Trachyphytum with habitats ranging from hot lowland deserts to cool mountain foothills and sagebrush shrublands. Due to its morphological similarities and sympatric distributions with several diploid, tetraploid, and hexaploid species, many less common taxa are lumped with *M. albicaulis* among museum accessions, leading to unrecognized patterns of diversity. Here we investigate patterns of molecular variation among museum specimens from the western USA, including many with known chromosome counts, using on DNA sequences from the plastid trnH-psbA, trnS-trnG, trnS-trnfM, ndhF-rpl32, and rpl32-trnL intergenic spacers. Preliminary results suggest that the most underrecognized species is the desert allo-tetraploid and putative progenitor of *M. albicaulis, M. obscura.*

PLTBIO-03 P U. **Molecular investigation of biogeographic origins among populations of *Mentzelia dispersa* (Loasaceae) from western North America.** *Brianna N. Douglas, Kaylee M. Dahl, Katie E. Howe, Joshua M. Brokaw, Abilene Christian University.*

Mentzelia dispersa is an annual plant found throughout western North America, extending from California to British Columbia and as far east as the Dakotas. In this study we examine chloroplast DNA in order to investigate the biogeographic origin of *M. dispersa*. We gathered samples from populations of *M. dispersa* throughout its range. We extracted DNA and performed PCR to amplify the ndhF-rpL32 intergenic spacer region of the chloroplast. DNA sequences were used to construct a haplotype network and compare populations of *M. dispersa* geographically. We found an apparent geographic structure to the genetic diversity of *M. dispersa,* with similar haplotypes usually found in the same region. The greatest genetic diversity was found in California, compared to the Pacific Northwest and central regions of the United States, where few other haplotypes are found. This suggests that California is the geographic origin of *M. dispersa*, a conclusion that is consistent with a possible northeastern expansion from California during previous and ongoing climate warming.

STEM Education Poster Session
Participants:
STM-01 P U. **PURSUE: undergraduate research journal, increases publishing opportunities for minority undergraduate STEM majors.** *Ineceia Carter, Ayanna Montegut, Tia Villeral, Yolander Youngblood, Prairie View A & M University.*

The mission of PURSUE: undergraduate research journal (ISSN 2575-159X), is to share original research work produced by undergraduates in the areas of (but not limited to) Science, Engineering, Technology and Mathematics (STEM). Articles in this journal are produced in conjunction with a faculty mentor and are peer-reviewed by scientists. The journal is open to all undergraduates. As the only active periodical listed with the Council of Undergraduate Research (CUR) that is housed at a public Historically Black College or University (HBCU), this journal especially encourages research and scholarly publications from African American students and other minorities. Publications are increasingly difficult at the undergraduate level in because students usually spend one semester, at the most two, with a faculty mentor then they compete with other graduate students and seasoned scientists for publication honors. Thus, undergraduates typically do not continue to pursue publishing. PURSUE: undergraduate research journal, gives undergraduates with credible relevant research a space to publish their peer-reviewed articles. As a result, more underrepresented minorities are publishing their research. This is especially true for students at PV. In the four issues that have been published since 2016, 72% of the articles in PURSUE are from students at HBCUs, 14% are from predominantly white institutions and 14% are from high school seniors. This also serves

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as a means for faculty to extend knowledge beyond the classroom and encourage other students to conduct quality research. PURSUE: undergraduate research journal, is reserved for articles that have undergraduates as the first author.

STM-02 P G. **A comparison of online and in-person graduate gross anatomy courses with an implementation of active learning.** *Libby Bradley, Emma Handler, Rustin Reeves, University of North Texas Health Science Center at Fort Worth.*

Active learning enables students to be fully engaged in their own learning through discussion, thought, creation, and investigation of the provided course content. Jigsaw, an active learning technique, promotes cooperative learning by placing students into small groups and encouraging peer teaching. The Jigsaw technique is well suited for gross anatomy courses at the graduate level because of the reliance on independent learning already present in laboratories. Here we compare the academic performance of an online versus in-person cohort of students enrolled in graduate gross anatomy courses with the implementation of the Jigsaw technique. In this analysis, both cohorts received Jigsaw implementation; however, the online cohort executed their strategies entirely virtually, while the in-person cohort met face-to-face. Additionally, we compare demographics, perceived preparedness, and perceived emotional health (i.e., confidence, anxiety, confusion, etc.) of both student cohorts while enrolled in the course. Historical data from previous student cohorts suggests that at the completion of the course (May 2021) the in-person cohort will perform well, if not better, with the implementation of the Jigsaw technique. Additionally, the online student cohort is expected to perform less well despite receiving similar learning implementations as the in-person cohort. Gross anatomy is an ideal experimental exercise for the implementation of active learning techniques as it is typically taught at the beginning of graduate health science programs with a vast amount of fundamental information for future courses. Currently, there is a lack of research comparing online and in-person graduate gross anatomy courses with the implementation of active learning. Additionally, there are no current comparisons of demographics or perceived emotional well-being pertaining to the implementation of the Jigsaw technique into either online or in-person graduate gross anatomy courses.

Systematics & Evolutionary Biology Poster Session
Participants:

SYST-01 P G. **Faunal comparison of Pleistocene localities at McFaddin Beach, Ingleside, and Moore Pit, Texas.** *Deanna Flores, William Godwin, Christopher J. Bell, Patrick J. Lewis, Sam Houston State University.*

Faunal comparisons between paleontological localities are important for defining biome composition and boundaries, and for understanding the pattern of regional environmental change and its impact on vertebrate communities. Such comparisons are most effective with large, diverse faunas from localities of comparable geological ages. Here I will compare faunas from three Rancholabrean Texas localities, McFaddin Beach (MB), Ingleside (IS), and Moore Pit (MP). The comparison will better place MB into the broader picture of the Texas Pleistocene. MB extends for ca. 20 miles along the coastline of Jefferson County, IS is in a barrier lagoon in San Patricio County, and MP is outside Dallas along the Trinity river. All three localities have large, diverse faunal assemblages. IS is located on the Coastal Plain similar to MB. The MP assemblage, while not on the coastal plain, consists of most taxa found in the Pleistocene of Texas. Taxa from the three sites indicating a Rancholabrean age include Bison spp. and Canis dirus. IS and MP have been only narrowed to Rancholabrean (240-11Ka). MB is Rancholabrean but hypothesized to be washing out from the Beaumont clay and interglacial deposits dated to 70-7Ka. Preliminary faunal comparisons show some common taxa, including Alligator mississippiensis, Bison spp., Equus spp., Canis dirus, and Mammut americanum. Some uncommon taxa are present in assemblages for only two sites: Tremarctos floridanus (MB & IS), Tapirus veroensis (MB & IS), and Tapirus haysii (MB & MP). MB, however, has some taxa that separate it from the other localities, such as Castoroides, Homotherium, Eremotherium, and Trichechus manatus bakerorum. These taxonomic differences may be a result of age or environmental differences between the three sites. The presence of Eremotherium at MB suggests it may have been a more suitable habitat for tropic/sub-tropic species similar to the Florida peninsula during colder periods.

SYST-02 P G. **Quadrate variation in the genus *Zygaspis*.** *Antonio Meza, Christopher J Bell, Patrick J Lewis, Sam Houston State University.*

Amphisbaenia is a clade of fossorial reptiles consisting of over 200 extant species in more than 20 genera. Most modern studies of cranial anatomy of amphisbaenians are based upon high-resolution X-ray CT scans. Most of those studies are based upon low sample sizes, and sometimes only a single specimen. We scanned 13 specimens from six species of the genus Zygaspis, Z. quadrifrons, Z. vandami, Z. niger, Z. violacea, Z. dolichomenta, and Z. kafuensis, whose collective

distribution spans most of southern Africa. The basic cranial anatomy of Z. quadrifrons is well described but was based on only a single specimen. That baseline description allows for both inter- and intraspecific variation to be estimated. We examined the right quadrate of two adult specimens from each species with the exceptions of Z. dolichomenta (one specimen) and Z. quadrifrons (four specimens). The quadrate bone is considerably diverse in shape across reptiles and has the potential to be a diagnostic element. The quadrates were segmented in the software program Amira. Landmarks were then placed on the bones and a Principal Component analysis (PCA) was performed. The majority of variation was accounted for in the first two Principal Components (PC1= 96.07% and PC2= 3.22%), indicating variation in overall size (PC1) and width (PC2). Qualitative variation was also observed in the number of foramen present on the quadrates. Our results demonstrate that inter- and intraspecific variation does exist and should be accounted for in functional and phylogenetic studies. Future analyses will incorporate other cranial bones, thus enhancing the understanding of the morphological variation within Zygaspis.

SYST-03 P G. **Species delimitation in the domed cavesnail (*Phreatodrobia nugax*) using integrative taxonomy.** *Taylor Villanueva, Kathryn Perez, University of Texas-Rio Grande Valley.*

The domed cavesnails, *Phreatodrobia nugax*, is a minute (<2 mm maximum size) snail endemic to the Edwards-Trinity Aquifer System of Central Texas. Several species of cavesnail that co-occur in samples from the aquifer are very challenging to distinguish from each other and from the domed cavesnail. Making this challenge more difficult is that the morphological variability in the domed cavesnail is extreme, including shells that are partially uncoiled, flat, tall, and everything in between. Previous molecular phylogenetic work supports the notion that what we are calling the domed cavesnail is polyphyletic, meaning that it is not clear what exactly is and isn't considered *P. nugax* at the species level. This provokes conservation and regulatory concern because several species of cavesnail are considered endangered, but we might not be able to reliably distinguish them from the domed cavesnail. In my work, I attempt to distinguish the domed cavesnail from other closely related cavesnails using molecular phylogenetics, geometric morphometrics, and animal dissections of *P. nugax* from different localities such as springs, seeps, and wells across its wide geographic range.

SYST-04 P G. **Investigating *Tryonia* springsnails through phylogeny and morphometrics.** *Houston Glover, University of Texas Rio Grande Valley.*

The isolated, spring-fed desert marshlands—or cienegas—of west Texas are home to a wide assortment of invertebrate life forms. The diversity of species in these cienegas is indicative of water quality, both in the springs themselves, as well as in the aquifer from which they are fed. Many of these invertebrates are members of closely related groups, but have been geographically separated for so long as to have diverged both genetically and morphologically to form distinct species. Because these species are often endemic to only a handful of sites, many of them are under threat of extinction. One such group that is relatively understudied is the genus of springsnails called Tryonia. Here, I present the beginnings of an ongoing study that will add to the knowledge base for this genus by constructing a phylogeny based on gene sequencing and morphometric data. Once complete, this work will aid in the construction of a broader phylogeny that will be a constructive part of the knowledge base necessary to conserve this genus and the threatened species within it.

SYST-05 P HS. **Orthologs for pigmentation genes in *Schistocerca gregaria* are candidates for body color change during locust phase transition.** *Sreeram Satish, Sai Prasada Manikonda, Baylor College of Medicine.*

Schistocerca gregaria, the desert locust, frequently swarms the plains of Africa and Asia, destroying the food supply for millions of people. The species transitions between differently pigmented solitarious and gregarious (swarming) phases. The genetic and biochemical bases of pigmentation are understood in several model organisms, most notably the fruit fly, *Drosophila melanogaster*. We hypothesized that pigmentation genes in *S. gregaria* orthologous to those in *D. melanogaster* may play a role in the color changes that occur during swarming. To identify candidate pigmentation genes, we used publicly available data from the FlyBase, NCBI, and OrcAE databases to search for three known D. melanogaster dark pigmentation genes, black, tan, and ebony, in the draft genome of *S. gregaria*. Due to the evolutionary gap between the two organisms, some orthologous genes were difficult to detect. To bypass this issue, we used the German cockroach, *Blatella germanica*, as an intermediate organism because it is more closely related to *Drosophila melanogaster* and has a well-annotated genome. We developed a workflow to annotate *D. melanogaster* orthologs in *S. gregaria* and found one candidate ortholog for ebony, one candidate ortholog for tan, and two candidate co-orthologs for black. We plan to confirm these candidate pigmentation genes by analyzing RNA from *S.gregaria* and related locust

species with completed transcriptomes. We will also analyze expression differences between swarming and non-swarming locusts and continue to look for other pigmentation genes. Ultimately, we want to knock out these genes in the desert locust to test their role in pigmentation.

Terrestrial Ecology & Management Poster Session
Participants:
TERR-01 P U. **Activity patterns of gray fox (*Urocyon cinereoargentius*) in an urban system.** *Saira Sitgreaves, Troy A. Ladine, East Texas Baptist University.*

From 14 Oct 2014 to 1 Dec 2020, a period of six (6) years, using trail cameras, we investigated the activity of the gray fox (Urocyon cinereoargentius) in an urban system. Our study is part of a larger study investigating community dynamics of mammals in our area. We found these foxes to be primarily crepuscular with peak activity found shortly after sunrise and just before sunset with minimal diurnal activity. Most activity occurred primarily in areas of dense canopy and underbrush, furthest from residential homes and roads. However, no variable exhibited statistical significance between high use (> 7% of pictures) and low use (< 7% of pictures). Setting aside the exception of the year 2020, monthly activity of the gray fox in our urban system exhibited little variation with slight increases in activity found in January and November. In 2020, monthly activity demonstrated an increase beginning in March and peaking in August before decreasing to match previous years. The increase in monthly activity observed may be due to the COVID-19 lockdown and simultaneous decrease in human activity relative to previous years.

TERR-02 P U. **Interaction between co-occurring populations of raccoons (*Procyon lotor*) and Virginia opossums (*Didelphis virginiana*) in an urban system.** *Cameron Castles, Troy A. Ladine, East Texas Baptist University.*

Common raccoons (Procyon lotor) and Virginia opossums (Didelphis virginiana) have a large niche overlap. As part of a study using trail cameras starting 14 Oct. 2014, the interaction between raccoons and opossums is investigated. Our data indicate possible niche separation through both spatial and temporal axes. Logistic regression analysis indicates raccoons are more active near permanent water sources and areas with higher canopy cover. The opossum, on the other hand, is more active near roads and areas with higher understory cover. Thus, our study indicates some niche separation based on habitat use. While both species are primarily nocturnal, the opossum is more active around midnight and the raccoon exhibits a peak just prior to sunrise and a smaller increase in activity just after sunset. Further investigation of temporal niche separation at a scale of activity pattern greater than 24 hr will be conducted.

TERR-03 P U. **A survey of mesopredators in East Texas using scent lures.** *Maria Hendrickson, Diane Neudorf, Sam Houston State University.*

Various scent lures are often used in combination with game cameras to survey for predators in a particular area. We examined the attractiveness of different scents to mesopredators in three locations in the southeast Texas Piney Woods region. The scent lures were chosen to determine whether man-made scents were more attractive to predators than naturally occurring scents. Scent lures included gray fox (*Urocyon cinereoargenteus*) urine, rabbit urine, bobcat (*Lynx rufus*) urine and Elizabeth Taylor White Diamonds perfume. Patches of dirt 1 m x 1 m were raked clear of grass and leaves, and a wooden stake was placed in the center, with a game camera set up to observe the station. Scent lures were made by soaking cotton rags in the scents for 24 hours and then nailing the rag to the stake at each lure station. Each scent lure was left out for 10 days to ensure time for discovery before being removed. The images from game cameras were then sorted through and each species that visited the scent station was recorded, as well as how frequently the lure was visited. We will present our findings on which baits were most successful in attracting mesopredators, as well as which types of predators visited the most frequently.

TERR-04 P U. **How stand age can affect carbon storage in a subtropical, deciduous forest.** *Amanda Scamardo, Tamara Basham, Collin College.*

Anthropogenic Carbon (C) emissions are contributing to climate change. In order to mitigate climate change, carbon emissions must decrease and carbon sequestration must increase globally. Carbon storage in forest ecosystems plays an important role in carbon sequestration. Carbon storage in forests is thought to increase and then plateau as forests age. In this study, we examined the role that forest age plays in carbon storage by comparing carbon storage between two areas of a subtropical, deciduous forest of different ages. The new growth forest was cleared for agriculture and has regrown since 1995; the old growth forest was never cleared. We hypothesized that the old growth forest would store more carbon due to the size of the trees and

accruement age of the forest. We tested this hypothesis in the Oak Point Nature Preserve in Plano, TX. We used species data and diameter-at-breast-height (DBH) collected from 14 78.5 m2 random plots, 7 plots in each forest type (new and old growth). Species and DBH data were entered into iTree - Eco V6 (itreetools.org) to estimate total carbon storage of individual trees. C storage estimates were then summed for each plot. Differences in C storage between forest types were tested using a linear mixed effects model with forest type as a fixed effect and plot as a random effect using the NLME package in R (version 4.0.2, R Foundation). The results of this study indicate that species composition differs between the two forest types, but carbon storage was not significantly higher in the old growth forest. Higher tree density and different species composition in the new growth forest may contribute to similar carbon storage in the two forest types. This study suggests that having a mixture of forest stand ages within forests may maximize carbon storage and species diversity.

TERR-05 P G. **A preliminary analysis of variation in shell morphology of the land snail *Haplocion pasonis* (Gastropoda: Urocoptidae) from west Texas.** *Cody Patterson, Ned Strenth, Nicholas Negovetich, Angelo State University.*

Haplocion (Holospira) pasonis is a desert-adapted land snail that has been reported from several widespread locations in west Texas and adjoining regions of northern Mexico. This widespread distribution is more extensive than the known distributions of most other holospirids from this region. This study was undertaken to determine if the shell morphologies are consistent throughout the known range of this species. This preliminary study was conducted on a subset of all H. pasonis specimens from the UTEP Biodiversity Collections. Specimens examined (n = 22) represented three distinct sample sites in Hudspeth and Presidio counties; several lots of only single individual shells from both west Texas and Chihuahua, Mexico were examined but excluded from statistical analyses. The number of whorls (11-12) were similar across all specimens. A permutational MANOVA using all measurement data showed no significant difference between populations (p<0.06). That same analysis of aperture length, aperture width, and total width did reveal significant differences between sample sites (p<0.05). Results of this preliminary study indicate consistency in the whorls count and total length with significant variation in aperture size, and total width between the two counties examined. Additional shell material as well as genetic analysis will be required to better understand the extent

of variation among the widely distributed Haplocion pasonis.

TERR-06 P G. **Nest box microclimate influences incubation behavior: a suburban and rural comparison.** *David Farris, Diane Neudorf, Sam Houston State University.*

Urbanization and human changes to the environment can remove critical resources like cavity- bearing trees that can be critical nesting habitat for many species of birds; nest boxes are often used to supplement or replace lost cavities. Although nest boxes are a common tool in conservation, the microclimates can be different from natural tree cavities. For birds in warmer climates, using potentially hotter and drier artificial cavities may influence their incubation and feeding behavior as well as fitness. This can be further exacerbated in habitats with less canopy cover such as found in more urban and suburban areas. By comparing nest boxes used by Carolina Wrens (Thryothorus ludovicianus) nesting in a suburban and a rural habitat, we hope to better understand how nest box microclimates can affect incubation and feeding behaviors. We monitored temperature and humidity inside and outside the nest box for active wren nests in both habitats. Video recordings of incubation behavior and feeding behaviors were taken during morning and afternoon sessions for a two-day period for each nest. We will discuss variation in microclimates for nest boxes in both habitats and differences in wren incubation and feeding behaviors.

TERR-07 P G. **Genetic analysis of beaver reintroductions in Texas.** *Drew Neyland, Monte Thies, Sam Houston State University.*

The restoration of Castor canadensis in Texas is one of the state's greatest conservation success stories. By 1900, overexploitation by fur trappers decimated beaver numbers in the state and the species was thought to be extirpated from east Texas. Between 1939 and 1942, 129 beavers were translocated from source populations along the South Llano River of Edwards and Kimble Counties in southwest Texas into 27 eastern counties. It is unknown the extent to which this extirpation and subsequent reintroductions has impacted the genetic composition of present-day beaver populations. Given the local extirpation in east Texas prior to 1900, our working hypothesis is that current east Texas populations are wholly connected genetically to populations from southwest Texas. To address this question, our current study is using mitochondrial DNA and microsatellite markers to determine the genetic

effect of this bottleneck and connect present day populations to relict populations. To make this determination, we have obtained samples from wildlife services, live trapping, incidental finds, and museum specimens from various regions across the state. Sample collection is currently being conducted in east Texas and the Big Bend National Park region and, once all samples are collected and DNA samples are processed, haplotype networks will be constructed to determine the origin of these populations. Genetic diversity indices will also be determined from the microsatellite markers. Field collection methods and preliminary results will be presented.

TERR-08 P G. **Metacommunity dynamics of medium- and large-bodied mammals in the LBJ National Grasslands.** *W. Craig McCain, David J. Hoeinghaus, Jaime E. Jiménez, University of North Texas.*

Patchiness is a common feature of landscapes in conservation entities as protected areas are often set aside or acquired as a series of patches within a matrix of private land. Effectiveness of such conservation areas is expected to be mediated by patch attributes and species traits. Information on metacommunity dynamics within the landscape can help prioritize key patches for additional protection or restoration as well as areas that may be benefitted by improved connectivity. This research is assessing drivers of metacommunity structure and dynamics of medium and large-bodied mammals in the LBJ National Grasslands. The Grasslands is comprised of multiple disconnected property units (patches) embedded in a matrix of privately owned land. We are using camera traps to survey mammal communities across seasons in thirty patches of various size, habitat conditions, and connectivity. Initial analyses will test whether observed patterns are better explained by island biogeography theory (IBT) or the habitat area hypothesis (HAH). For IBT, each property unit is considered a patch or "island" and the mammal communities are shaped by patch size and relative connectivity. In contrast, the HAH predicts that the amount of habitat in the local landscape around the sampling point determines community attributes. Research is currently underway, and this poster presentation describes our study design and expected findings.

TERR-09 P NS. **Host by geographical distances across the Gracillariidae.** *Richard James Wilson Patrock, Texas A & M University Kingsville.*

The Gracillariidae is a family of plant mining micro-lepidoptera that are rightfully seen as mostly host-specific. At the generic and higher levels, many show wide host breadths. Given that many host switches require variable evolutionary changes, I followed these changes described from data in Gracillariid.net and recent literature on a global scale along insect and host phylogenetic trees and geographical areas. Phylogenies were derived from the literature and host patterns followed that of the source material or recent modifications of the APG-IV system. Results are discussed and displayed on the poster.

SATURDAY, FEBRUARY 27

ORAL SESSION #3

007. Mathematics & Computer Science
Participants:
8:30   007-01 U. **Chemical espionage: modeling the relationship between the *Pieris brassicae* butterfly and *Trichogramma* wasps.** *Dashon Mitchell, Dr. Christopher Mitchell,* Tarleton State University

Our project, Chemical Espionage, describes the situation of the butterfly species Pieris brassicae, the large cabbage white butterfly, which uses chemical signals to attract mates. This, however, presents a new problem for the females as the chemical aphrodisiac can attract too many males and make it difficult for her to lay her eggs in a secure locale. To combat this, males of the species emit an anti-aphrodisiac which deters other males from approaching the mated female. However, the use of this anti-aphrodisiac has an unexpected consequence for the butterflies as it attracts two species of the Trichogramma wasp, parasitic wasps which can detect the anti-

aphrodisiac and will use it to locate mated females so they can prey on the eggs she lays. Once a Trichogramma wasp locates a mated female butterfly, they land on the female and ride on it to find where the female lays her eggs. Once located, the wasps will lay their eggs and the larva of the wasps will consume the eggs of the butterfly. The optimal solution for these butterflies is one in which a steady population of eggs are laid to replenish the butterfly population while reducing the amount of eggs lost to wasps. The best solution for the wasps, however, is one in which a balance is struck between the amount of anti-aphrodisiac used and the growing population of the butterflies. In order to find the equilibrium between these two scenarios where both can coexist without driving the other to extinction we created a system on differential equation to model the situation. We started by modeling only the butterfly populations and then introduce the wasps. After parameterizing the model, we search for equilibrium and stability. Simulations are done to show the different scenarios between the two species.

8:45   007-02 U. **Increase in exposure rates of the Eastern Equine Encephalitis Virus from the black-tailed mosquito to avian species: a mathematical approach.** *Aurod Ounsinegad, Dr. Christopher Mitchell, Tarleton State University.*

The Eastern Equine Encephalitis Virus (EEEV) is an erratic and deadly neurological disease that spans across the northeastern coast of the United States. To determine the rate at which the virus is spread between the Black-Tailed Mosquito (Culiseta melanura) and select avian species we began by analyzing the migration patterns of both the mosquito and the avian species. It was found through this that certain species of avians shared similar, or even identical, flight patterns with the Black-Tailed Mosquito. Through this research, we develop and analyze a system of Ordinary Differential Equations (ODEs) to gain insight on how and when transmission of the virus to avians is at its highest. We incorporate a host stage-structured model where the avian host group is split into two categories, adults and young-of-the-year birds (YOY). Using this we explored the extent to which fluctuations occurred in transmission rates

according to host/vector abundances, mosquito biting rate, and type of host. We hypothesize that YOY avians are more readily exposed to the mosquito vector as they lack a defense mechanism, unlike their adult counterpart. By utilizing our system of ODEs, interpreting the reason as to why virus transmission spikes at specific times, and incorporating an avian stage-structured model we are given the opportunity to properly present a solution to our observed hypothesis.

9:00   007-03 U. **The development of an in-house algorithm and Java scripts to define and identify gene clustering arrays in annotated genomes.** *Jared Rodriguez, Dr. Robert Moore, Wayland Baptist University.*

The clustering of genes on a genome can indicate shared control mechanisms as well as genetic lineages of organisms. The process for identifying a gene cluster array from a customized list of genes, however, can prove to be tedious and time consuming when dealing with large quantities of genomes. To alleviate the tedious work of locating and defining gene cluster arrays we developed an in-house java script program and algorithm with the ability to cycle through a provided database of annotated genomes and calculate the number of genes that would classify as clustered relative to the genome or larger dataset as a whole. This methodology has already been used in another joint project of ours to analyze and re-define tRNA gene clusters in 15,000 bacteria genomes and exhibits potential for future applications in other gene types as well.

9:15   007-04 G. **Convolutional neural network for salamander classification.** *Preston Ward, Tarleton State University.*

Museums across the country have a vast amount of salamander samples in their archives. Unfortunately to the naked eye, these species can be indistinguishable from one to the next. The goal of this project is to create a deep learning model that is able to take in a picture of a salamander, and return that salamanders classification. Right now, the only way to classify these salamanders is to sequence them, and classify them from that. This takes time, and

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equipment a lot of places may not have. The hope is by building this model, all one has to do is take a picture of the specimen, and the model can return its classification with high accuracy. The model we built is a Convolutional Neural Network(CNN), and we took an iterative approach in building this model, first by getting a fairly accurate base model then using various techniques to dig into the layers of the network to see where improvements could be made and what the network was visualizing in its deciding factor between different species.

9:30   007-05 N. **An examination of Latinx bilingual preservice elementary teachers' mathematical proficiency and language use when solving mathematical tasks.** *Maria E. Diaz, Jair J. Aguilar, Victor M. Vizcaino, University of Texas-Rio Grande Valley.*

Elementary teachers find challenging to implement mathematical problem-solving tasks with their students. Thus, it is crucial for teacher preparation programs to develop pre-service teachers' self-confident and ability to solve non-routine mathematical tasks, while considering factors such as the language used to communicate their strategies and solutions. The purpose of this mixed-method study is to examine Latinx Pre-Service Bilingual Elementary Teachers' (LPBET) mathematical proficiency as they solve a series of non-routine mathematical tasks. Also, the study seeks to explore how language is used when communicating strategies and solutions. Participants were eight LPBETs enrolled in a mathematics methods course. The LPBETs solved the non-routine mathematical tasks administered every other week during a semester. The tasks were completed as homework, and the LPBETs were asked to record thinking-aloud their strategies and solutions. Data shows that participants have a low conceptual understanding, but a high procedural fluency, which is related to the process and algorithms used to solve the tasks with a variety of strategies. The language used to communicate processes and solutions differ in terms of the clarity, conceptual understanding, procedural fluency, and strategies. LPBETs showed a limited academic vocabulary when explaining their solutions and strategies. This study has the potential to impact future

generations of LPBETs by identifying their ability to solve and communicate mathematics tasks and thus, improve their instructional practice. Increasing LPBETs ability to communicate and solve non-routine tasks will transfer to their students and consequently, facilitate them to teach 21st Century skills such as critical analysis, decision making, and team-building.

9:45   **What is undergraduate research in math and who gets to do it?** *Distinguished invited speaker: Alicia Prieto-Langarica, Youngstown State University.*

008. Physics & Engineering
Participants:
10:30   008-01 U. **Experimental investigation of soiling losses on photovoltaic modules with artificially deposited dust of different particle sizes.** *German Rodriguez Ortiz, Thomas E. Gill, Deidra R. Hodges, Malynda Cappelle, University of Texas at El Paso*

The accumulation of dirt (dust and sand) on the surface of photovoltaic (PV) modules, known as soiling, has detrimental effects on their power output. Soiling reduces the amount of energy that is harnessed by a PV system because it blocks, scatters, or reflects part of the sunlight. The short-circuit current (Isc) is the most affected value, where, under certain conditions, losses can be as high as 80%. During the last few years, soiling has gained the attention of researchers worldwide. As of 2018, Texas has 2.3 GW in solar PV capacity installed, and has been increasing at a rate of more than 50% annually since 2010. However, west Texas is one of the dustiest regions of North America, increasing the hazard of soiling. Here we show preliminary data where an artificial dust and sand deposition technique was used to simulate outdoor natural deposition. We have simulated soiling under controlled laboratory conditions, using local sediment and sieving it to three samples with different particle sizes, namely <53 μm, <73 μm, and <104 μm. The Isc losses were up to 30%; these results are similar to those obtained in outdoor conditions. Our results demonstrated a correlation between soiling losses and dust particle size, where smaller particles have a

greater negative effect on the Isc output. We anticipate our project to be the starting point of a series of experiments to develop an artificial dust deposition technique to simulate and compare to outdoor conditions testing the effect of deposition of different compositions on Isc. For example, variables such as humidity, temperature, wind speed, dust size, shape, hardness, mineral composition, etc. play an important role in soiling but their effects are not well understood. Our studies where these variables can be varied and tested will increase our knowledge of the PV soiling phenomenon.

009. Terrestrial Ecology & Management
Participants:

11:00   009-01 U. **Conservation potential of symbolic state herpetofauna in the United States.** *Erin McGilvray, Travis Laduc, University of Texas at Austin.*

State legislative bodies designate state symbols from a variety of categories, including many from nature, to serve as representations of the state's values, environment, and economic interests. All 50 U.S. states have official tree, flower, and bird symbols; 48 states have fish and insect symbols; 44 states have mammals. In contrast, official herpetofaunal symbols are significantly underrepresented, with only 28 states having reptile symbols and just 23 states having amphibian symbols. This discrepancy is likely tied to common public biases against many reptiles and amphibians based on a fear of harm to people or property, negative depictions in folklore and pop culture, and a lack of familiarity. Symbolic state herpetofauna could be used as educational tools to help mediate these concerns among the public. Among state reptile and amphibian symbols, few are listed as endangered or critically endangered by the International Union for Conservation of Nature Red List -- four reptiles and one amphibian. For those states lacking symbols, this could be a missed opportunity for conservation. Though symbolic species do not necessarily receive statewide protections, the added public attention focused on state symbols has benefited conservation efforts by increasing awareness and concern for these flagship species and their habitats. States currently lacking these symbols should consider the potential conservation uses of designating official state reptiles and amphibians.

11:15   009-02 U. **Shifts in seasonal activity pattern of male white-tailed deer (*Odocoileus virginianus*) in an urban system.** *Dakota Courtney, East Texas Baptist University.*

From 14 October 2014 through 21 November 2020 we used trail cameras to investigate seasonal shifts in activity of male white-tailed deer (Odocoileus virgnianus). We hypothesized there would be no seasonal shifts in activity as its primary predators, with the exception of the coyote (Canis latrans), have been mostly extirpated from the area.   Our findings do not support our hypothesis as there was a significant increase in activity during the months of November through January compared with the three month period immediately prior. These late fall-early winter months coincide with the hunting season and the rut in the area. A significant increase in activity also occurred starting two weeks prior to the start of hunting and continued through the two weeks after the end of hunting season. The time period during hunting season did not exhibit a significant increase in activity of male deer. The study site is located within the city limits of Marshall, TX. Thus, there is no hunting on the site. Male deer may be timing their movement patterns to avoid hunting outside of the city limits.

11:30   009-03 U. **Home range and spatial movement of Texas horned lizards (*Phrynosoma cornutum*) in the Southern High Plains of Texas.** *Sarah Macha, Dr. Andrew Kasner, Wayland Baptist University.*

This study was conducted May-Aug 2020, continuing a telemetry study of Texas horned lizards (Phrynosoma cornutum) at Running Water Conservancy, Hale County, Texas. Twenty-three adult lizards (9 males, 14 females, mass>15g) were equipped with a VHF radio-transmitter and located up to 24/month (3-4 days/week, 3-4pts/day) to determine home range and movements. Average home range for lizards with at least 40 locations for the study was 3055m2 (range=512-5674) for female lizards (n=8) and 2408m2 (range=131-6000) for male lizards (n=7). Lizards moved an average 10m per/day (range=1-108). Monthly averages were calculated for lizards with at least 20 locations

recorded for the month. Average home range in May was 598m2 (range=34-1461m2) for females (n=4) and 1874m2 (range=1115-3318) for males (n=4). Average home range in June was 1391m2 (range=170-2720) for females (n=10) and 794m2 (range=195-2798) for males (n=8). Average home range in July was 526m2 (range=90-1483) for females(n=9) and 628m2 (range=82-1704) for males (n=9). Average home range for August was 149m2 (range=18- 739) for females (n=8) and 137m2 (range=5-301) for males (n=7). Home ranges were largest in May and June when mating was occurring, and smallest in August when lizards began to aestivate (up to half of August locations were stationary for some lizards due to dormancy). Earliest date of aestivation was 11 Aug, and last marked lizard to aestivate was 6 Sept.

11:45   009-04 G. **Choose the right side: staying on underside of leaves negatively affects the growth of tobacco hornworm caterpillars.** *Sakshi Watts, Rupesh Kariyat, University of Texas-Rio Grande Valley.*

Plants have evolved an array of physical and chemical defense mechanisms to defend against herbivores with trichomes (hair-like appendages on leaves and stems) being one of them. Caterpillars, a major group of insect herbivores are generally found on the abaxial (underside) leaf surface, which is considered as an avoidance mechanism against biotic and abiotic stresses. Since trichomes act as the first line of defense that caterpillars have to encounter before feeding, we examined the correlation between abaxial vs adaxial (above side) trichome density and caterpillar feeding behaviour, and growth. A combination of field, lab and microscopy experiments were performed using a Solanaceae specialist caterpillar, tobacco hornworm, Manduca sexta (Lepidoptera: Sphingidae), and multiple host species. We found that although abaxial leaf surface had significantly more trichomes, M. sexta caterpillars overwhelmingly preferred to stay on abaxial leaf surface. Consequently, caterpillars took significantly longer to commence feeding on abaxial leaf surface. In addition to this, manipulative lab-based diet experiments showed that staying on abaxial leaf surface with higher trichomes also affected caterpillar growth. Taken

together, our study shows that while caterpillars prefer to feed on abaxial leaf surface, they accrue feeding delays and developmental constraints, and thereby potentially have a reduced impact on their host plants.

12:00   009-05 G. **Can purple corn extract be a potential bio insecticide against insect herbivores?** *Sukhman Singh, Rupesh Kariyat, University of Texas-Rio Grande Valley.*

Polyphenols are botanically derived compounds that have long been studied for their potential insecticidal properties and with many potential sources under exploration. Due to their biodegradable nature and lower persistence in the environment they can be used as a safe alternative to other chemical pesticides. Their very low availability in plants makes the extraction process expensive and thus hinders their commercial utilization. Using a simple and inexpensive method, we extracted polyphenols from purple corn pericarp. In previous studies, we demonstrated that purple corn pericarp negatively affects the growth and development of tobacco hornworm (Manduca sexta), a specialist insect herbivore on Solanaceae with downstream effects on their progeny. Further, we explored whether this extract had any effect on the growth and development of a generalist insect pest (the fall armyworm, Spodoptera frugiperda) which has been reported to feed on more than 150 plant families). We found that purple corn pericarp rich in polyphenols negatively affected the growth and development not only in their larval but also in their pupal stage. Our findings suggest that there is potential to develop commercial level product from purple corn pericarp that can be used as a bio-pesticide. Future work is focused on testing its efficacy under field conditions.

12:15   009-06 G. **Home range, habitat and microhabitat selection of the three-toed box turtle (*Terrapene carolina triunguis*) on a habitat island in North Texas.** *Sara van der Leek, Scott Kiester, Kenneth Steigman, Andrew Gregory, Jaime E. Jimene, University of North Texas.*

Three-toed box turtle (Terrapene carolina triunguis) is a long-lived species native to the

southern United States. In Texas, this species is designated a "species of greatest conservation need" and as "vulnerable" by the IUCN. Twenty-four (24), three-toed box turtles were tracked once a week on an isolated and anthropogenically disturbed habitat island using VHF telemetry. Tracking occurred during the spring, summer, and fall of 2020 to provide insight into their home range sizes, movements, and habitat use. Microhabitat measurements were recorded at turtles' locations and at random locations to determine what microhabitat characteristics turtles are selecting on this disturbed landscape. Turtle microhabitats were associated with a high percentage of leaf litter ground cover and moderate-heavy understory cover. Turtles were typically found in forested habitat types. Only one juvenile turtle was found over the course of the study and all other turtles were estimated to be >20 years old. No sources of mortality were detected during the study period; however, 4 turtles lost their radio-transmitter during the study and their fates are unknown.

12:30   009-07 G. **Foul smelling terpene-rich trichomes mediate herbivore plant interactions.** *Ishveen Kaur, Rupesh Kariyat, University of Texas-Rio Grande Valley.*

Insect herbivory leads to initiation of a suite of structural and chemical defenses in their host plants. However, how species variation affects defense trait expression in closely related species is less understood. In order to test this, we investigated the role of trichomes (hair like appendages on leaves) in two plant species of Cucurbitaceae family as we observed that species difference affected herbivore incidence and feeding in common garden experiments. Using desktop electron microscopy, we identified different morphotypes and density difference for trichomes. We found that Cucumis sativa has significantly lower number of trichomes as compared to Lageneria siceraria. Moreover, these species also vary in the density and morphotype of their trichome type- with L. siceraria having significantly more glandular trichomes when compared to C. sativa. To further examine whether these differences affected herbivory, we collected volatile organic compounds in glandular trichomes, identified and quantified through Gas-Chromatography and Mass-Spectral libraries. We found that terpenes such as β-ocimene, caryophyllene and humulene showed highest peaks followed with fatty acid derivatives, previously known to be herbivore deterrents. Further, we removed glandular trichomes from both the species and added them to artificial lepidopteran diet to study the effects of compounds of glandular trichomes on growth and development of cabbage loopers (Trichoplusia ni) (Lepidoptera: Noctuidae). Taken together, we show that the trichomes in L. siceraria acts as both chemical and physical defenses to mount an effective defense strategy against herbivores, thereby negatively impacting growth and development.

010. Geosciences
Participants:
1:00   010-01 G. **Deposition and diagenesis of the Blossom Sand, Panola County, Texas.** *Hannah Chambers, Stephen F. Austin State University.*

The Blossom Sand is a formation within the Late Cretaceous Austin Group. The Blossom Sand, which crops out in northeast Texas, can be found in the subsurface of southwest Arkansas, western Louisiana, and the East Texas Basin. It ranges in thickness from 50 to 90 ft (164-295.3 m) and consists of primarily illitic sandstone. In the Carthage Field of Panola County, Texas, the Blossom Sand is a historic gas reservoir located at depths of approximately 2,000 ft (609.6 m) below the surface. Since the discovery of the Carthage Field in 1918, the Blossom Sand has produced approximately 26 BCF of gas along with minor amounts of oil. Despite its notoriety in the Carthage Field, there is very little research that has been conducted on this unit. The origin of its sediments, clay minerals, and depositional style have gone unknown. This study provided insights into the depositional environment and diagenetic history of the Blossom Sand using a combination of analytical methods including well log correlations, thin section analysis, x-ray diffraction (XRD), x-ray fluorescence (XRF), and scanning electron microscopy (SEM). The data derived from each method was used to establish the Blossom Sand's mineralogy, porosity, permeability, and clay characteristics, and used to determine depositional environment and diagenetic history of the unit. Understanding the

depositional environment and diagenetic features within this gas reservoir can aid in enhanced recovery of the Blossom Sand and similar sandstone gas reservoirs.

1:15   010-02 G. **Geochemical characterization of Utica shale play using XRF-based chemostratigraphy in Ohio.** *Barbara M. Kemeh, Julie M. Bloxson,* Stephen F. Austin State University.

The Utica shale is an extensive gas shale play within the Appalachian Basin, expanding from Quebec through New York, into Pennsylvania, West Virginia and Ohio. Currently a target for gas exploration, it is also the source rock for much of the Paleozoic reservoirs throughout the basin. However, the Utica-Point Pleasant lithology varies significantly across the Appalachian Basin which can make it challenging to characterize. Here we show that chemostratigraphy reflects changes in depositional and facies characteristics of the Utica and Point Pleasant formations in Ohio. X-ray fluorescence (XRF) combined with lithologic descriptions as well as x-ray diffraction (XRD) and total organic carbon (TOC) data performed by Core Laboratories, was used to investigate changes in the detrital and paleo-productivity distribution between the carbonate rich Lexington Limestone through argillaceous carbonate mudstones in the Utica shale. In depth analysis regarding the existence of bottom water anoxia environment was not performed due to the depletion of redox trace elements. We identified nine chemofacies using Hierarchical Cluster Analysis (HCA) which reflect the geochemical variation up section. There is not a dominant chemofacies in the Utica shale while the lower Point Pleasant Formation is characterized by paleo-productivity enriched chemofacies. Furthermore, the variability in chemofacies is due to formations of more mixed mineralogy as a result of intermittent, sustained periods of increased sediment delivery into the basin as a result of the ensuing Taconic Orogeny. In conclusion, there are noticeable changes from the Point Pleasant Formation into the Utica shale in core 6430, representing changes in sediment provenance and productivity.

1:30   010-03 G. **Inferences on basin thermal maturity and source rock potential within the Midland Basin through evaluation of clay mineral diagenesis and organic maturity.** *Hunter Green, Texas Tech University.*

The use of mineral diagenetic indices and organic matter maturity are useful tools for reconstructing the evolution of sedimentary basins and critical for assessing the potential of source rocks and unconventional reservoirs. In this study, the relationship of clay mineral diagenesis and organic matter maturation indices were used to constrain the maximum burial depths and temperatures of Pennsylvanian and Permian shale strata within the Northern Midland Basin. A variety of organic and inorganic analytical methods were applied to fine-grain sample fractions (<2 µm) to obtained geochemical and mineral phase presence. X-ray diffraction scans show a progressive increase in ordering of mixed layered illite-smectite (I-S) phases (R0 to R1) as well as an increase in illitic phases within I-S with depth. Rock-Eval pyrolysis data show up to 9.5 wt.% TOC throughout and decrease in hydrogen index (HI) with depth with mostly type II kerogen present. Inorganic and organic maturation indices indicated that sediments were subjected to conditions of within the early oil window with maximum paleotemperatures ranging from <100 to 140 °C and buried up to 2.5 to 4 km, respectively. Data from Rock-Eval were used to determine calculated vitrinite reflectance (%Ro), which indicate maturation in the early oil window (0.64 to 0.77). The data presented here show good correlation between inorganic and organic maturation indices within the Northern Midland Basin and can be further applied in a regional context to better understand the complex burial and geotectonic evolution of the southern margin of Laurentia during the Late Paleozoic.

1:45   010-04 N. **Development of rill marks on the beach face at Bryan Beach, Freeport, Texas.** *R. LaRell Nielson, Stephen F. Austin State University.*

Well developed rill marks are present on the beach face at Bryan Beach near Freeport, Texas. These rill marks are produced as the tide goes out by water draining from the berm and bars that are found on the beach face. They develop in zones where there is a higher permeability in the

berm and bars that run parallel to the beach face. These zones contain course clasts and fossil fragments and a small amount of clay. Below and above each permeable zone, the sand contains fewer large clasts and shell fragments and larger amounts of clay resulting in the zone being less permeable. Rill marks are produced by a thin film of water that flows out of the sand and down the beach face following the breaking of each wave as the tide goes out. Rill marks are divided into five different types: fringing, conical, branching, meandering, and bifurcating. All five types of rill marks are found on the beach face at Bryan Beach. The type of rill mark present is determined by: the angle of the slope on the berm or bar face, the amount of porosity and permeability of the sand, and wave impact direction and intensity. They are best developed on stormy days with high tides. Rill marks are rarely preserved in the rock record because the next high tide destroys the rill marks that developed during the last low tide.

ORAL SESSION #4

011. STEM Education
Participants:
8:30   011-01 U. **PLTL Ambassador Program: expanding peer leading to early college students.** *Alissa G. Saenz, Jonathan A. Tipo, Geoffrey B. Saupe, James E. Becvar, University of Texas at El Paso.*

The University of Texas at El Paso (UTEP) has seen remarkable strides in the success rate of General Chemistry students through the implementation of Peer-Led Team Learning (PLTL) over the past twenty years. This was done not only by facilitating the learning of General Chemistry topics for students, but by introducing strategies of facilitated learning, studying, time management, and critical thinking. These influential techniques could be applied within rigorous Early College High School (ECHS) programs for those who are simultaneously part-time college students and full-time high school students. ECHS students need a better understanding of what to expect for university-level courses; the success rate in collegiate level STEM courses is low for these students, despite the rigorous nature of the ECHS program, likely due to a lack of adequate preparation. To assist with the preparation in local ECHS programs, we are implementing the PLTL Ambassador Program to initiate a pilot program from the Chemistry Peer Leading at UTEP to the Northwest Early College High School in El Paso, TX. In this program, we plan to aid students as they make the transition into a higher education environment by equipping them with the necessary tools and techniques to succeed. Our plan includes introducing new study habits, learning techniques, and ways to time manage in their high school level chemistry course. We plan to assess the effectiveness of this program by doing monthly evaluations as well as comparing their course scores after each testing period. Our hope is that participants will take these techniques and apply them holistically in other areas of their academics to become a more prepared and engaged student. PLTL has countless benefits for both the peer leader and the students, and we strive to diffuse these benefits to not only UTEP students, but those in the greater El Paso community.

8:45   011-02 U. **Video editing: a valuable tool to enhance peer-led team learning for remote learning.** *Enid Martinez, Dania de la Hoya, Lester Ibarra, Jacob Najera, Adam Boyea, Mahesh Narayan, Geoffrey B. Saupe, and James E. Becvar, University of Texas at El Paso.*

Remote learning during the COVID-19 pandemic has opened the door for creative use of technological skills to engage students and instructors alike for the purpose of communicating complex and abstract concepts into a manageable format such as educational videos. The general chemistry courses at the University of Texas at El Paso have engaged Peer-Led Team Learning (PLTL) strategies over the past twenty years to enhance facilitation of learning. We have found that educational videos integrate new concepts with existing knowledge and enhance learning in PLTL Workshop. The video creation process requires a thorough understanding of a concept in order to present it in a concise manner. To transform an idea for a video into an effective educational tool and minimize time spent on weeding out verbal tics and extraneous information from an explanation,

writing a script helps the narrator stay on track, speak at consistent pace, and avoid mistakes. Key factors that elevate the quality of the video to engage the viewer through visual and auditory processing channels include incorporation of text and symbols that emphasizes important information, condensing information in under five minutes, and designing tutorial-style figures and images that illustrate the material being narrated. To avoid overwhelming the viewer with a high cognitive load, video editing is essential in removing unnecessary visual or audial distractions, adding images to the recorded video file and rearranging clips to maintain viewer attention, and manipulating soundtracks to balance narration volume, speed and tone. Training all current and future peer leaders with iMovie, due to its ease of use and availability on campus equipment, benefits the PLTL program in all aspects of instruction.

9:00   011-03 U. **Changing the learning facilitation workbook each semester.** *Carolina Melendez, Raymundo Aragonez, Korina Avitia, Sofia Delgado, Jonathan Tipo, Madeline Olivas, Geoffrey B. Saupe, James E. Becvar, University of Texas at El Paso.*

Workbooks authored by Peer Leaders and practitioners facilitate learning in Peer-Led Team Learning (PLTL) workshops in general chemistry at the University of Texas at El Paso (UTEP). Workbooks grant authorship credit to the writers of the original content. Earnings by the non-profit Lead For America Corporation (LFAC) from sale of workbooks provide financial support for PLTL Program costs. The First Semester General Chemistry Workbook is a Peer Leader's and student's most valuable resource. The accessibility of the information and question bank included is unparalleled compared to other materials for learning facilitation. One of the main ways a Peer Leader uses the workbook is to present practice problems and assign homework to students. It is common practice to take these problems and count them toward their overall workshop grade. The primary goal of revising the workbook is to preserve the integrity of the student's work. Each semester, the homework problems at the end of each module are modified in order to prevent previously graded copies from being distributed and used. These revisions to

the homework problems ensure the prevention of academic dishonesty between the students. The secondary goal to revising the workbook is to enhance the quality of the included information. As learning techniques are constantly being developed throughout the semester, the workbook must reflect these advancements. Images, text material, and even the methodology for comprehending information and solving problems are modified as needed in order to reflect the discoveries during the semester. The successful revision strategy involved assigning individual modules to teams of two to three people. Each team had one person reviewing the reading material while the other member(s) would focus on revising the homework problems.

9:15   011-04 U. **Quality control in on-line peer-led workshops.** *Edna Tepezano, Paulina Torres, Brittney Baca, Lester Ibarra, Raymundo Aragonez, Jeremiah Davis Bell, Diego Maldonado, Carolina Melendez, Geoffrey Saupe, James E. Becvar, University of Texas at El Paso.*

The General Chemistry Program at the University of Texas at El Paso has had a successful Peer-Led Team Learning (PLTL) intervention for the past twenty years. Students enrolled in a large section lecture are co-enrolled in a small learning community called Workshop, which is overseen by undergraduate Peer Leaders who previously mastered the content and completed a pre-semester training. The fall 2020 semester required an all on-line experience for Workshop. This change presented challenges for the Peer Leaders and resulted in a revamped oversight process of evaluation and quality control of Workshop function. In conducting evaluations, it is evident that each Peer Leader has their own style in managing a Workshop. Most experienced Peer Leaders seem confident in their knowledge of the subject, while new Peer Leaders appear more hesitant in their explanations. Evaluators believe these reviews are beneficial particularly to new members of the PLTL program because it gives them reassurance and thus increases their confidence. It is also useful to have another perspective to determine if improvements need to be made. Some Peer Leaders started the semester with a lot of insecurities, doubts, and a fear of public speaking, but gained confidence

and certainty in their abilities to lead their peers. Evaluators also reap several benefits such as learning from both the innovative ideas as well as the mistakes other Peer Leaders might make to analyze themselves and their workshops. Peer leading does not only impact individuals professionally and academically, but also shapes who they are outside of the workshop. Suddenly, Peer Leaders begin overcoming some insecurities and weaknesses they have struggled with for years and become stronger and better human beings in the process. Workshop evaluations have proven to have great value and serve as guidance in this lifelong learning journey.

9:30   011-05 N. **Teaching during the pandemic: HyFlexing.** *Joni H. Ylostalo, University of Mary Hardin-Baylor.*

As the SARS-CoV-2 started its spread across the globe in the Spring of 2020, Universities were forced to implement alternative modes of teaching to engage students. This generated numerous challenges for the faculty, students, and University administration. Here, I describe an adaptation of the HyFlex model of teaching, coined CRUflex, that was implemented at UMHB and the experiences with this transition. After the emergency online teaching during Spring of 2020, UMHB transitioned into CRUflex model of teaching for the Fall of 2020. In this model, students could take any class in three different modalities, face-to-face, online synchronously, and online asynchronously, and transition between any of these modalities at will during the semester. This generated challenging classroom dynamics and student successes varied greatly. The added freedom allowed safer practices of learning as the classrooms were not crowded, however, this freedom might have also encouraged laxed responsibilities by some students. The challenges for faculty were also significant, especially in the front end, as all of the courses had to be transitioned to online, and in many cases re-designed, to fit the online environment. More challenges were faced in generating the best activities and assessments that would be engaging for students but also provide reliable learning evaluation data. Thorough evaluation of the courses ended up being extremely valuable and the added lecture videos have enhanced the course delivery

allowing students to re-watch the lessons later. Furthermore, generation of all online assessments have generated usable materials for the coming semesters.

9:45   011-06 N. **Academic community supports undergraduate success, especially during the isolation of a pandemic.** *Julian Davis, University of the Incarnate Word.*

Undergraduates, particularly those who are financially disadvantaged and / or under supported outside school face many challenges as they progress through school. Strong academic support, in the form of mentoring by peers and faculty, study sessions, and professional development activities, has been shown to enhance student performance in courses and increase retention. These activities also have a positive impact on student morale, particularly those without encouragement and assistance outside their school environments. The covid-19 pandemic has presented an additional layer of challenges to college students in general and has further widened the disparities in students' resources. Our Cardinal Chemistry Scholars (C2S) Program, funded by an NSF S-STEM grant, has been providing financial, academic, professional, and mentoring support to financially disadvantaged undergraduates since the fall of 2018. The positive impact this type of program and the supportive academic community it fosters on undergraduates has been well-documented. Preliminary results from the spring suggest it is even more important during the covid-19 pandemic. Fall 2020 course grades and other metrics are not yet available, but our initial look at student performance this semester, which is the first one to be affected by the pandemic from start to finish, support this conclusion as well. We hope our analysis of the C2S program and feedback from student scholars will prepare us to better support students as the pandemic continues.

012. Freshwater Science
Participants:
10:30   012-01 U. **Population density differences of the invasive zebra mussel in two Central Texas lakes.** *Josiah S. Moore, Samuel E. Poster, Jason L. Locklin, Robert F. McMahon,*

Jessica M. Konkler, Alex J. Flory, Temple College.

Dreissena polymorpha (zebra mussels) are among the most invasive species in North America. Since they were first reported in Texas in 2009, zebra mussels have invaded 30 Texas reservoirs. To better understand the population dynamics at southern latitudes, we studied populations of mussels at two central Texas reservoirs: Stillhouse Hollow Lake and Belton Lake. To estimate densities, four sets of 20x20 cm plates (four replicates per set) were suspended bimonthly from a floating marina in each lake at four equally-spaced depths from surface to sediment between September 2019-July 2020. Samplers were assessed monthly to estimate densities and settlement through time at various depths. Mussel lengths were measured on a separate set of samplers suspended 6 m from the water surface to estimate growth rates. Water temperature and dissolved oxygen were logged hourly at three depths in both lakes during the study. Preliminary results suggest that two cohorts (spring and fall) occur in both lakes, and mussel densities are 40X greater at Stillhouse Hollow Lake compared to Belton Lake. A minor fall settlement event resulted in a max density of 296 ± 424 m-2 in Stillhouse Hollow (February) and 98 ± 164 m-2 in Belton (May) followed by a major settlement event following the spring spawn of 80,348 ± 120,324 m-2 (August) in Stillhouse Hollow and 3,461 ± 8,928 m-2 (July) in Belton. Mussel growth rates between September 2019-June 2020 were 80.6 μm d-1 and 101.3 μm d-1 in Belton and Stillhouse Hollow, respectively, which is among the highest reported for zebra mussel growth in North America.

10:45 012-02 G. **Mercury contamination characterized by microbial Hg methylation genes in Martin Lake, East Texas.** *Sharon Schmidt, Javid McLawrence, Anil Somenahally, Ri-Qing Yu, University of Texas at Tyler.*

The number one emitter of atmospheric mercury (Hg), Luminant's Martin Lake Steam Station, is located on Martin Creek Lake in Martin Creek Lake State Park in Tatum, Texas. The power plant emits atmospheric Hg while burning coal to generate electricity. The surrounding lake water is also used as cooling water for the plant, and it is released back into the lake after use. The atmospheric Hg emitted from the Martin Lake Station may drop on Martin Creek Lake; however, the fate and concentration of Hg in the lake ecosystem have not been studied. Inorganic Hg in the sediment could be methylated by anaerobic microbes into neurotoxicant methylmercury (MeHg), although the dominant groups of Hg-methylating microbes are unknown in the lake. This toxic form of mercury can bioaccumulate along the aquatic food web, potentially causing detrimental health effects on local populations. Sediment and pore water samples in Martin Lake were investigated over five seasons in 2019 and 2020. Biogeochemical analyses of sulfate, iron (III), total organic content, and others found that sulfate concentrations were significantly higher than the levels in nearby lakes, and iron levels fluctuated among different sampling sites in Martin Lake. Sites near the cooling water runoff had higher water temperatures than other areas of the lake. After extracting genomic DNA from sediment samples, Hg-methylating genes were detected from most sites around the lake. Archaeal hgcA and Deltaproteobacterial hgcA genes have been detected and quantified via qPCR with average copy numbers in the thousands per gram of soil. It is hypothesized that sampled areas surrounding the power plant will have higher concentrations of MeHg and more abundant hgcA genes due to atmospheric deposition and cooling water runoff from the power plant. We anticipate that our study could be used in the future to inform the public about the risks of mercury contamination in lakes that can negatively impact public health.

11:00 012-03 G. **Seasonal dynamics of food resources downstream of different tributaries in Cibolo Creek, Texas.** *Namrata Giri, Brian G. Laub, University of Texas at San Antonio.*

Food resources for fish, such as algae and leaf litter, may be impacted by urban development. The goal of the project is to assess the variability in food resources in different seasons and across environmental factors such as water quality, below different tributaries of a creek undergoing urban development and wastewater inputs. We sampled benthic organic matter and algal biomass in Cibolo Creek in south-central Texas,

at sites below three tributaries – Currey, Menger, and Browns Creek. Currey and Menger Creek are perennial streams carrying wastewater effluent, whereas Browns Creek is a natural ephemeral stream. Summer season sampling was done June 6-20; fall season sampling was done October 22-24; winter season sampling was done January 14-23 and spring season sampling was done March 23-24, 2019. Due to COVID, spring season sampling for Browns Creek could not be completed. None of the measured food resources, including fine particulate organic matter (FPOM), ash free dry mass (AFDM) for algae, chlorophyll-a, and coarse particulate organic matter (CPOM) differed significantly between sites within seasons. Sites below each tributary exhibited different seasonal patterns in food resources, which may be related to urban impacts such as wastewater effluent or urban runoff. However, only Menger differed significantly in FPOM, AFDM, and Chlorophyll-a between seasons. The findings will help to understand an adverse effect of urbanization on the creek which leads to scarcity or a shift in types of food resources for fish.

11:15   012-04 N. **Seasonal patterns of spring discharge at Silver Falls, Crosby County, Texas.** *John E. Stout, United States Department of Agriculture.*

Beneath the high plains of the Llano Estacado lies the southern extension of the Ogallala Aquifer, which provides a key source of groundwater for the region. Along the eastern fringes of the Llano Estacado, there are numerous natural springs that discharge from the Ogallala formation and provide a valuable source of freshwater for ranches located in the Rolling Plains of Texas. Large scale irrigation has altered hydrological conditions, which has influenced the flow of springs along the eastern escarpment. In late 2012, the author began a study of a spring located at Silver Falls in Blanco Canyon, east of Crosbyton, Texas. The goal was to monitor the discharge of this naturally flowing spring over a period of seven years to establish temporal patterns. Measurements of spring discharge over a seven-year period did not show an appreciable reduction associated with the depletion of the Ogallala Aquifer. However, discharge at Silver Falls was found to follow a seasonal pattern of declining flow during the summer followed by a

recovery starting in late fall and reaching maximum flow during the winter and early spring. Whereas seasonal variations of spring discharge can be measured precisely, the cause of these seasonal patterns is less certain. It is likely that the combined effects of groundwater extraction for irrigation and the growth and transpiration of natural vegetation contribute to the seasonal patterns of groundwater discharge observed at Silver Falls.

013. Marine Science
Participants:
11:45   013-01 U. **eDNA metabarcoding analysis** of **anthropogenic effects on shark (Selachimorpha) diversity along the Texas gulf coast.** *Madelyn Knauss, Stephanie Lockwood, Texas Tech University.*

Metabarcoding with eDNA uses collected samples of DNA from the environment to detect species. Traditional diversity reports, such as visual counts and camera traps, can vary in accuracy due to information gaps, and levels of diversity can be influenced by differing water chemistry and anthropogenic impacts. In this study, we explore the use of metabarcoding with environmental DNA by relying on the precise identification using shed DNA from seawater samples in order to avoid the issue of misidentifying the morphological characteristics of species. This study draws on previous research to identify White sharks in the Pacific Ocean by using the MiFish universal primers to target the 170 bp COI gene fragment. This study utilizes this primer set to identify shark species in the Texas Gulf Coast region. Researchers will compare and record correlations between prior species lists, as well as the salinity, dissolved oxygen, temperature, anthropogenic impact, and pH levels to diversity levels of sharks. Then, we will compose a diversity report analyzing where hotspots occur and outline future conservation guidelines that monitor local populations for areas of higher shark diversity. By using seawater samples to identify species in each area, we virtually eliminate potential risks associated with direct handling and also increase accuracy of detection. Utilizing more accurate data helps biologists form more effective conservation strategies, which is increasingly

important as anthropogenic effects intensify. We anticipate identifying a range of diversity based on water chemistry, water depth, and human impacts. Identifying this range, specifically regarding threatened species such as sharks, provides foundation for future conservation and management plans that will account for a changing environment.

014. Conservation Ecology
Participants:
12:15 014-01 U. **A comparison of Carolina Wren nestling begging behavior and growth in urban and rural environments.** *Sara Moore, Dr. Diane Neudorf, Sam Houston State University.*

Given the alarming population declines of bird species globally and the inevitable expansion of urbanization, the need to understand how birds respond to human disturbance is critical to understanding which species may succeed in urbanized habitats. The objectives of this study were to compare: 1) nestling begging behavior; 2) nestling condition; and 3) nest success of Carolina Wrens (Thyrothorus ludovicianus) in urban and rural environments. We tested the hypothesis that urban wrens will be in poorer condition due to less food availability and potentially greater disturbance. We predicted urban wrens would fledge at lower body mass (which can be an indicator of future survival) and that they would beg more and louder than their rural counterparts. Over two field seasons we measured nestling condition at day 6 and day 9 of the nestling period in 38 nests. We also recorded nestling vocalizations at 3 urban nests in 2020. We will present our findings from the 2019 and 2020 seasons.

016. Plant Biology
Participants:
1:15 016-01 U. **DNA barcoding in the species of *Chlorococcum* algae.** *Emily Martinez, University of Mary Hardin-Baylor.*

Chlorococcum is a genus of algae in the Chlorococcaceae family. *Chlorococcum* algae have many different species that are indistinguishable to the eye. All of the single-celled organisms appear the same under a microscope: small, round, and green. These species cannot be distinguished by appearance alone. In this research, DNA barcoding was used to determine the differences between the species. DNA barcoding is a method of distinguishing species by identifying a segment of DNA from a gene that is different in each species. Barcoding is a worldwide endeavor to give each organism a unique barcode. In this study, DNA extraction, PCR, and bioinformatics were used to determine a gene that could be used for DNA barcoding in the *Chlorococcum* genus. Many genes were explored, including the *TufA* gene and the ribosomal large subunit gene on several different *Chlorococcum* species. These genes were the most successful in differentiating between the different *Chlorococcum* species. The *TufA* gene sequence from *C. aquaticum* and *C. oleofaciens* had shown a significant enough difference to consider it a possible gene to distinguish between the species.

1:30 016-02 G. **Phylogenetic analysis of New World cypresses (Hesperocyparis; Cupressaceae): comparative sequencing of two newly developed chloroplast intergenic spacers.** *Alexander Sholl, Randall Terry, Lamar University.*

The New World Cypresses (Hesperocyparis; Cupressaceae) are a group of 16 morphologically-cryptic species geographically centered in western North America and adjacent Mexico. Although previous molecular phylogenetic studies have resolved relationships among basal lineages of the genus with strong support, it has become increasingly clear that recovery of relationships within the two principal Hesperocyparis lineages (i.e., the Arizonica and Macrocarpa clades) will require considerable effort aimed at collecting comparative data from a variety of sources. As a part of this continuing effort, we report results from comparative sequencing of two newly developed intergenic spacers from the chloroplast genome (ndhF-rpl32 and trnS-ycf3) for assessing interspecific relationships within the Macrocarpa and Arizonica clades of Hesperocyparis. Parsimony, Maximum Likelihood, and Bayesian analyses of approximately 1.4 kilobase pairs of aligned sequence support previously described relationships among the basal lineages of the genus as well as strengthen support for species-

level relationships within the Arizonica and Macrocarpa clades. Additionally, variation in simple sequence repeats was observed that could be useful in resolving population-level relationships. Data presented here, when combined with previously published sequences from noncoding chloroplast regions, provide the most well supported hypotheses of interspecific relationships among the New World cypresses published to date.

1:45   016-03 G. **Morphology and anatomy of the seed coat in the Texas species of *Argemone* (Papaveraceae).** *Shelby Conway, David E. Lemke, Texas State University.*

The genus Argemone (Papaveraceae) comprises 32 New World species of annual or perennial herbs or subshrubs, eight of which are native, or have been introduced, to Texas. This study used light microscopy and standard histological techniques, as well as scanning electron microscopy and confocal laser scanning microscopy, to examine the morphology and anatomy of the seed coat of the Texas species of the genus. All exhibit a surface sculpturing pattern that is best described as alveolate or areolate, although differences in seed size and microsculpturing patterns allow for distinctions to be made among the species.

2:00   016-04 G. **Preliminary observations on the structure of extrafloral nectaries in Cactaceae.** *Jackson F. Burkholder, David E. Lemke, Texas State University.*

Extrafloral nectaries (EFNs) are nectar-producing structures that are formed on vegetative portions of the plant body and that typically do not play a role in pollination. Several studies have indicated that EFNs encourage ants and other arthropods to visit a plant and to protect it in return for an energetically-rich extrafloral nectar reward. EFNs were first observed on members of the cactus family (Cactaceae) over 100 years ago, but their structure has been little-studied. At least four morphologically different kinds of EFNs have been documented in Cactaceae: highly modifed spines that are short, broad, and blunt; nectaries that resemble ordinary spines with no obvious modifications; modified foliage leaves associated with an areole; and regions of epidermal tissue below and not associated with an areole. Preliminary observations in Coryphantha and Glandulicactus show that the EFNs, which likely represent modified spines, consist of a parenchymatous, vascularized stalk that supports a distinct layer of secretory tissue with a heavily cuticularized epidermis.

Graduate Student Oral Presentation Competition
2:30 to 6:30
(Please see pages 18-20 for these abstracts.)