

The 24th Annual Meeting of the Ecological Integration Symposium (EIS)



Rudder Tower, Texas A&M University

College Station, Texas, April 4-5, 2024

Abstract memories of EIS 2024

Thanks to Everyone Who Helped Make this Meeting Possible ...

The Ecological Integration Symposium gratefully acknowledges the following for their support, sponsorship, and hard work in putting together this year's annual meeting.

EIS 2024 Organizing committee

Hayden Roberts (hcr@tamu.edu)

Jackson Linde (jackson.linde@tamu.edu)

Oluwaseun D. Ajileye (ajileye .5@tamu.edu)

Adeyemi Adeyinka (adeyinka08@tamu.edu)

Nicole Scavo (nicole.scavo@tamu.edu)

Austin Ehrie (ajehrie@tamu.edu)

Adekola Owoyemi (ludtson@tamu.edu)

Jorge Medina-Duran (jorgemedinad@tamu.edu)

Cara Webster (cfjwebster17@tamu.edu)

Malik Nkrumah(maliknkrumah@tamu.edu)

Texas A&M Faculty

Heath Blackmon (hblackmon@bio.tamu.edu) – Opening Remarks

Courtney Fitzpatrick (cfitzpatrick@bio.tamu.edu) – Closing Remarks/ Faculty Advisor

Welcome

We would like to welcome you to the 24th annual meeting of the Ecological Integration Symposium (EIS 2024). The EIS is an annual interdisciplinary event that brings together a diverse group of leading scientists and students from the fields of ecology, evolutionary biology, and conservation. The symposium provides an excellent opportunity for both local and visiting students to showcase their work and engage in meaningful dialogue with the invited speakers.

Continuing the tradition of EIS since its inception in 2000, we are a graduate student-run event that is open to the public and free to attend.

The organizing committee is grateful to our sponsors for their support and to the large body of faculty, students and public who have made this event possible.



Ecological Integration Symposium 2024

Global Innovations in Ecology

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Plenary Speakers

Steven J. Cooke

Carleton University

Dr. Steve Cooke is a Canadian biologist specializing in ecology and conservation physiology of fish. He is best known for his integrative work on fish physiology, behavior, ecology, and human-dimensions to understand and solve complex environmental problems. He currently is a Canada Research Professor in Environmental Science and Biology at Carleton University and the editor-in-chief of scientific journals such as *Conservation Physiology* and *Fisheries*. Dr. Cooke earned his bachelor's degree in environmental studies at the University of Waterloo in 1999 and his doctorate degree at the University of Illinois at Urbana-Champaign in 2002. Cooke's research has contributed to many aspects of the biology, conservation and management of fish and aquatic ecosystems. Often, Cooke uses novel technology, like EMG transmitters, and telemetry techniques to understand the behavior and physiology of free-living animals. Recently he provided a framework for the application of telemetry techniques to enable IUCN Red List ranking. Cooke uses interdisciplinary approaches (ranging from behavior to genomics) to study complex conservation and management problems. Notable awards given to Dr. Cooke includes being a recipient of the Award of Excellence from the Fisheries Management Section of the American Fisheries Society (AFS) in 2005 and becoming a Natural Sciences and Engineering Research Council E.W.R. Steacie Memorial Fellow in 2015. He also was elected to the Royal Society of Canada's College of New Scholars, Artists, and Scientists and served as the Secretary and member of the council from 2017-2019. With over 500 publications, Dr. Cooke is considered a world leader in fisheries and has made substantial contributions to deepen our understanding of conserving freshwater biodiversity.

Pamela Soltis

University of Florida, Florida Museum

Professor Pamela Soltis is a highly respected American botanist, renowned for her contributions to plant genetics and evolutionary biology. Dr. Soltis earned her bachelor's degree in biology from Central College in 1980, graduating summa cum laude. She pursued further studies at the University of Kansas, obtaining an M.Phil. with honors in botany in 1984 and a Ph.D. in botany in 1986. After her Ph.D., she began her academic career as an assistant professor in the Department of Botany at Washington State University in 1986. She was promoted to associate professor in 1992 and to full professor in 1998 in the Department of Botany and School of Biological Sciences. In 2000, she joined the University of Florida and the Florida Museum of Natural History as a curator. At the University of Florida, she served as the University of Florida Research Foundation Research Professor from 2006 to 2009 and co-directed the UF Computational Biology Program from 2009 to 2012. Professor Soltis focuses primarily on the patterns and processes that shaped the tree of life, particularly studying the diversity and evolution of angiosperms (flowering plants). She employs genomic methods, natural history collections, and computational modeling to explore phylogeny, phylogeography, and polyploidy of angiosperms. Having published over

400 scientific papers, Soltis is recognized for her influential contributions to the understanding of genetic and genomic attributes in the success of polyploids. Soltis has also held significant positions in various scientific societies. She served as the president of the Botanical Society of America in 2007–08 and has been involved with the Society for the Study of Evolution, the American Society of Plant Taxonomists, the American Genetics Association, and the Society of Systematic Biologists, serving as its president as well. Additionally, she has contributed as an associate editor for the journals "Evolution" and "Systematic Biology" and is a member of the University of Kansas Women's Hall of Fame. Her work has been recognized with several awards. She received the 2002 Dahlgren Prize in Botany from the Royal Physiographic Society of Sweden and, along with her husband Douglas Soltis, won the 2006 Asa Gray Award. Soltis was named a highly cited researcher by Reuters in 2014 and was elected to the National Academy of Sciences in 2016.

Patricia C. Wright

Stony Brook University

Dr. Pat Wright is a scientist and distinguished professor in the Department of Anthropology at Stony Brook University, New York and is the Founder and Executive Director of the Centre Valbio, a research and training center in Ranomafana, Madagascar. Current research includes investigating the growth, tooth eruption patterns, and ontogeny of various lemur species, the nutritional composition of lemur foods, the relationship between lemur foods and medicinal plants, the role of parasites on populations, and the effects of habitat disturbance on lemur populations. Wright also conducts biodiversity surveys in tropical forests of Madagascar to address conservation problems. She has received the prestigious MacArthur Fellowship and three medals of honor from the Malagasy government. After Wright discovered a new species of lemur in 1986, she helped establish its habitat as a national park and a UNESCO World Heritage Site. She has published over 200 scientific papers, authored four books, and has given hundreds of lectures to museums, universities, and societies throughout the US and Europe.

Nancy Grimm

Arizona State University

Dr. Nancy Grimm is an inter- and transdisciplinary ecosystem ecologist and Virginia M. Ullman Regents Professor of Ecology at Arizona State University. Dr. Grimm studies the interactions of climate change, human activities, resilience, and biogeochemical processes in desert and urban stream ecosystems. She was founding director of the Central Arizona–Phoenix Long-term Ecological Research program and served as its principal investigator for 19 years. She co-directed the Urban Resilience to Extremes Sustainability Research Network from 2015–2022 and now co-directs the international network of networks, NATURA (NATure-based solutions for Urban Resilience in the Anthropocene) and the graduate scholars network, Earth Systems Science for the Anthropocene (ESSA). Dr. Grimm is a member of the U.S. National Academy of Sciences and Fellow of the American Association for the Advancement of Science, the American Geophysical Union, the Society for Freshwater Science, and the Ecological Society of America. She is a past president of the

Ecological Society of America and the North American Benthological Society (now Society for Freshwater Science), past program director for the U.S. National Science Foundation, and senior scientist for the U.S. Global Change Research Program. She was awarded the 2019 Sustainability Science Award from the Ecological Society of America as part of an international team consensus on how ecological research in urban areas can improve sustainability and resilience to natural disasters. Grimm is known for her support of long-term research, and her dedication to mentorship and collaboration. Along with her colleagues and students, Grimm has made greater than 200 contributions to scientific literature.

Maria Diuk-Wasser

Columbia University

Dr. Maria Diuk-Wasser is a professor in the Department of Ecology, Evolution & Environmental Biology at Columbia University. She earned a Ph.D. in Biology from the University of California, Los Angeles and completed her post-doctoral training in Epidemiology & Public Health at Yale University. She was an assistant professor in the Division of Epidemiology of Microbial Diseases at the Yale School of Public Health before moving to her current position at Columbia. Professor Diuk-Wasser is interested in elucidating the environmental and anthropogenic factors driving the emergence of vector-borne and zoonotic diseases. Her research integrates laboratory, field and a range of modeling approaches to predict human disease risk. Her current focus is on how pathogen interactions at multiple scales (within host, population, community and regionally) influence the recent emergence of tick-borne pathogens in the United States. In endemic areas, she studies how human behavior and landscape modification influence human infection and disease. Her current research focuses on tick-borne pathogens, but she has also worked on West Nile virus, malaria, dengue and leptospirosis. Other research interests include landscape ecology, population and community ecology, evolutionary ecology, behavioral ecology and conservation biology.

Contributed Abstracts

Texas Tropical Network (TTN) Symposium

Title: 60 Years of Ecological Insight from the Manu Elevation Gradient

Presenting author: Erik Iverson

Affiliation: Integrative Biology (UT Austin)

Abstract: Tropical elevation gradients provide some of the most important natural laboratories for studying ecology and evolution because of the wide variety of microclimates they offer within a limited area and their dynamic geological and evolutionary histories. The Andes Mountains, the longest in the world and the tallest in the Western hemisphere, have been particularly useful for biogeographic research since the days of Alexander von Humboldt, Aimé Bonpland, and Francisco José de Caldas. The Andes have hosted many studies that make use of their extensive elevational and latitudinal clines, and transects of major importance have been established in all Andean countries. Over the past 60 years, an elevational transect in the Manu Biosphere Reserve of Southeastern Peru has emerged as particularly important for global ecology and evolutionary biology, with surveys of all major organism groups and many ecological properties and functional traits taking place across 4000 vertical meters of relatively pristine vegetation communities. The Manu region is now home to a growing number of research stations and major investments in permanent scientific research infrastructure, increasing the importance and capacity of its elevation gradient for answering questions about global change and biodiversity loss. Here, we chart the development of scientific inquiry along the gradient and describe the major findings of 60 years of transects, surveys, and experiments, contextualizing their importance for informing the discipline of ecology and evolution as a whole. We then look at the present and future conservation challenges of the region and the investments that will be needed to ensure that the Manu gradient remains one of the world's foremost natural laboratories of global environmental change.

Title: Size, Diet, and Habitat Associations of a Recently Described Peacock Bass Species, *Cichla cataractae*

Presenting author: Benton Fry

Affiliation: Texas A&M EEB

Coauthors: Kirk Winemiller, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Although it is a relatively small country (215 km², about the size of the state of Idaho), Guyana has among the highest diversity of freshwater fishes on Earth. This biodiversity is threatened by multiple human impacts, ranging from gold mining to climate change. Research in the last few decades has revealed a wealth of undiscovered aquatic biodiversity. One example of this is the newly discovered peacock bass, *Cichla cataractae* (endemic to the Essequibo River Basin). *Cichla cataractae* was discovered by biologists in

2018 (locals already knew of the species) co-existing with a well-known species of peacock bass, *C. ocellaris* (the type species for the genus). A field expedition was completed between January 7, 2023, and March 24, 2023 in the Rupununi, Rewa, and Essequibo Rivers, where 1011 peacock bass were collected by angling. 207 were *C. cataractae*. This expedition aimed to collect information on biotic and abiotic factors associated with the niche breadth of these two species. Recreational grade side-scanning sonar was used to map all available habitats where *Cichla* spp. are present. Each peacock bass was measured for total length, weight, and mouth gape width, gut contents were removed via a modified gastric lavage technique, and eye color was recorded as a measure of gonad development. Preliminary results from this study will report on the size distribution, habitat associations, and diets of *C. cataractae*, emphasizing the impact of novel field methods on surveying fishes in remote areas.

Title: Use of RFID to Assess Survival Rates of In-Situ Nests Between Mass and Solitary Strategies

Presenting author: Leah Spoolstra

Affiliation: Texas A & M, Department of Ecology and Conservation Biology

Coauthors: Dr. William Grant (Department of Ecology and Conservation Biology, Texas A&M University), Dr. Beth Silvy (Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University), and Dr. Gerard Kyle (Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University)

Abstract: Populations of sea turtles have been depleted due to anthropogenic and climatic pressures, such as habitat degradation, overexploitation and illegal trade, and fishery-related mortalities. Sea turtles in the genus *Lepidochelys* express a unique behavioral nesting polymorphism with 3 distinct strategies: solitary, mixed, and mass. Reproductive synchronization, referred to as 'arribadas,' is considered to be an advantageous behavior as brief occurrences of prey at high densities reduce the probability of an individual getting preyed upon; however, beaches where arribadas occur typically demonstrate poor hatching success attributed to high predation, destruction, temperature, nest density, and microbes. Ostional, Costa Rica, one of the most important rookeries for *Lepidochelys olivacea*, legalized the extraction of sea turtle eggs in 1987 to conserve natural resources while providing socio-economic improvements. Legal extraction occurs strictly during the first 36 hours of each arribada when nest loss is considered to be the highest. Despite the global importance of Ostional for the reproduction of *L. olivacea*, little is known about natural embryo mortality between nesting strategies and events. My research focuses on estimating the rate of natural embryo mortality and the probability of nests surviving to produce hatchlings based on disturbance events, spatial and temporal distribution, and nesting strategy to support legal egg harvesting. For the first time, passive radio frequency identification (RFID) was used for nest monitoring to determine the fate of in-situ solitary and arribada nests. I categorized the causes of nest loss and estimated the survival probability for nests from two distinct reproductive strategies based on multiple variables to contribute to local management decisions regarding resource extraction.

Title: The canopy frogs of Gabon

Presenting author: Ed Basham

Affiliation: The University of Texas at Austin

Coauthors: Abraham Bamba-Kaya (Institute de Recherches Agronomiques et Forestières, Libreville, Gabon) & Gregory F.M. Jongsma (Department of Natural History, New Brunswick Museum, Saint John, NB E2K 1E5, Canada)

Abstract: Tropical forests are vertically complex and offer unique niche opportunities in the form of resources, climate, and habitat gradients from the forest floor to the canopy. Rainforest amphibians have diversified within this vertical space resulting in partitioned niches and corresponding morphological, behavioral, and reproductive traits. However, a lack of data regarding the vertical niche space used by amphibian species has prevented a nuanced analysis of the form-function relationship between traits and vertical height. We performed 74 ground-to-canopy surveys for amphibians in the tropical rainforest of Gabon and described the vertical stratification patterns of the assemblage in terms of richness, abundance, and species-specific vertical niches. We determined that the community shift in richness and abundance between the ground and understory was pronounced, while the community change from understory to canopy was gradual. We analyzed the relationships between amphibian traits with vertical height using linear mixed effects models, finding strong support (>60% variance explained) that frogs with bigger toes in relation to their length access greater height in the canopy. This relationship provides support for the form-function hypothesis; that morphology changes predictably to meet the functional demands of species along niche gradients. Furthermore, we documented differences in the vertical heights of species according to their reproductive modes, highlighting the potential impact of reproductive mode diversity on the vertical stratification patterns of amphibian assemblages.

Title: Range expansion dynamics of Green Jay (*Cyanocorax yncas*) in Texas revealed through population genomics

Presenting author: Brian Stokes

Affiliation: University of Texas

Coauthors: Timothy H. Keitt, Department of Integrative Biology, University of Texas

Abstract: Climate change is rapidly shifting the geographic range of thousands of species, but empirical research has not fully addressed the complexities of this global ecological trend. The goals of this study were to 1.) investigate how the landscape structures gene flow during range expansion and 2.) characterize genetic changes across the newly colonized areas. We use the range expansion of green jay (*Cyanocorax yncas*) in South Texas as a model system to explore the relationship between an expanding population and the landscape. Historically, green jay were found within about 50 km of the Rio Grande in South Texas. Green Jay have steadily expanded their northern range limit to about 300 km north of the Rio Grande. Using whole genome sequencing data from green jay (n=65) captured throughout 30 sites in Texas and Mexico covering the range expansion area, we

compared measures of genetic variation and heterozygosity with regional landscape and climatic variables. We developed models of land use by green jay and statistically compared these with empirical measures of genetic connectivity to characterize the likely pathways of expansion. Our findings indicate that expansion pathways are likely dependent on resource distribution in time and space. Additionally, we identify some genes which may be linked to climate adaptation at the sub-population level within the newly expanded area.

Title: Metagenomic insights into the genotypic, environmental, and temporal drivers of the coral reef microbiome

Presenting author: Carly Scott

Affiliation: Integrative Biology, University of Texas at Austin

Coauthors: Emily Nixon, University of California San Diego; Mikhail Matz, Integrative Biology, University of Texas at Austin

Abstract: Coral spawning happens in a once-per-year mass event, where individuals from many species release gametes into the water column within hours of each other. This large biomass pulse from spawning may have a large effect on the reef microbiome during this time of year. Since the coral microbiome is established horizontally from the environment, shifting changes in environmental microbial abundance may affect the colonization dynamics of offspring on the reef. Here, we generated whole genome shotgun sequencing data to quantify short-term temporal dynamics in the coral-associated community (*Orbicella faveolata*), reef benthos, and water column through a four-week experiment on St. Croix, USVI centered on spawning. All substrate types showed significant over-time community change. However, these patterns differed drastically by geography, with reefs separated by <10 km exhibiting different baseline communities and temporal patterns. For the coral associated community, we found temporal factors (time and heat stress), local environment, and host genotype were similarly important in determining microbial community structure. This opposes the current paradigm which often assumes that the local environment is the most important determinant of coral-associated microbial communities. Together, these results highlight the importance of fine-scale temporal and geographic factors in determining the coral reef microbial community. The significant genotype-level response to change we found indicates that a “personalized” approach may be necessary in understanding the coral holobiont. By using a reference-agnostic approach, we were able to identify significant diversity (200 species) not present in existing databases. Future research can incorporate time series, genotype, and metagenomic data to better understand which taxa are responsible for coral holobionts’ response to the environment.

Title: Seed dispersal dynamics across intact and regenerating tropical forests by a threatened frugivore

Presenting author: Eric Wuesthoff

Affiliation: Rice University

Coauthors: Lovasoa Ratolojanahary, Université d'Antananarivo; Rahelison Anevoka, Association des Guides de Maromizaha; Tojoharilala Fenohasina Merison; Association des Guides de Maromizaha; Jonah Ratsimbazafy, Groupe d'Étude et de Recherche sur les Primates; Amy E. Dunham, Rice University

Abstract: In tropical ecosystems, forest remnants are frequently embedded within a matrix of degraded, human-modified landscapes. Many gaps in understanding remain how frugivorous animals, like many primates, move within and between these habitats and how this may affect patterns of seed dispersal. Additional insights can offer invaluable information regarding the pivotal role frugivores perform in ecosystem processes across habitat types and may offer valuable insights for guiding forest restoration initiatives. We investigated patterns of seed dispersal by brown lemurs (*Eulemur fulvus*) within and between intact and regenerating rainforest through an ongoing field study in Maromizaha, eastern Madagascar. Our team conducted day-long follows of two *E. fulvus* social groups, recording location and identity of feeding plants where animals consumed fruit and identifying taxa of seeds dispersed in fecal deposits. From January – September 2023, we conducted 565 hours of follows, encompassing both dry and rainy seasons at our site. We found that plant species composition of lemur diets and seed fecal contents varied between seasons. Despite changes in the dietary composition, we did not observe significant differences between rainy and dry seasons in the distances traveled by lemur groups during our observation periods, suggesting that fruit resources may be equally available. We also recorded evidence of dispersal of seeds between regenerating and intact forest areas, showing a use of degraded habitats by *E. fulvus* the possible influence of these primates on plant communities in and around these sites. These preliminary results from our ongoing data collection highlight potential importance of large-bodied frugivores for seed dispersal beyond intact habitats, which is particularly important in Madagascar primates are key in facilitating this ecological process. Our findings will provide important evidence for conservation practice in Madagascar, including the community managers at Maromizaha who work to restore degraded forests and promote healthy lemur populations.

Title: Niche overlap in transition zones: the relevance of biogeographic areas in niche evolution

Presenting author: Maria A. Hurtado-Materon

Affiliation: Ecology and Evolutionary Biology Program, Texas A&M University.

Coauthors: Baltazar Gonzalez (Centro de Investigación Esquel de Montaña y Estepa Patagónica (CIEMEP), Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET) y Universidad Nacional de la Patagonia “San Juan Bosco” (UNPSJB). Roca 780, Esquel (P.C. 9200). Chubut, Argentina. Laboratorio de Investigaciones en Evolución y Biodiversidad (LIEB), Facultad de Ciencias Naturales y Ciencias de la Salud, UNPSJB. Esquel (P.C. 9200). Chubut, Argentina), A. Michelle Lawing (Department of Ecology and Conservation Biology, Texas A&M University, College Station, TX 77843) and Gabriel M. Martin (Centro de Investigación Esquel de Montaña y Estepa Patagónica (CIEMEP), Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET) y Universidad Nacional de la

Patagonia “San Juan Bosco” (UNPSJB). Roca 780, Esquel (P.C. 9200). Chubut, Argentina. Laboratorio de Investigaciones en Evolución y Biodiversidad (LIEB), Facultad de Ciencias Naturales y Ciencias de la Salud, UNPSJB. Esquel (P.C. 9200). Chubut, Argentina)

Abstract: Evoregions represent biogeographic regions where most of the resident species stem from one or a few in situ radiations. Transition zones are regions where multiple diversification and colonization events had been placed, and therefore less related to in situ diversification events. Colonization events could or could not be coupled with niche evolution. Therefore, transition zones can represent zones where several species colonize, but in the absence of niche evolution, those zones do not present independent evolutionary history. However, in cases where colonization is associated with niche evolution, transition zones are particularly relevant in terms of evolutionary history because they represent zones where independent evolutionary processes have occurred. Because transition zones are associated with geographic barriers and heterogeneity habitat, we expect species habitat in transition zones to have colonized and diversified in terms of niches in response to new environmental conditions, making their niches more differentiated between them compared with species that are only in the evoregions. We used ecological niche models to evaluate the relevance of transition zones in the evolution of Carnivora niches.

Title: Urbanization at the cost of biodiversity? Examining implications of urban growth on habitats and Key Biodiversity Areas in Indonesia

Presenting author: Abir Chaudhuri

Affiliation: Geography, Texas A&M University

Coauthors: Rakibul Ahasan, Ph.D. student, Department of Geography, Texas A&M University Burak Güneralp, Associate Professor, Department of Geography, Texas A&M University

Abstract: Urban land expansion has caused habitat loss and fragmentation across the world, and the rate has been higher in developing countries that are also the most biodiverse. Indonesia, a developing country with a rich biodiversity, has experienced significant urban growth over the last few decades. In this study, we asked where recent urban land expansion caused the largest habitat losses across the country, which species were the most affected, and if the protected status of Key Biodiversity Areas (KBAs) made any difference in terms of habitat loss to urban land expansion. To this end, we studied urban growth and its impact on habitats over a 23-year period (from 1992 to 2015) across the country as well as in and around its KBAs. Our results show that, during this period, urban land increased by 67.5% in the country and by around 8% within its KBAs. Sumatra and Kalimantan showed the highest urban expansion rates among the islands, at 124% and 99% respectively. The number of KBAs encroached by urban land cover increased by 30% overall across the period, with more protected KBAs (37% increase) being impacted than unprotected ones (29% increase). To further understand how urbanization affected habitats critical for biodiversity conservation, we analyzed urban land expansion within the ranges of threatened species across the country and within KBAs for amphibians, birds, mammals, and reptiles. Java, with the largest initial urban land area in the country,

experienced the greatest impact of urban expansion on the KBAs, species habitats, and biodiversity in the island.

Title: Abiotic and biotic factors that shape *Cassiopea* organism-environment interaction in response to global change

Presenting author: Ziyu Wang

Affiliation: Texas A&M University, Department of Biology

Coauthors: Marie Strader (Department of Biology, Texas A&M University, College Station, TX) Colin Jeffrey Anthony (Marine Laboratory, University of Guam, Mangilao, GU)

Abstract: *Cassiopea*, a genus of epibenthic scyphozoans, thrives in human-disturbed environments, displaying remarkable adaptability. In the Strader Lab, we aim to understand *Cassiopea xamachana* as a model to understand mechanisms underlying organismal responses to environmental change. *C. xamachana* have been observed in novel northern habitats off the coast of Florida, suggesting a range expansion. Through citizen science and physiological experiments, we aim to understand potential abiotic and biotic factors that may be promoting their range expansion. This includes 1) leveraging iNaturalist data to model the nuances of range expansions, phenotypic variations, and habitat dynamics; 2) delving into the role of abiotic cues, particularly light intensity, in triggering metamorphosis, with a focus on strobilation induction. Strobilation, a crucial aspect of the jellyfish life cycle, is pivotal in facilitating their dispersal. iNaturalist observations suggest a potential northward range expansion in Florida. Moreover, these observations suggest that habitat variability may influence phenotypic diversity. In controlled lab experiments, we demonstrate that polyps exposed to 200 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$ under continuous 24-hour light exhibit a notable advancement in the onset of strobilation compared to the 12:12h light/dark cycle. Conversely, the absence of light precluded strobilation. Furthermore, at 120 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$, polyps displayed robust planuloid bud production, with 44% of the population producing at least one bud per day. These findings underscore the remarkable adaptability of *C. xamachana* to diverse environmental conditions, emphasizing the intricate interdependence between organisms and their habitats.

Environmental Monitoring and Conservation

Title: Environmental DNA analysis for detection of *Poeciliopsis* in northern Sonora, Mexico.

Presenting author: Alanna Fulkerson

Affiliation: Department of Ecology and Conservation Biology, Texas A&M University

Coauthors: Alejandro Varela-Romero(2), Alexandre Gutierrez-Barragán(2), Doug Duncan(3), Mariana Mateos(1).

- 1) Department of Ecology and Conservation Biology, Texas A&M University,
- 2) Departamento de Investigaciones Científicas y Tecnológicas, Universidad de Sonora,
- 3) Retired.

Abstract: Several species of *Poeciliopsis* occur in Sonora state, Mexico; *Poeciliopsis jackschultzi* (Rio Concepcion Topminnow), is listed as endangered by the IUCN Red List, and whether it is still extant is unknown. The major threats appear to be habitat loss/degradation and invasive species. Survey efforts are hampered by the inability to use external morphology to distinguish *P. jackschultzi* from its co-occurring congeners: the Gila topminnow, *Poeciliopsis occidentalis*; and asexual hybrids whose maternal progenitor is the Headwater topminnow, *Poeciliopsis monacha*. Environmental (e)DNA provides a promising and non-invasive alternative for biodiversity and ecosystem monitoring. Here, we present the results of a metabarcoding eDNA based method aimed at detection of teleosts. We collected and filtered in situ water samples in 2022 and in 2023, based on known localities and historical occurrence of *Poeciliopsis* of interest. After DNA extraction, samples were subjected to Polymerase Chain Reaction (PCR) with the MiFish primer set, which targets a 163-185 bp region of the mitochondrial 12S rRNA gene of teleosts, and is diagnostic for our target taxa. After filtering sequenced reads, we obtained ~238 million reads associated with 2925 unique features. Unfortunately, we did not detect a single feature assigned to *P. jackschultzi*, suggesting that it was absent or at an abundance below our detection ability. After subsequent filtering, the most frequent features were assigned to the native cyprinids Sonoran Chub, *Gila ditaenia* (>147 million), and Longfin dace, *Agosia chrysogaster* (~146 million) followed by those assigned to *P. occidentalis* (> 14 million) and *P. monacha* (~ 23 million). We also detected features assigned to non-native fish known to occur in this region; Green sunfish, *Lepomis cyanellus* (~ 89 million), Bullhead, *Ameiurus melas* (> 12 million), and Western mosquitofish, *Gambusia affinis* (~ 10 million).

Title: It's all over but the drying. Managing for a post-Ogallala world

Presenting author: Ed Rhodes

Affiliation: Texas A&M University Department of Rangeland, Wildlife and Fisheries Management

Coauthors: Humberto Perotto-Baldivieso, Department of Rangeland, Wildlife and Fisheries Management, TAMU; Evan P Tanner, Department of Rangeland and Wildlife Sciences, Texas A&M - Kingsville; William Fox, Department of Rangeland, Wildlife and Fisheries Management, TAMU; Jay P Angerer, USDA-ARS, Miles City, MT

Abstract: The Ogallala Aquifer is the largest freshwater aquifer in North America, supplying irrigation water to one of the most agriculturally productive regions in the world. The Ogallala currently supports 30% of all the crop and livestock production in the United States. In the southern portion of the aquifer, natural recharge is low to nonexistent. While improvements in technology and crop genetics have increased overall water use efficiency, the Ogallala is still a diminishing resource. It is estimated that much of the Ogallala underlying the Southern High Plains will be depleted or nearing depletion by 2100. Coupled with this trend is the fact that up to one-quarter of the soil types in the region may not be suitable for dryland crop production. The impending drawdown of the Ogallala will

have dramatic repercussions on the US and world food supply chains. By integrating a mosaic of restorative practices such as rangeland reseeded, perennial improved pastures, and regenerative practices such as integrated crop and livestock systems, scientists and land managers have the opportunity to develop interdisciplinary research and management programs around the rehabilitation of the land, and reestablishing lost (as well as developing new) ecosystem services to this region. We propose that future research and extension efforts focus on interdisciplinary research aimed at addressing current and future potential land uses that can maximize ecosystem services and protect soil resources in a changing and uncertain climate. University curricula must adapt to prepare the next generation of land managers for this monumental task facing this region, as it is one that may become a test case for other regions globally.

Title: Mapping Aboveground Biomass in Oregon and California with ICESat-2 and Ancillary Data

Presenting author: Mei-Kuei Lu

Affiliation: Department of Ecology and Conservation Biology, Texas A&M University

Coauthors: Sorin Popescu & Lonesome Malambo, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Biomass mapping is important for understanding the carbon stocks of the forests and fuel assessment which can provide precious insights for management and scientific purposes. In this study we demonstrated how to utilize ICESat-2 data along with other data sources to predict biomass for the Northwestern and California coastal forests in 2016 and 2020. The model built incorporated the Landsat time series data, GEDI height data, LANDFIRE vegetation data and ICESat-2 derived height data to produce wall-to-wall biomass map. Results showed that the produced maps have high accuracy and the corresponding uncertainty maps were also created. The maps were validated with different independent validation datasets respectively: 2016 AGB map was validated with the FIA biomass hexagon data ($R^2 = 0.769$; $RMSE = 55.26$ Mg/ha) and 2020 AGB map was validated with GEDI 2019 to 2021 average biomass data ($R^2 = 0.655$; $RMSE = 73.93$ Mg/ha). GEE, a powerful cloud computing platform which provides parallel computing for fast computation, multiple commonly used satellite images and machine learning algorithms, is useful for large scale geospatial data analysis. These results show the reliability of the maps and the methods used in the study can be used to scale up the analysis from regional to national scale. Future study can include the upcoming NiSAR mission and the GEDI biomass data via flexible data fusion method for more accurate biomass mapping.

Title: Amphibian Exposure to Microplastic Pollution Linked to Hydroperiod Dynamics in an Urban IRES System

Presenting author: Andre Felton

Affiliation: University of Texas at San Antonio

Coauthors: Sue-Ellen Gibbs-Huerta, and Jeffrey Hutchinson

Abstract: Microplastic pollution is ubiquitous across ecosystems and considered one of the fastest growing sources of pollution globally. Rivers serve as major unilateral pathways of MP transport between terrestrial and marine ecosystems, yet our understanding of MP migration along rivers and exposure routes into co-occurring aquatic organisms is still limited. In this study, MP distributions and anuran activity was monitored monthly at 24 sites in two urban ephemeral rivers (Leon Creek and Salado Creek) in San Antonio, Texas between June 2021 and May 2022. Microplastics were detected in surface water and sediment at all sites ranging from 2.1 to 30.48 items L⁻¹ and 123.51 to 1359.1 items kg⁻¹. Fibers were the most abundant (~89%) MP morphotype followed by foams (7%) in both surface water and sediment samples. Potential MPs were marked and analyzed using Fourier Transform Infrared Spectroscopy (FTIR) for confirmation and polymer identification. Half of all ephemeral pool sites contained co-occurring tadpoles at various developmental stages and metamorphosed juveniles. Four different species were observed among 8 sites throughout the study. Results regarding MP intake are currently being processed and MP identifications/characterizations can be reported during presentation. As the global extent of IRES systems is projected to increase with continued climate change, understanding how MP concentrations behave with altered hydroperiod regimes can provide information regarding ecologically relevant levels that co-occurring organisms experience and entry-routes to food web interactions.

Title: Imidacloprid exposure is detectable in over one third of wild bird samples from diverse Texas ecoregions

Presenting author: Meredith Anderson

Affiliation: VIBS and EEB in Texas A&M

Coauthors: Meredith J. Anderson a, e, 1, Alan Valdiviezo d, 1, Mark H. Conway b, Christina Farrell c, R. Keith Andringa a, Amy Janik e, Weihsueh A. Chiu d, Ivan Rusyn d, Sarah A. Hamer e a. Ecology and Evolutionary Biology Interdisciplinary Program, Texas A&M University, United States of America b. Master Bird Bander, Lower Rio Grande Valley, TX, United States of America c. Master Bird Bander, San Marcos, TX, United States of America d. Department of Veterinary Physiology and Pharmacology, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, United States of America e. Schubot Center for Avian Health, Department of Veterinary Pathobiology, School of Veterinary Medicine and Biomedical Sciences, Texas A&M University, United States of America

Abstract: Avian decline is occurring globally with neonicotinoid insecticides posed as a potentially contributing factor. Birds can be exposed to neonicotinoids through coated seeds, soil, water, and insects, and experimentally exposed birds show varied adverse effects including mortality and disruption of immune, reproductive, and migration physiology. However, few studies have characterized exposure in wild bird communities over time. We hypothesized that neonicotinoid exposure would vary temporally and based on avian ecological traits. Birds were banded and blood sampled at eight non-agricultural sites across four Texas counties. Plasma from 55 species across 17 avian families was analyzed for the presence of 7 neonicotinoids using high performance liquid chromatography-tandem mass spectrometry. Imidacloprid was detected in 36 % of

samples (n = 294); this included quantifiable concentrations (12 %; 10.8–36,131 pg/mL) and concentrations that were below the limit of quantification (25 %). Additionally, two birds were exposed to imidacloprid, acetamiprid (18,971.3 and 6844 pg/mL) and thiacloprid (7022.2 and 17,367 pg/mL), whereas no bird tested positive for clothianidin, dinotefuran, nitenpyram, or thiamethoxam, likely reflecting higher limits of detection for all compounds compared to imidacloprid. Birds sampled in spring and fall had higher incidences of exposure than those sampled in summer or winter. Subadult birds had higher incidences of exposure than adult birds. Among the species for which we tested more than five samples, American robin (*Turdus migratorius*) and red-winged blackbird (*Agelaius phoeniceus*) had significantly higher incidences of exposure. We found no relationships between exposure and foraging guild or avian family, suggesting birds with diverse life histories and taxonomies are at risk. Of seven birds resampled over time, six showed neonicotinoid exposure at least once with three showing exposures at multiple time points, indicating continued exposure. This study provides exposure data to inform ecological risk assessment of neonicotinoids and avian conservation efforts.

Title: Understanding the Role of Aliefs on University Student Views on Predator Culling Contests

Presenting author: Abigail Meeks

Affiliation: Texas State University

Coauthors: Dr. Christopher Serenari (Texas State University), Anna Self (Texas State University)

Abstract: Worldviews often dictate individual and group beliefs, which then result in select behaviors. We posit that aliefs, understudied habitual mental states that activate normally negative automatic responses to a stimulus such as extreme heights, interfere in this process. Aliefs are not wholly rational, and their nature may result in individuals acting against their previous beliefs or knowledge. Though, the alief concept has yet to be applied to wildlife issues. In this study, we sought to measure aliefs through voting behavior and in the context of predator calling contests (PCCs). Predator calling contests are contests in which a large number of predators are culled with prizes given to the highest number killed or largest harvest. To explore the role of aliefs, we measured a) belief that a worldview embracing PCCs exists, b) the role of science and ethics in moderating behavior-belief connection, c) intention to vote for a PCC ban, and d) moderating influence of science and hunting ethics. To activate aliefs, we showed respondents pictures from PCCs followed with a question about how they would vote on a PCC ban right now. We emailed a link to a quantitative survey instrument to 10 Texas universities with chapters of The Wildlife Society. Responses from 168 students indicate that they believe a worldview embracing PCCs exists but would vote to ban PCCs (82%). Regression results suggest that one's belief about the existence of an alternative worldview was statistically significant ($p < 0.05$) on a respondent's decision to ban PCCs. The interaction between belief and science was statistically significant ($p < 0.05$) indicating that science may be a powerful moderator for ethics and voting behavior. Though if used improperly, scientific information may be

alienating to individuals. Understanding factors affecting decision making of stakeholders, including the role of aliefs, in controversial wildlife issues is critical for future management.

Evolution & Population Genetics

Title: Exploring the Evolutionary Dynamics of Achiasmatic Meiosis

Presenting author: Andres Barboza Pereira

Affiliation: Texas A&M University, Department of Biology

Coauthors: Heath Blackmon, Department of Biology, Texas A&M University

Abstract: Crossing over during meiosis has a dual role in cellular function and maintenance of genetic diversity. In species with chromosomal sex determination, reduced recombination between sex chromosomes is common. Sexually antagonistic variation, where an allele benefits one sex but is costly to the other, has been the primary hypothesis to explain the evolution of reduced recombination. However, other hypotheses have been proposed (e.g., epistasis, haploid and diploid selection, and reduction in aneuploidy). One mechanism to reduce recombination is achiasmatic meiosis. We investigate achiasmatic meiosis' evolutionary dynamics through a mathematical model, evaluating the support for alternative hypotheses for the evolution of reduced recombination.

Title: Measuring interspecific admixture in federally endangered Houston toads (*Bufo* [=Anaxyrus] *houstonensis*) at the main recovery site within designated Critical Habitat

Presenting author: Ferris Zughaiyir

Affiliation: Texas State University, Aquatic Resources and Integrative Biology

Coauthors: Shashwat Sirsi, David Rodriguez, and Michael R.J. Forstner, Department of Biology, Texas State University

Abstract: Evaluating introgression rates between two sympatric species is crucial when one of the species is threatened with extinction. We measured interspecific admixture in endangered Houston toads (*Bufo* [=Anaxyrus] *houstonensis*) with sympatric Gulf Coast toads (*Bufo* [=Incilius] *nebulifer*) at the Griffith League Ranch (GLR), Bastrop County, TX. From multilocus genotypes and mitochondrial sequence data, we evaluated the level and direction of admixture for contemporary populations (2020-2021) of both species. Prior assessments (2000-2008) detected higher genetic admixture in Houston toads than was indicated by phenotypic assessments. From 2000-2008, asymmetric backcrossing was observed with F1 hybrids backcrossing more frequently with Houston toads. During this previous assessment, Houston toads were at critically low numbers relative to more abundant Gulf Coast toads. An increase in Houston toad abundance and therein larger breeding aggregations was considered a potential means to alleviate hybridization for this endangered species. Hypothetically, under decreased rarity fewer opportunities for hybridization would occur. We observed an increase in the size of Houston toad breeding

aggregates detected on the GLR during our study, potentially from population supplementation efforts. However, we also found increased interspecific admixture in Houston toads. We speculate that warmer environmental conditions earlier in the year may enable additional overlap in breeding activity for these sympatric toads. We suggest further investigation into breeding periods for these toads to evaluate assumed temporal isolation in breeding activity. Our study suggests additional management strategies are required to mitigate the breakdown in premating isolating mechanisms, to alleviate hybridization and its associated problems in an endangered species.

Title: Insights into Subterranean Connectivity within the Aquifer of the Yucatán Peninsula: Population Genetics and Distribution of *Typhlatya* species.

Presenting author: Gabrielle Vaughn

Affiliation: Texas A&M University- San Antonio, Department of Natural Sciences

Coauthors: Lauren Ballou (Department of Biology, Berea College), David Brankovits (Molecular Ecology Group, Water Research Institute, National Research Council of Italy (IRSA CNR)), Efrain Chavez-Solis (Department of Sciences at Universidad Nacional Autónoma de México (UNAM)), Fernando Calderón- Gutiérrez (Department of Natural Sciences, Texas A&M University- San Antonio), Thomas M. Iliffe (NA/ Galveston, Texas, USA), Nuno Simões (Department of Sciences at UNAM) and Elizabeth Borda (Department of Natural Sciences, Texas A&M University- San Antonio)

Abstract: Species of the anchialine cave dwelling shrimp genus *Typhlatya* (Atyidae) are broadly distributed among karst subterranean estuaries (KSEs) worldwide. Found within anchialine habitats, where the ground water is stratified with fresh/brackish and saline water, *Typhlatya* species are commonly observed throughout the aquifer of the Yucatan Peninsula, Mexico. Recent phylogenetic work demonstrates the presence of at least five species, where four (*T. pearsei*, *T. mitchelli*, *Typhlatya* sp. A, *Typhlatya* sp. B) were associated with the meteoric lens of inland and coastal caves, and one (*T. dzilamensis*) identified as a salinity generalist and restricted to coastal caves with a distribution extending into marine caves in Belize. All five species were also observed as syntopic within the Ox Bel Ha cave system. This study will assess the population genetics and structure via deeper within species sampling from ~30 inland and coastal caves of the Yucatan Peninsula, including marine caves in Belize. Analyses of mitochondrial (COI, 16SrRNA, and CYTB) and nuclear (ITS and 28SrRNA) gene data will yield a better understanding of species distributions and connectivity among cave systems across the Peninsula (and beyond).

Title: Non-random recolonization after a hurricane yields rapid evolution by spatial sorting

Presenting author: Nikunj Goel

Affiliation: Department of Statistics and Data Sciences, University of Texas at Austin

Coauthors: Mattheau S. Comerford, Boston Department of Biology, University of Massachusetts, Boston, Massachusetts, 02125 Anastasia Bernat, Pacific Northwest National

Laboratory Scott P. Egan, Department of BioScience, Rice University, Houston, Texas, 77005 Thomas E. Juenger, Department of Integrative Biology, The University of Texas at Austin, Austin, Texas Timothy Keitt, Department of Integrative Biology, The University of Texas at Austin, Austin, Texas

Abstract:

Non-random survival due to extreme events can fuel rapid evolution by natural selection. However, recent work in evolutionary theory suggests that extreme events can fuel rapid evolution even without differential survival. For example, in metapopulations, extreme events can locally extirpate populations. These extinctions may cause non-random recolonization from nearby intact populations because of variation in a genetically determined dispersal trait. When these immigrants reproduce, the mean trait value in the recolonized patches changes relative to populations in nearby patches. However, this mechanism of evolution—or spatial sorting—has never been documented after an extreme event. In 2017, Hurricane Harvey struck Greater Houston, causing local extinction in soapberry bug metapopulation. Fortuitously, this happened during a survey, revealing that the mean wing length of recolonizing insects was longer than in extant populations. Combining this survey data with a novel quantitative genetics model of spatial sorting suggests that the strength of selection (std. $\beta=1.2 \pm 0.11$) was in the top three percentile of selection events observed in natural systems. Moreover, genetic crosses suggest wing length is heritable ($h^2 = 0.58 \pm 0.2$), indicating rapid evolution in soapberry bug metapopulation. Our study is the first to document spatial sorting after an extreme event and underscores the role of non-random migration in maintaining microevolutionary variation.

Plant Ecology and Adaptation

Title: Growing beyond Earth: Telomere tales of *Arabidopsis thaliana* in lunar regolith simulant and on the International Space Station

Presenting author: Borja Barbero Barcenilla

Affiliation: Texas A&M, Biochemistry and Biophysics

Coauthors: Dorothy E. Shippen, Biochemistry and Biophysics, Texas A&M

Abstract: NASA envisions sustainable colonies on the moon and on Mars by 2050, and plants will play pivotal roles in these endeavors. Here we investigate how the telomeres and telomerase of *Arabidopsis thaliana* are impacted by space flight and growth on extraterrestrial soil simulants. We report that telomere length is steady in plants grown on the International Space Station (ISS), although telomerase enzyme activity is strongly induced, increasing by up to 150-fold in roots. Ground-based studies affirmed telomerase activity is elevated in *Arabidopsis* by diverse environmental stressors, and this induction is independent of telomere length changes. There was a strong inverse correlation between genome oxidation and telomerase activity levels, suggesting plant telomerase may harbor a redox protective role that can help to facilitate survival in harsh environments. Recent studies show that *A. thaliana* can be successfully cultivated in lunar regolith, but arrests at

a terminal vegetative state and activates multiple stress responses. We found that pre-washing the simulant with an antioxidant cocktail facilitated seed setting and viable second-generation plants, but plants grown in lunar regolith simulant displayed increased genome oxidation and reduced biomass compared to Earth soil cultivation. Moreover, growth in lunar regolith simulant resulted in progressive telomere shortening and reduced telomerase enzyme activity for a variety of different *A. thaliana* accessions and in a variety of different regolith simulants. These findings highlight both the promise and the challenges of ensuring genome integrity for successful plant growth in extraterrestrial environments.

Title: Can Plants Spy On Their Friends? Plants Detect Belowground Insect-Damaged Neighboring Plants And Enhance Aboveground Defenses

Presenting author: Gage Strozier

Affiliation: Horticultural Sciences

Coauthors: Rachel Kurian Department of Electrical Engineering Texas A&M, Jayda Arriaga Biological Sciences Interdisciplinary Program Texas A&M, Morgan Thompson Department of Entomology Texas A&M

Abstract: Plants transmit ecologically relevant messages to neighboring plants through chemical cues. For instance, insect herbivory triggers the production of herbivore-induced plant volatiles (HIPVs), which can enhance neighboring plant defenses. HIPVs are emitted from directly damaged plant tissues and from systemic, non-damaged tissues. Although volatile-mediated interplant interactions have been observed both above- and belowground, it remains unknown whether belowground herbivory induces systemic HIPVs aboveground that influence neighboring plants. To explore how belowground herbivory affects interplant interactions aboveground, we characterized systemic HIPVs from squash induced by belowground striped cucumber beetle (*Acalymma vittatum*) larval herbivory. We exposed squash 'receiver plants' to systemic HIPVs or volatiles from non-damaged plants. We then measured herbivore resistance by challenging 'receiver plants' with aboveground-feeding herbivores: adult beetles (*A. vittatum*) or squash bugs (*Anasa tristis*). We discovered belowground-damaged plants emitted more (E)- β -ocimene, a key volatile from the systemic HIPV blend, than non-damaged controls, and that exposure to systemic HIPVs enhanced neighboring plant resistance to aboveground squash bugs, but not adult beetles. Further investigations into the mechanism of interplant interaction revealed β -ocimene alone can elicit plant resistance against squash bugs. Overall, our findings reveal a novel form of volatile-mediated interactions between plants spanning across aboveground-belowground plant systems.

Title: Water availability and diversity drive rooting strategies in herbaceous plants: insights from a biodiversity experiment

Presenting author: Sarah Ortiz

Affiliation: UT Austin - Department of Integrative Biology

Coauthors: Damla Cinoglu, Caroline E. Farrior, Amelia A. Wolf; all affiliated with Department of Integrative Biology, UT Austin

Abstract: The rapid decline of plant diversity within ecosystems has prompted substantial interest in the ecological consequences of biodiversity loss. Understanding the relationship between biodiversity and ecosystem function (BEF) is crucial for insight into the mechanisms governing ecosystem stability. Despite considerable efforts, a predictive understanding of the consequences of biodiversity loss, particularly in interaction with other global change factors, remains unclear. We conducted a BEF experiment in which we explicitly manipulated plant species richness phylogenetic diversity, and water availability (no additional water, +100% average rainfall). In Spring 2022 we collected species-level trait data that was used to generate shoot, root, and whole plant functional diversity metrics. At peak growth, we harvested biomass to be used as a proxy for productivity. Here, we compared metrics of biodiversity with respect to their predictive power of ecosystem function and explored how singular traits explain resource use in communities. We found a significant increase in productivity with species richness ($p = 0.003$), no relationship between PD and productivity ($p = 0.64$), and a resilience of productivity to variation in water availability across richness ($p = 0.24$) and PD ($p = 0.802$). We saw an increase in productivity as shoot functional diversity increased ($p = 0.011$, $R^2 = 0.043$), but including root traits did not increase the variance explained ($p = 0.016$, $R^2 = 0.036$). However, the community weighted mean of specific root length explains soil nitrogen in our plots ($p < 0.0001$). This relationship changes across water availability ($p = 0.009$), suggesting that rooting strategies and water availability interact to explain nitrogen acquisition in communities. Our results highlight the importance of species richness and shoot functional diversity in predicting community productivity, while emphasizing the role of root traits in the context of nitrogen acquisition and its interaction with water availability.

Title: The Ecological and phylogeographic correlates of hybridization in vascular plants

Presenting author: Lydia Morley

Affiliation: TAMU, ECCB/EEB

Coauthors: Katie Sanbonmatsu, Daniel Spalink

Abstract:

The pervasiveness of hybridization across the tree of life has become increasingly accepted in recent decades, especially within vascular plant taxa. Interspecific gene flow is coming to be recognized not just as an aberrant, albeit common, phenomenon, but an evolutionary process that is inextricably linked to speciation itself. Thus, we seek to understand not just how frequently hybridization occurs, but the conditions under which lineages are driven to hybridization. In this project, we hypothesize that the probability of hybridization and its success should be driven largely by the eco-geographic contexts under which parental species speciated and subsequently hybridized. We gathered a massive dataset of over 3 million vascular plant occurrence data, phylogeographic information, ecological, and environmental data to produce generative models that predict both hybrid occurrence and

hybrid abundance globally and regionally. We hypothesize that important variables for determining hybrid abundance are related to ongoing historical and cyclic disruption of evolved niche spaces. We also show that lineages don't hybridize uniformly across their range, but they exhibit spatial patterns of variation in hybridization tendency. In general, this study emphasizes the fact that, like divergence, gene flow is a regular evolutionary event predicted by historical, geographic, and phylogenetic factors.

Diet, Metabolism, and Morphology

Title: Of Mice and Museums: utilizing natural history collections to investigate the relationship between cranial morphology and habitat

Presenting author: Brandy Craft

Affiliation: Texas A&M University - ECCB

Coauthors: Haley N. Ellis(1), Grace L. Martindale(1), Thomas C. Yllander(1), Natalie M. Hamilton(1,2), and Sharon A. Jansa(3), and Jessica E. Light(1)

(1)Texas A&M University, College Station, TX, USA, (2)University of Alaska Fairbanks, Fairbanks, AK, USA, (3)University of Minnesota, St. Paul, MN, USA

Abstract: The *Peromyscus maniculatus* species complex is a broadly distributed rodent group consisting of nine species, stretching from Alaska and Canada south to Mexico. This group inhabits broad environmental gradients ranging from tropical and temperate rainforests to arid scrublands and deserts. Due to substantial intraspecific and interspecific variation, the *P. maniculatus* species complex serves as a model system for various evolutionary and ecological studies. This preliminary investigation examines how habitat affects skeletal morphology within the *P. maniculatus* species complex. The capacity to utilize food resources is linked to biting proficiency, which is influenced by craniomandibular morphology. Therefore, the skull shape of *Peromyscus* species can be expected to be associated with diet. As *Peromyscus* are generalized omnivores, their diet and subsequent craniomandibular morphology may differ in varying habitats due to food availability. Utilizing computed tomography (CT) scanning technology on fluid-preserved specimens from natural history collections, we employ geometric morphometric analyses to test the hypothesis that closely-related *Peromyscus* species exhibit size and shape variation in craniomandibular morphology in correlation with the environment.

Considering the diverse food resources available in different environments, we anticipate observing distinct variations in skull morphology between forested and non-forested areas. We assessed these differences by analyzing 3D shape data from landmarks positioned along homologous regions of the skull and utilized ANOVA to compare cranial shapes between forested and non-forested habitats. Our preliminary findings reveal a statistically significant correlation between skull shape and habitat type. Specifically, we noted an expansion in the overall roundness of the braincase and a reduction in the nasal area. The observed patterns of variation suggest a biological adaptation to the environment, prompting the need for further investigation.

Title: Comparative Shape Differentiation in Forelimb and Hindlimb Morphology across Habitats in the *Peromyscus maniculatus* Species Complex

Presenting author: Haley Ellis

Affiliation: Texas A&M University, ECCB

Coauthors: Brandy A. Craft(1), Grace L. Martindale(1), Thomas C. Yllander(1), Dept. ECCB & Texas A&M Natalie M. Hamilton(1),(2), Dept. Mammalogy, University of Alaska, Sharon A. Jansa(3), Dept. Mammalogy, University of Minnesota and Jessica E. Light(1), Dept. ECCB, Texas A&M

Abstract: The North American Deer Mouse (*Peromyscus maniculatus*) species complex has one of the largest geographic distributions of rodent assemblages in North America, extending from northwestern Canada and Alaska, south into the United States, and eastward to central Mexico. This widespread species inhabits numerous environmental gradients, with ecological diversity ranging from tropical and temperate rainforests to woodlands, grasslands, arid deserts, and alpine habitats. Variable morphology may result due to environmental pressures produced by each of these environments. Indeed, the incidence of local adaptation influencing parts of the appendicular skeleton has been well-documented in vertebrate species. For example, previous research found that forest-dwelling *P. maniculatus* have both longer and additional vertebrae than those from non-forested environments, leading to overall longer tails. The objective of this study was to explore and characterize how environmental gradients influence the morphology of long bones within the *P. maniculatus* species complex. We hypothesized that members of this rodent group will exhibit variation of shape in fore- and hindlimb morphology in association with habitat type, where we anticipate species that inhabit dense forested regions will display specialized limb variation compared to those in non-forested regions. To test our hypothesis, we implement 3D morphometrics to compare shape change across long bones. We used Computed Tomography (CT) scanning technology to scan fluid-preserved specimens sourced from natural history collections. Our analysis focuses on landmark data obtained from both fore- and hindlimbs. We used an analysis of variance (ANOVA) to statistically assess morphological differences between rodents in forested and non-forested habitats. This study highlights the importance of examining postcranial elements concurrently in the study of ecomorphology.

Title: The Mighty Power of a Micronutrient: How Tryptophan & Zinc Impact Mass Reared Insect Larvae

Presenting author: Kiley Stout

Affiliation: Department of Entomology

Coauthors: Jeffery K. Tomberlin, Department of Entomology, Texas A&M University. Erin M. Harris, Department of Entomology, Texas A&M University.

Abstract: Formulating diets for mass-produced insects is a key aspect of such systems. Failure to do so can result in mortality, poor growth, and low survivorship or reproduction. Historically, for the insects as food and feed industry, efforts have primarily focused on

macronutrients, such as protein or carbohydrates. However, essential micronutrients, such as amino acids, minerals, and vitamins, also have similar impacts. A slight variation outside the required amount of a single micronutrient could be the difference between survival and death. A diet imbalanced in micronutrients could interrupt associated metabolic pathways and interactions vital for insect development. Tryptophan, an essential amino acid, has been shown to increase protein content, survivorship and body weight of insects when given supplemental dietary concentrations. Select metabolites of tryptophan impact zinc storage, demonstrating how one micronutrient can directly impact another. Larvae of *Hermetia illucens* (L.) (Diptera: Stratiomyidae) and *Cochliomyia macellaria* (F.) (Diptera: Calliphoridae), which are mass-produced and used as feed, were placed in 50mL Falcon tubes in groups of 20 on their respective control diets with a doubled concentration of tryptophan, zinc, or a combination. Replicates were held at 27 °C and 65% relative humidity until the first 50% of the larval feeding stage was reached. Larval survivorship, feed conversion ratio, and weight were collected. Larval length and width were calculated using ImageJ software. Results demonstrated that supplementation of micronutrients did impact the life-history traits of both species, which can have implications within the mass-reared insect industry for diet optimization.

Title: Triatomine vector host preference in an experimental cafeteria: the impact of *Trypanosoma cruzi* infections

Presenting author: Jordan Salomon

Affiliation: TAMU eeb - VIBS

Coauthors: Jordan Salomon¹, Jeffery Tomberlin², Gabriel L. Hamer², Sarah A. Hamer²
¹Ecology and Evolutionary Biology Interdisciplinary Program Texas A&M University
²Entomology Department of Texas A&M University
³Veterinary Integrative Biosciences Department at Texas A&M University

Abstract: Triatomines are the insect vector of the Chagas disease parasite, *Trypanosoma cruzi*, which blood feeds on a diversity of hosts including mammals, birds, and herpetofauna, but only mammals are *T. cruzi* reservoirs. Accordingly, the transmission of *T. cruzi* is dependent on triatomines encountering mammalian hosts. We hypothesize *T. cruzi*-infected triatomines exhibit a preference for mammalian versus non-mammalian hosts, as compared to uninfected triatomines. We created a dual-choice olfactometer to expose individual, *T. cruzi*-infected and uninfected, starved triatomines to pairwise combinations of no host, dog, human, and chicken. Among the 25 negative control trials where a triatomine had the choice between two empty chambers, 20% of uninfected triatomines and 30% of uninfected triatomines chose an empty chamber. Of the 57 positive control trials where a host and an empty chamber were offered, 77% (17/22) of the active uninfected triatomines chose the host, whereas 58% (7/12) of the active infected triatomines chose the empty chamber over the host. In trials comparing two host options (n=80), uninfected triatomines were less active in the olfactometer (45%, 18/40) than *T. cruzi*-infected triatomines (55%, 22/40). Furthermore, uninfected triatomines displayed a preference towards dogs over chickens and humans. However when triatomines were *T. cruzi*-infected, no preference towards any of the hosts we detected. Contrary to our

hypothesis, *T. cruzi*-infected triatomines did not display a preference for mammalian hosts, however our data suggests differences in foraging behaviors between *T. cruzi*-infected and uninfected triatomines. These differences could lead to increased transmission via ingestion of a *T. cruzi*-infected triatomines and should be considered when deploying host-targeted endectocides.

Modeling Techniques in Ecology

Title: PaleoPhyloGeographic Models: Integrating paleontological, neontological, and spatial data in a phylogenetic comparative framework

Presenting author: Alexandra Howard

Affiliation: Ecology and Conservation Biology, Texas A&M University

Coauthors: Maria A. Hurtado-Materon (Texas A&M University), Julio A. Rivera (Henry M Jackson Foundation), J. Jaime Zúñiga-Vega (Universidad Nacional Autónoma de México), Emília P. Martins (Arizona State University), and A. Michelle Lawing (Texas A&M University)

Abstract: The fossil record combined with paleoclimate data provides an unparalleled resource to understand how species have responded to climate in the past and to predict how species will respond in the future. Understanding how species spatially respond to climate allows us to answer questions about range shifts and how communities organize in geographic space. Methods that project climatic niches into deep time typically do not account for the evolution of the climatic niche and as such may not accurately detect areas of ancient diversification. Here, we present PaleoPhyloGeographic Models (PPGM), that fill this gap by testing for the evolution of the minimum and maximum climatic tolerances and uses the detected evolutionary change to reconstruct ancient climate envelopes across the changing paleoclimate of the past. Our approach implements these models for any occurrence data with an associated phylogenetic framework. We show the utility of PPGM using a case study of *Sceloporus*, a genus of lizards found across North America. Previous work has shown that while modern diversity of *Sceloporus* is concentrated in Mexico, this genus initially diverged and evolved in the climate of the northern USA. Building on these previous findings, we examine the longevity of sympatric congener species communities throughout deep time (i.e. residence time). We also examine how communities assemble across their geographic range and whether different assembly patterns result in concert with changing climate. By integrating paleontological, neontological, and spatial data into a phylogenetic comparative framework, PPGM facilitates the study of macroevolution in a spatial context, and also answers questions that directly relate to conservation management and how communities of organisms organize and persist throughout time and across geographic space.

Title: Measuring and Preserving the Texas A&M Century Tree with Mobile LiDAR

Presenting author: Hailey Schmidt

Affiliation: Texas A&M - Dept. of Rangeland, Wildlife, & Fisheries Management

Coauthors: Mackenzie Nelson, Department of Ecology and Conservation Biology, Texas A&M University; Justinn Jones, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: The Century Tree, a symbol of Texas A&M University in College Station, Texas, USA, has stood since the late 1800s, embodying tradition and scholarship. To aid in its preservation, we utilized mobile light detecting and ranging (LiDAR) remote sensing technology to assess the physical attributes of this tree and generate a digital 3D model. Our study aimed to evaluate the effectiveness of laser measurements compared to traditional methods, estimate the tree's commercial value based on LiDAR, and explore the potential contribution of LiDAR to preserving items of cultural significance. Data collection and analysis occurred in spring 2023, employing allometric equations from the U.S. Department of Agriculture and equipment owned by Texas A&M AgriLife Research. Results revealed that LiDAR measurements offered superior precision in estimating tree height and diameter at breast height (dbh) compared to field methods, particularly in an urban setting. LiDAR consistently produced height values with less variation and greater precision ($\sigma_1 = 0.058$, $\sigma_2 = 0.618$), suggesting a reduction in the need for invasive or destructive sampling. The ability of LiDAR to create detailed digital renderings contributes to preservation efforts by memorializing landmarks like the Century Tree in the digital record. These digital representations not only aid preservation efforts, but also serve as valuable archival records for future generations. Our study highlights the utility of LiDAR in examining and conserving iconic natural and cultural landmarks. By providing precise measurements and detailed digital representations, LiDAR technology offers a non-invasive and effective means of monitoring and preserving valuable assets like the Century Tree at Texas A&M University.

Title: Leveraging the past to predict the future: the range dynamics of porcupines through time

Presenting author: Katie Sanbonmatsu

Affiliation: ECCB - TAMU

Coauthors: Katie Kobara Sanbonmatsu, Lydia Morley, Danielle Dillard, Heather L. Prestridge, Jessica E. Light (Department of Ecology and Conservation Biology, Texas A&M University)

Abstract: Ecological Niche Modeling (ENM) has developed as one of the most important tools for scientists and policymakers in the 21st century. It can be a critical tool for understanding how climate change will impact biodiversity. This suite of methods and algorithms are widely used both to predict future distributional changes and to understand historical range and niche dynamics. While most authors do this separately, we believe that a better understanding of the past is essential for accurate predictions of the future.

The North American Porcupine (*Erethizon dorsatum*) is not only a critical species for ecosystem health and function, but also an American Icon. Recent evidence suggests that *E. dorsatum* may currently be undergoing range expansions, but it remains unclear if they are moving to track a certain part of their niche, or if they're simply expanding or shifting their

niche occupancy. Here, we use ENMs to illuminate how *E. dorsatum* geographic range and ecological niche occupancy have shifted together through time. Then, we use this information to inform predictions for how *E. dorsatum* may respond to future climate change scenarios.

To do so, we implemented a novel approach of both hindcasting and forecasting ENMs to address two important questions. First, how have porcupines moved to track available niche space in the past several centuries? Second, based on these projections, how will porcupines change their range in the 21st century? To this end, we utilized large publicly available occurrence datasets for both *E. dorsatum* and its two most important predators (*Puma concolor* and *Pekania pennanti*) to develop several models that ultimately describe how this enigmatic mammal may respond to Anthropogenic change.

Title: Integrating Ecology and Economics for Achieving Effective Weed Management Decisions

Presenting author: Purushottam Gyawali

Affiliation: Department of Soil and Crop Sciences, Texas A&M University, College Station, TX

Coauthors: Karen Lindsey, Department of Agricultural Economics and Agribusiness, University of Arkansas, Fayetteville, AR

Ankita Ratouri, Agricultural and Biological Engineering, Purdue University, West Lafayette, IN

Steven Mirsky, United States Department of Agriculture, Agricultural Research Service, Beltsville Agricultural Research Center, Sustainable Agricultural Systems Laboratory, MD

Michael Popp, Department of Agricultural Economics and Agribusiness, University of Arkansas, Fayetteville, AR

Jason Norsworthy, Department of Crop, Soil, and Environmental Sciences, University of Arkansas, Fayetteville, AR

Muthukumar Bagavathiannan, Department of Soil and Crop Sciences, Texas A&M University, College Station, TX

Abstract: Adopting integrated weed management strategies is imperative to effectively tackle the challenge of herbicide-resistant weeds, where knowledge-based tools play a crucial role in achieving sustainable weed management, while maximizing economic returns. Decision support systems (DSSs) are invaluable tools for farmers and practitioners, aiding in the formulation of effective weed management plans. They empower users to evaluate the benefits of implementing best weed management practices and understand the potential consequences of neglecting them. In this context, a simulation model, WEEDS (Weed Ecological and Economic Decision Support System), is in development to guide weed management decision-making. Specifically targeting troublesome broadleaf and grass weed species across major agronomic cropping regions in the United States, the model is an extension of the Palmer Amaranth Management (PAM) model, initially designed for *Amaranthus palmeri* management in the Mid-Southern US. The

ongoing improvements to the WEEDS model include the integration of common waterhemp (*Amaranthus tuberculatus*) and barnyardgrass (*Echinochloa crus-galli*), problematic grass weed species. This version of the WEEDS tool simulates the long-term population dynamics of common waterhemp and evaluates economic outcomes, including Net Present Value, across various crop rotations such as corn, soybean, and cotton. While adaptable to different weed species and geographical regions throughout the United States, current efforts primarily focus on common waterhemp within the Midwestern and South-Central US. The development of the WEEDS model represents a significant step towards aligning agricultural practices with ecological well-being. By providing a practical decision-support tool, it contributes to the establishment of effective weed management practices, ensuring biodiversity preservation, soil health, wildlife habitat, and resilience to climate change.

Invasive Biology

Title: Behaving Invasively: Tracking Behavioral Syndromes Across Invasion Scales

Presenting author: Breann Richey

Affiliation: TAMU EEB ECCB

Coauthors: Michelle Lawing, Texas A&M University; Gil Rosenthal, University of Padua; Marco Zuffi, University of Pisa Museum of Natural History; Loris Di Vozzo, University of Pisa; Mirko Guasconi, University of Pisa

Abstract: Invasive species are a critical threat to global biodiversity. Invasive species modify ecosystem function, redefine global biogeographic patterns, successfully outcompete for resources, change ecosystem dynamics, and shift the trajectory of evolutionary lineages. Climate change has compounded the risk of biological invasion, resulting in unprecedented rates of new introductions. Despite the increasing prevalence of species invasions, relatively little is known about the ecological and evolutionary mechanisms facilitating invasion success. Behavior is an often overlooked mechanism of successful invasions, yet behavioral patterns are an important facilitator in the success of species invasions. This study implements an invasion behavioral syndrome to identify the roles of aggression, boldness, exploration, and neophilia across invasion stages. In this study we identify differences in invasion related behaviors between native and invasive populations of a globally invasive species, the Italian wall lizard, *Podarcis siculus*. Here, we compare data from 4 populations which differ in population age, invasion status, and invasion stage to identify how these behaviors differ across invasion status and time since invasion. This study aims to determine how invasion syndrome behaviors contribute to the invasive success of *P. siculus* across the Tuscan archipelago and mainland, and emphasizes the importance of behavioral flexibility of invasive species when they encounter novel environmental challenges. By highlighting the adaptive behaviors that contribute to invasion success in a particularly relevant and globally invasive species, this study offers valuable insights for understanding the role of behavior in invasion success.

Title: Trends in anthropogenic introductions of frogs across space and time

Presenting author: Griffin Nicholson

Affiliation: Department of Ecology and Conservation Biology, Texas A&M University

Coauthors: Lee A. Fitzgerald, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Biological invasions of anurans (frogs and toads) continue to increase, but, outside of a few exceptions such as the Cane Toad (*Rhinella marina*) invasion in Australia, anthropogenic introductions of non-native anurans have been mostly overlooked. To begin to address the global challenge posed by anuran invasions, it is critical to understand the broad patterns of these introductions. With this urgency in mind, we present here our assessment of taxonomic, spatial, and temporal trends of anthropogenic anuran introductions. As part of these trends, we determined the anthropogenic pathways of transport of non-native anurans and evaluated the relative frequency of occurrence of these pathways through time and space. Similarly, we assessed the geographic sources and sinks of anthropogenic anuran introductions and determined whether there is temporal and spatial heterogeneity in these sources and sinks. Our analyses are based on our collation of a new database of anuran invasions, which combines records and data from journal articles, natural history and geographic distribution notes, guidebooks to herpetofauna and invasive species, and citizen science and museum specimen databases. We found a continued increase in introductions of non-native anurans and that the pathways of these introductions have changed over time from primarily intentional introductions to now predominantly accidental introductions. Despite some past concerns, non-native anurans are not often introduced via the pet trade. Spatial heterogeneity exists in pathway usage and the sources and sinks of anthropogenic anuran invasions. Further research can expand these analyses to other groups of herpetofauna and can direct action towards the control of transport of non-native anurans.

Title: Impacts of invasive threats on native lizards and improving coexistence potential

Presenting author: Nicole Stevens

Affiliation: EEB/ECCB

Coauthors: Lee Fitzgerald, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Invasive species are one of the largest contributors to global biodiversity loss, especially on islands. Introduced species lack long-term coevolutionary relationships with native species in their new environments and these novel interactions often contribute to rapid population decline. Risks to native fauna can include direct predation, competition, habitat loss, and genetic changes imposed by introduced species. Our ongoing work has assessed the impacts of invasive threats on native lizards on both island and continental scales. We have examined global trends in how different factors, such as the threat type imposed by the invasive species, affect conservation status of various lizard species. Preliminary results show that mammalian predators, especially cats, are the most common

recorded threat to lizard populations and, as expected, island-dwelling lizard species are at higher risk of extinction. My talk will expand on examples of these invasive threat/native lizard systems and how to achieve higher levels of coexistence. For example, St. Croix ground lizards (*Pholidoscelis polops*) have been extirpated from much of their island range from introduced mammalian predators. Ongoing research suggests that modern landscape heterogeneity and uneven predator density may facilitate coexistence despite continued threat presence. Removal of invasive species is the most effective way to ensure the continued success of native fauna, but it is not always feasible. With research-based conservation translocations, lizard populations may be able to establish even where invasive species are still present.

Title: Exploitative competition: An invasion mechanism of the invasive lacertid lizard *Podarcis siculus*

Presenting author: Paige Hudson

Affiliation: Texas A&M University, Psychological Brain Sciences, Ecology and Conservation Biology

Coauthors: Breann Richey and Dr. Michelle Lawing, Ecology and Conservation Biology, TAMU

Abstract: Invasive species pose a significant threat to biodiversity by disrupting habitats, monopolizing resources, and displacing native species. Understanding the mechanisms behind the success of invasive species is crucial for predicting population dynamics and devising effective conservation management strategies. The Italian wall lizard, *Podarcis siculus*, is a globally invasive lacertid native to the Italian Peninsula. As *Podarcis siculus* continues to increase its native and near-native range it has displaced multiple populations of endemic lizard species. Affected native lizards are typically completely eradicated or forced into less optimal habitats. By measuring competitive exclusion through resource use and guarding, this study aims to understand the direct mechanisms through which *Podarcis siculus* successfully outcompetes native lizards. This research employs observational and experimental methods to assess the interactions between *P. siculus* and resources such as heat, food, and shelter, when in isolation versus in sympatry with *Sceloporus consobrinus*, the Prairie lizard, a similarly-sized lizard which is sympatric in *P. siculus*'s invasive range. Through this study we will quantify the magnitude of heterospecific species interactions between the Italian wall lizard and affected native species, as well as identify the behaviors that contribute to a successful invasion and exclusion of native species. Results from this study have the potential to provide critical information about resource acquisition that could be utilized in implementing proactive and sustainable conservation practices.

Species Range and Dispersal

Title: Effects of Range Management on the Plateau Spot-tailed Earless Lizard, Year 2 Results

Presenting author: Kathryn Steffen

Affiliation: Rangeland, Wildlife, and Fisheries Management

Coauthors: Danielle Walkup, Department of Rangeland, Wildlife, and Fisheries Management & Natural Resources Institute, Texas A&M University Mycha Van Allen, Natural Resources Institute, Texas A&M University Eden Fielder, Natural Resources Institute, Texas A&M University Corey Fielder, Natural Resources Institute, Texas A&M University Teresa Kenny, Natural Resources Institute, Texas A&M University Toby Hibbitts, Natural Resources Institute, Texas A&M University Roel Lopez, Department of Rangeland, Wildlife, and Fisheries Management & Natural Resources Institute, Texas A&M University Wade Ryberg, Natural Resources Institute, Texas A&M University Doug Tolleson, Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University Paul Crump, Texas Parks and Wildlife Department

Abstract: The plateau spot-tailed earless lizard (*Holbrookia lacerata*) was recently under review for federal listing due to perceived population declines. Its range includes the semi-desert grasslands of the Edwards Plateau in Central Texas. On a microhabitat scale, previous research has shown that *H. lacerata* is most often encountered on bare ground and less frequently in dense or brushy vegetation. Our research objective is to better understand which rangeland management practices cultivate microhabitat landscapes preferred by *H. lacerata*. Our second year of surveys concluded in 2023 at the Texas A&M AgriLife Research Station at Sonora in Edwards County. The Sonora Station has researched long-term control, grazing, and fire management treatments for decades, providing a well-documented landscape that focuses on rangeland practices already implemented in this region. A diverse habitat mosaic may be preferable to our target species and rangeland practices such as these are regularly used to control patches of woody vegetation and encourage such landscapes. We conducted detection surveys for *H. lacerata* using a stratified random sampling design with forty 0.8-ha circular survey plots across four treatments: control, graze, burn, and burn and graze. In year two we began vegetation surveys with a sampling design derived from the point-centered quarter method, as well as started tracking *H. lacerata*. Preliminary results show that individuals were found primarily within grazed (n=36), burned (n=22), or burned and grazed plots (n=10), with only six individuals captured in the control plots. We will continue to conduct surveys for *H. lacerata* and collect habitat data in 2024.

Title: Demographic Structure of Alligator Snapping Turtles (*Macrochelys temminckii*) Along a Fishing Pressure Gradient

Presenting author: Luke Micek

Affiliation: Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University

Coauthors: Christopher M. Schalk, Southern Research Station, US Forest Service Cord B. Eversole, Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University David R. Stewart, US Fish and Wildlife Service Jessica L. Glasscock, Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University

Abstract: The alligator snapping turtle (*Macrochelys temminckii*) is a state threatened species in Texas and a candidate for being listed as federally threatened. However, there is a lack of information on the demography of *M. temminckii* in the western portion of its range. Passive fishing gear (e.g., trotlines, limblines, juglines) has been identified as a threat to *M. temminckii*, but its impact on populations has yet to be quantified. We estimated the demographic parameters of *M. temminckii* in habitats of varying intensities of passive fishing pressure, while also quantifying the extent of passive fishing gear in aquatic habitats. From June – December 2023, we surveyed for *M. temminckii* and conducted passive fishing gear surveys at three study sites in east Texas: Alazan Bayou WMA (unfished), the Attoyac River (fished), and Shawnee (fished). We observed differences in age and sex ratios, and body size distribution of *M. temminckii* among the fished and unfished study sites. Furthermore, catch per unit effort (CPUE) of *M. temminckii* was lower at both fished sites (i.e., Attoyac and Shawnee) compared to the unfished site (i.e., Alazan). Passive fishing gear was abundant at the Attoyac and Shawnee study sites, however, the majority of devices appeared to be abandoned and all were illegally deployed (i.e., abandoned with no gear tag). These results highlight the threat recreational fishing imposes on *M. temminckii* populations and the need for increased surveillance and removal of illegal passive fishing gear.

Title: Patterns of microhabitat use by Texas tortoises in a southern Texas coastal rangeland

Presenting author: Camryn Kiel

Affiliation: Texas A&M Department of Rangeland, Wildlife, & Fisheries Management

Coauthors: Toby J. Hibbitts, Natural Resources Institute, Texas A&M University, and Biodiversity Research and Teaching Collections, Department of Ecology and Conservation Biology, Texas A&M University

Andrea B. Montalvo, East Foundation

Abstract: Understanding habitat relationships at multiple scales aids in producing effective management recommendations for wildlife species. For example, macrohabitat associations can be useful in conducting species surveys across a broader geographic range, while assessing microhabitat associations examines more specific resource use and has utility in forming site management plans. Limited research exists on such relationships for the Texas tortoise (*Gopherus berlandieri*), a species listed as threatened in Texas, where it ranges in the southern portion of the state. Generally, Texas tortoises are known to use thornscrub grassland vegetation. However, thornscrub grassland is a broad term that does not describe the finer scale variation in vegetation class cover within this vegetation community across space. We attached radio transmitters to Texas tortoises and assessed their microhabitat associations on a coastal rangeland in southern Texas to determine more detailed patterns of resource use. We examined the vegetation cover types and overall canopy cover at 1m above ground used by tortoises at the East Foundation's El Sauz Ranch in Kenedy and Willacy Counties. We collected microhabitat data at 253 tortoise locations, along with 2 random locations for each tortoise location (506 random locations) to compare microhabitat use to availability. Texas tortoises appear to use areas with higher

overall canopy cover and woody vegetation cover than is generally available, although they exhibit use of a variety of vegetation cover types. These finer scale assessments of Texas tortoise microhabitat use are necessary to inform recommendations for management action throughout their range to support their conservation.

Title: Sexual dimorphism in dispersal traits for the highly invasive Western Mosquitofish

Presenting author: Rose Blanchard

Affiliation: TAMU ECCB

Coauthors: Christopher Kopack, Department of Ecology and Conservation Biology, Texas A&M University Michelle Lawing Department of Ecology and Conservation Biology, Texas A&M University Joshua Perkin Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Dispersal, and the ability to move to novel environments is vital for surviving in a changing world. The ability to move to new environments allows organisms to access favorable habitat, increase the likelihood of finding a mate, and/or flee a degrading habitat. Studies have shown that between, and within species, individuals who disperse are not a random subset, and thus may differ in morphology. Studies on intraspecific differences, however, almost always focus on differences between male individuals, with a lack of research into differences between the sexes and the role that sexual dimorphism can play on dispersal capabilities. The Western Mosquitofish (*Gambusia affinis*) is a wonderful model species for this, given that they are sexually dimorphic, and are adept dispersers, which allows them to invade waterbodies worldwide. This study focuses on the sexual dimorphism in *G. affinis* and the influence it may have on the individual sexes ability to disperse. We utilized linear measurements, and dispersal traits to test if sexes differ in morphology related to dispersal capability. Random forest models identified which of the dispersal traits differ the most between males and females. Analyses on these dispersal traits revealed that not only do females and males differ significantly in morphology, but that females have amassed more dispersal beneficial traits than the males, and thus are predicted to have a higher dispersal capability. Given that most dispersal studies focus on male individuals, the inclusion of females is vital, especially given that they have a morphology that suggests higher dispersal capabilities, as well as the fact that most populations of this species are highly female bias. This study calls for continued investigation into female morphology, a field of study which is widely ignored.

Community Dynamics

Title: Spatially intensive fish inventories conducted 70 years apart reveal strong spatial footprints of reservoirs in a regulated temperate river

Presenting author: Johnathan Ellard

Affiliation: Texas A&M University - Dept. of Ecology and Conservation Biology

Coauthors: Rebecca Mangold, Department of Ecology and Conservation Biology, Texas A&M University Anastasia Umstott, Department of Biology, Stephen F. Austin State University Carmen Montaña, Department of Biology, Stephen F. Austin State University Kole Kubicek, Department of Biology, Lamar University Kevin Conway, Department of Ecology and Conservation Biology, Texas A&M University Joshua Perkin, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: River regulation and fragmentation affect flowing water ecosystems on a global scale, but there is rising interest in managing these alterations to benefit biodiversity and ecosystem goods and services provided to humans. A critical first step in developing management plans is estimation of historical ecological states and subsequent deviations from these states. In this study, we repeated an historical, spatially intensive fish survey conducted 70 years ago (1954-1955) in the Sabine River of Texas to assess spatiotemporal change in the fish fauna. We used the same sampling gears and visited the same locations as the previous survey, but excluded sites that are now inundated by reservoirs that did not yet exist during the historical survey. Non-metric multi-dimensional scaling plots revealed a temporally persistent (i.e., present during both periods) longitudinal gradient in fish assemblage composition, but the pattern was weaker in the second survey because sites closest to impoundments had the most altered fish assemblages. The species that contributed most to temporal change included decline of small-bodied minnows but increases by basses, sunfishes, and shads. When we divided the riverscape into three segments, the segments nearest to the upstream and downstream reservoirs showed significant declines in species richness, while the middle segment most distant from a reservoir showed no change. This work provides guidance on conservation and management of regulated rivers by delineating the spatial footprints of reservoirs and identifying the fish species most affected by this globally pervasive form of environmental change.

Title: Long-term changes in fish assemblage structure across the Neches River Basin

Presenting author: Rebecca Mangold

Affiliation: Texas A&M University

Coauthors: Johnathan Ellard, Department of Ecology and Conservation Biology, Texas A&M University Anastasia Umstott, Stephen F. Austin University, Kole Kubicek, Lamar University, Kevin Conway Department of Ecology and Conservation Biology, Texas A&M University, Carmen Montaña, Stephen F. Austin University, and Joshua S. Perkin Department of Ecology and Conservation Biology, Texas A&M University

Abstract: River regulation and fragmentation caused by dam construction are primary threats to large river fish assemblages on a global scale. However, there is increased interest in restoration of riverine ecosystems through flow regime management that mimics natural flow regimes. Long-term ecological perspectives considering historical, pre-regulated conditions and contemporary, post-regulation conditions provide valuable insight for guiding restoration decisions. In this study, we investigate stream fish

assemblage change over a 67-year period (1956 versus 2023) in the Neches River Basin of Texas. We resampled 26 sites from a historical assemblage survey conducted on the Neches River, Angelina River, and Pine Island Bayou. We used transformed abundance data, Bray-Curtis dissimilarity, and non-metric multidimensional scaling (NMDS) to quantify shifts in fish assemblage structure. The NMDS revealed truncated spatial variation through time along NMDS1 (i.e., spatial homogenization) and a distinct temporal shift in assemblage structure along NMDS2. When we mapped site-species change through time, we found the greatest levels of change occurred primarily near three reservoirs that were constructed between 1956 and 2023, while there was relatively little change at sites with greater distances from reservoirs. The majority of assemblage change was driven by species additions, not losses, including increased prevalence of fishes that typically inhabit reservoirs (bass, sunfish) or tributary streams (minnows). Our results help inform flow management by establishing historical baseline conditions, revealing the locations and fish species that have contributed to long-term shifts, and highlighting the potential for restoration (e.g., through natural flow regime mimicry) given limited loss of rare, riverine fishes.

Title: Partitioning Spatial Variation in Stream Fish Beta Diversity, East Texas

Presenting author: Anastasia Umstott

Affiliation: Stephen F. Austin State University

Coauthors: Maggie Moses, Department of Biology, Stephen F. Austin State University
Rebecca Mangold, Department of Ecology and Conservation Biology, Texas A&M University
Johnathan Ellard, Department of Ecology and Conservation Biology, Texas A&M University
Kevin Conway, Department of Ecology and Conservation Biology, Texas A&M University
Joshuah Perkin, Department of Ecology and Conservation Biology, Texas A&M University
Kole Kubicek, Department of Biology, Lamar University
Carmen Montaña, Department of Biology, Stephen F. Austin State University

Abstract: Understanding the mechanisms that influence patterns of biodiversity and community assembly at different spatial and temporal scales can aid in predicting changes in natural resources and prioritizing conservation management actions. East Texas streams harbor rich freshwater biodiversity; however, recent changes in land uses over the last decades appear to be major drivers of influencing in species richness, abundance, and distribution in this region. In this study, standardized surveys were conducted at 60 stream reaches throughout the Neches River basin and Sabine River basin, during the summer season, to examine the spatial scale (i.e., ecological region, basin, sub-basin) patterns influencing fish assemblages at local stream sites. I hypothesized significant differences in beta diversity across all regional scales. To assess this, we performed dissimilarity analyses to examine the differences in dispersion among fish assemblage compositions across all spatial scales. In addition, an additive diversity partitioning (ADP) was used to examine the relative contributions of each spatial scale to total beta diversity. Likewise, the ecological uniqueness, or species dissimilarity, of each site was calculated by local contributions to beta diversity (LCBD) partitioning. At the ecological region and sub-basin scales, we did not observe variation in beta diversity. However, at the basin scale significant differences in

beta diversity was observed. The ADP analysis suggested that the smallest spatial scales (between and within sites) explain more than half of the total beta diversity, while the LCBD suggest that five stream sites within the Neches River basin significantly contributed to the dissimilarity of all sites. Finally, species replacement (turnover) was dominant across all spatial scales. The findings of this study emphasize the importance of both broad and local-scale conservation efforts in order to maintain overall diversity and inform conservation practices.

Title: Why are there so many darters in East Texas streams? Exploring local stream environmental predictors of darter diversity and their conservation status.

Presenting author: Jordan Lindholm

Affiliation: Stephen F. Austin State University

Coauthors: Anastasia Umstott, Stephen F. Austin State University Rebecca Mangold, Texas ATM University Johnathan Ellard, Texas ATM University Joshua S. Perkin, Texas ATM University Kevin Conway, Texas ATM University Kole Kubicek, Lamar University Carmen G. Montana, Stephen F. Austin State University

Abstract: Darters, also known as “sand perches,” are members of the family Percidae, the second richest group of freshwater fishes in North America. They inhabit freshwater environments, have benthic lifestyles, and exhibit ecomorphological adaptations to variation in water depths, flows, and substrates. Their small slender bodies allow them to “dart” between and under structures found in swift-moving streams. Despite their remarkable adaptations and phenotypic differentiations, darters face conservation challenges due to anthropogenic threats. Rivers in East Texas are home to a high diversity of darters with over 15 species occurring in the region, including 5 species of Greatest Conservation Need (SGCN). In summer of 2023, we conducted standardized surveys across 60 streams in the Neches River and Sabine River basins to examine local environmental variables that could explain the distribution of darters within these basins. Given their affinity for running water and benthic lifestyles, we hypothesized that water flow and substrate composition will be the main drivers of darters diversity and their assemblage structure in these streams. A redundancy analysis performed on abundances and local habitat variables across all streams revealed that assemblage structure is influenced by substrate composition (e.g., sandy bottom), water discharge, and depth. However, when assemblages were examined by river basin, water discharge, temperature, conductivity, and sandy substrates were better predictors of the assemblages for streams in the Neches River basin, while sandy substrate alone was main predictor for assemblages in the Sabine River basin. As expected, evidence of darter habitat-affinity was observed across sites in both river basins. Our findings can aid in planning conservation decisions for darters and other SGCN in east Texas. The next steps in this research will be ecomorphological analysis of darter species in these basins to better assist in improving understanding of fish responses, vulnerability to land use changes, and conservation needs of stream fishes in Texas.

Title: Local predictors of the distribution of two endangered shiners (*Sharpnose Notropis oxyrhynchus* and *Smalleye N. buccula*) in the upper Brazos River, Texas

Presenting author: Chase Nimee

Affiliation: Department of Biology, Stephen F. Austin State University

Coauthors: Mike Curtis, Department of Biological Sciences, University of North Texas Kaley Cave, Department of Biological Sciences, University of North Texas David Hoeinghaus, Department of Biological Sciences, University of North Texas Zacchaeus Compson, Department of Biological Sciences, University of North Texas Carmen G. Montaña, Department of Biology, Stephen F. Austin State University

Abstract: Patterns of distribution and relative abundances in ecological communities depend on a complex interplay between regional- and local-scale processes. Regional processes may shape distributions due to species' broad physiological tolerances and potential for dispersal, whereas local processes associated with habitat filtering and biotic interactions determine the presence and relative abundances of species that are capable of colonizing a potentially suitable location. Understanding local drivers of community structure has important implications for management and conservation of imperiled species. In this study, we investigated the relationship between local abiotic and biotic variables and the distribution of federally endangered Sharpnose (*Notropis oxyrhynchus*) and Smalleye (*N. buccula*) shiners endemic to the upper Brazos River, Texas. Stream reaches of the upper Brazos River are dynamic, and changes in the historical hydrology of this area due to anthropogenic activities have raised conservation concerns for imperiled fishes, including these two endangered shiners. Over one year, we conducted monthly field surveys of fishes and quantified environmental parameters at 22 sites in the Salt Fork [SF], Double Mountain Fork [DMF], and Brazos River mainstem [BRM]. In general, Sharpnose and Smalleye shiners were broadly distributed along the BRM and DMF but were largely absent from the SF. Variation in distributions across seasons was explained by local factors, including wetted width, depth, flow, and conductivity. Furthermore, Random Forest Models demonstrated significant relationships between instream conditions and the presence of Sharpnose and Smalleye shiners. For example, important predictors of the presence of Smalleye included the absence of macrophytes, low temperatures, and high amounts of woody debris, whereas less algae, greater canopy cover, and continuous flow throughout the year appear to be driving Sharpnose distributions. These findings emphasize the importance of environmental variables related to hydrology and habitat structure in shaping the distribution of two imperiled species in the upper Brazos River.

Title: Building up ecological indicators for the assessment and recovery of estuarine ecosystems in the wake of external disturbances

Presenting author: Bailey Lin

Affiliation: Texas A&M University at Galveston, Department of Marine Biology

Coauthors: Hui Liu, Department of Marine Biology, Texas A&M University at Galveston

Abstract: Estuaries are vulnerable to natural and anthropogenic disturbances. Over the past few decades, Galveston Bay, Texas, has experienced man-made disasters (oil spills, chemical pollutions etc.), and major hurricanes. Ecosystem management requires high-

quality ecosystem components data that is collected through carefully designed monitoring programs, which are often insufficient in reality but are highly necessary for managers and stakeholders. This project is designed to monitor long-term zooplankton dynamics (i.e., species composition, abundance, and diversity) along with environmental factors including salinity, temperature, and Chl-a in order to inform science-based decision making regarding estuarine ecosystems. Since September 2022, monthly sampling has been ongoing along a salinity gradient in the bay using two mesh plankton nets (100 μm and 200 μm) along with environmental factors including salinity, temperature, and Chl-a. Data from September 2022 to January 2023 indicate strong associations between the diversity index and zooplankton density. Data also indicates that during this time period the copepod species *Acartia tonsa* had the highest total relative abundance throughout Galveston Bay. Additionally, we will explore the relationship between zooplankton abundance and distribution in relation to environmental variables in the bay. The results of this research will contribute to our understanding of estuarine zooplankton dynamics in terms of prudent management of estuarine ecosystems after external perturbations.

Title: Mapping the Microbial Landscape of Porites Corals: the effect of age, environment, and genotype

Presenting author: Raegen Schott

Affiliation: The University of Texas at Austin

Coauthors: Carly B Scott, Department of Integrative Biology, The University of Texas at Austin. Mikhail Matz, Department of Integrative Biology, The University of Texas at Austin.

Abstract: Coral reefs face unprecedented challenges due to climate change and human activities. The interplay between corals and their associated microbiomes offers a potential avenue for understanding and bolstering coral resilience. The *Porites* species complex is notorious for harboring a significant amount of cryptic genetic structure. How this complex genetic structure shapes the microbiome, however, is still unknown. Here, we show that age, local environment, and host genetics all are drivers of microbial community assembly. To gain a deeper understanding of this, we looked at differences in microbial diversity and taxa between juvenile and adult massive *Porites* from three sites at Orpheus, Island Australia. Massive *Porites* can live to be over 400 years old, which provides long-term insight into microbial flexibility. We calculated microbial community beta diversity across sites and age classes in addition to determining differentially abundant taxa between groups. We found that adults have significantly less community diversity than juveniles, indicating microbial winnowing over time. We also identified *Endozoicomonas* as the largest differentially abundant taxon between age classes; this bacteria is widely thought to beneficially contribute to the coral holobiont, as it likely plays a role in nutrient cycling and amino acid synthesis. Furthermore, there were differences in diversity and abundant taxa between sites, this includes differentially abundant microbiota such as *Endozoicomonas* and the often-pathogenic *Vibrio*. Together, these results demonstrate that the coral holobiont becomes more specific with time and certain environments likely select for a specific community.

Title: Response and resilience of karst subterranean estuary communities to precipitation impacts

Presenting author: Fernando Calderon Gutierrez

Affiliation: Texas A&M University - San Antonio; Department of Natural Sciences

Coauthors: Thomas M. Iliffe (NA / Galveston, Texas, USA), Elizabeth Borda (Texas A&M University - San Antonio; Department of Natural Sciences), German Yañez (Circulo Espeleologico del Mayab), Jessica Labonté (Texas A&M University at Galveston; Department of Marine Biology)

Abstract: The impact of meteorological phenomena on ecosystem communities of karst subterranean estuaries (KSEs) remains unknown. KSEs are characterized by vertically stratified groundwater separated by a halocline, and host endemic aquatic cave adapted fauna (stygobionts). In October 2015, eight days of heavy precipitation caused the first recorded mortality event in the KSE. This event was marked by a halocline shift 5 m deeper. The present study aimed to provide insights into resilience of KSEs faunal communities to temporal shifts in temperature and precipitation. Cave water temperature decreased on average 0.0068°C per mm of accumulated precipitation over four days. Biological surveys (2012-2021) conducted within cave systems El Aerolito and La Quebrada, in Cozumel, indicated that change in community structure was not detected and stygobionts were resilient, however, marine species inhabiting the caves were impacted. Overall, stygobiont communities of KSEs remain resilient to short-term meteorological phenomena despite density shifts of some community members.

Poster Session 1

Texas Tropical Network Posters

Title: Exploring the diversity of cichlid fishes in rivers of Guyana, South America

Presenting author: Megan Beeksm

Affiliation: Stephen F. Austin State University

Coauthors: Sophie Scott, Stephen F. Austin State University Lily William, Stephen F. Austin State University Takiya Jackson, Texas A&M University Kendall Hastings, Texas A&M University Calvin Young, Texas A&M University Chelbie Gilkes, University of Guyana Akeem Sinclair, University of Guyana James Vankley, Stephen F. Austin State University Donald B. Burt, Stephen F. Austin State University Leslie Winemiller, Texas A&M University Kirk Winemiller, Texas A&M University Carmen Montana, Stephen F. Austin State University

Abstract: Neotropical rivers are notable exceptional for their high diversity and endemism of fishes. Fishes in the family cichlidae (i.e., cichlids) are taxonomically and morphologically diverse and occupy a variety of habitats making them ideal organisms for exploring morphological aspects related to habitat use and trophic ecology. In May 2023 during the

early phase of the rising water season which occurs from April to August, we surveyed assemblages of cichlids inhabiting floodplain lakes and main channel of the Rupununi River in Guyana using multiple types of fishing gears. Given the diversity of morphological adaptations, we expected to see a relationship between fish morphology and habitat use. Surveys of littoral habitats yielded 18 cichlid species contained in 12 genera. Although survey effort differed among locations, more species were collected from floodplain lakes (n=17) compared to sites in the river channel (n=4). Cichlid species richness was greater than previous reports for the same area of the Rupununi River which reported nine species. We measured 28 morphological traits related to swimming performance, habitat use, and trophic ecology on 104 preserved specimens. A principal components analysis (PCA) performed on log-transformed morphological data suggested two dominant gradients in morphospace: First gradient (PCA1) ordinated cichlid species between elongate, wide bodies and deep, laterally compressed bodies, while the second gradient (PCA 2) ordinated species between short snout with small mouth gape to long snout with large mouth gapes. Our surveys highlight the diversity of cichlids in the Rupununi region in South America during the rising water season; but also provide baseline data for assessing freshwater biodiversity using morphological traits that can help predict responses of species to land, water, and habitat changes. Given the rapid expansion of anthropogenic activities in the region, we expect our results can help to promote research in rivers of Guyana because there is a sense of urgency of exploration of these rivers to document biodiversity before it disappears and the status of these ecosystems.

Title: Water availability and extreme events under climate change scenarios in an experimental watershed of the Brazilian Atlantic Forest

Presenting author: David Costa

Affiliation: TAMU Department of Ecology & Conservation Biology

Coauthors: David de Andrade Costa^{1,2}, Yared Bayissa², Mariana Dias Villas-Boas³, Jader Lagon Junior¹, Antônio J. Silva Neto⁴, Raghavan Srinivasan² ¹ Federal Fluminense Education, Science and Technology Institute, Campos, RJ, Brazil; david.costa@iff.edu.br, jlagonjr@gmail.com, ² Department of Ecology and Conservation Biology, Texas A&M University, College Station, TX 77843, USA; yared.Bayissa@ag.tamu.edu, raghavan.srinivasan@ag.tamu.edu ³ CPRM—Geological Survey of Brazil, Rio de Janeiro, Brazil; email: mariana.villasboas@cprm.gov.br ⁴ Department of Mechanical Engineering and Energy, Universidade do Estado do Rio de Janeiro, Nova Friburgo, RJ, Brazil; ajsneto@iprj.uerj.br

Abstract: Climate change has become a global concern, exacerbating weather and climate extremes, and leading to significant adverse impacts and associated losses and damages. According to the Intergovernmental Panel on Climate Change's (IPCC) sixth assessment report – AR6, approximately 3.3 to 3.6 billion people are estimated to reside in highly vulnerable contexts. Hydrological modeling plays a crucial role not only in assessing the potential impacts of climate change on water resources but also in evaluating the effectiveness of mitigation actions. This study focuses on evaluating the effects of climate change on water balance and extreme events in the Brazilian Atlantic Forest region. By

incorporating precipitation and temperature variability from 32 global climate models and their ensemble means, along with two regionalized climate models, the study aims to comprehend the projected climate change boundaries on water balance at the watershed level. The Soil and Water Assessment Tool (SWAT) is utilized for this purpose. The findings highlight the critical implications of climate scenario boundaries outlined in the sixth IPCC report for the Atlantic Forest region of southeastern Brazil. They underscore the significant consequences of climate change on rainfall patterns and streamflow, which vary depending on the specific IPCC climate scenarios utilized. Furthermore, the study emphasizes the importance of refining rain discretization methodologies, particularly in mountainous regions like the Atlantic Forest, where high variability exists, and global climate models struggle to capture finer-scale variations. Even regional climate models with a resolution of 20 km fail to adequately represent this variability in mountainous regions. The study emphasizes the need to prioritize adaptation and mitigation strategies to better prepare for the diverse impacts of climate change, including flooding events and water scarcity, which can have profound effects on regional economies.

Title: How high do they go? Comparison of maximum food chain length in channel and floodplain habitats of the Rupununi River, Guyana

Presenting author: Takiya Jackson

Affiliation: Texas A&M University

Coauthors: Calvin Young, Texas A&M University Kendall Hastings, Texas A&M University Kirk Winemiller, Texas A&M University Leslie Winemiller, Texas A&M University Sophie Scott, Stephen F. Austin State University Megan Beeksma, Stephen F. Austin State University Lily Williams, Stephen F. Austin State University Carmen Montaña, Stephen F. Austin State University Donald Burt, Stephen F. Austin State University James VanKley, Stephen F. Austin State University

Abstract: We collected fishes from several channel and floodplain habitats of the Rupununi River, Guyana, during the end of the low-water season. We used stable isotope analysis of fish tissue samples to test the hypothesis that food chain length (maximum vertical trophic position of top-predator fishes) was longer in floodplain lakes than the river channel, with the former having higher aquatic productivity. Based on comparison of nitrogen stable isotopes ratios (an indicator of vertical trophic position) of predatory fishes and fishes feeding near the bottom of food chains, we infer that maximum food chain length was only slightly longer in floodplain habitats. Top predators in the river channel were large piscivorous piranhas and payaras (Characiformes) and catfishes (Siluriformes); in floodplain lakes the top predators were small scale and fin-feeding piranhas. Interestingly, several small zooplanktivorous fishes (anchovy, characiformes, dwarf cichlid) were at trophic positions similar to or higher than the positions of piscivorous piranhas, catfishes, croakers, and peacock bass. We conclude that fishes at the top of food webs in Rupununi floodplain lakes are supported by aquatic primary production via two predominant pathways: microphagy vs. macrophagy. In contrast, food chains in the river channels tend to transfer biomass to fishes of successively larger size (macrophagy).

Title: Intraspecific Diel Temporal Niche Conservatism and Assemblage-Wide Overlap in Neotropical Bats

Presenting author: Kaitlyn Patterson

Affiliation: Department of Biology, Texas State University

Coauthors: Ivan Castro-Arellano, Department of Biology, Texas State University

Abstract: Studies of food and habitat niche partitioning have a long standing in ecology. However, studies about the role of temporal activity patterns as a potential mediator of species interactions are scarce. Knowledge about mammalian temporal niches could aid our understanding of patterns of species richness and composition in each community, a major goal in ecology. The purpose of this project is to evaluate intraspecific temporal niche conservatism against geographical variation while concurrently assessing temporal overlap within each local community in neotropical bats. Mist-netting data being contributed from various researchers will be analyzed with a null model approach using a specific algorithm (i.e., ROSARIO) developed for time analyses. Circular statistics will be used for diel pattern characterizations and pairwise species comparisons at local communities. The activity patterns will then be compared within each species to ascertain if geographical variation or temporal niche conservatism is the dominant pattern for neotropical bats. We expect species will exhibit intraspecific temporal niche conservatism over geographical variation, as well as steady patterns of interspecific temporal overlap within local sites. Overall results from this study will continue to augment our understanding of the structure of neotropical bat assemblages.

Title: Freshwater fish diversity in a river of the Guiana Shield: The Rupununi River – Guyana

Presenting author: Sophie Scott

Affiliation: Stephen F. Austin State University

Coauthors: Megan Beeksma, Department of Biology, Stephen F. Austin State University Lily Williams, Department of Biology, Stephen F. Austin State University Takiya Jackson, Department of Ecology and Conservation Biology, Texas A&M University Kendall Hastings, Department of Ecology and Conservation Biology, Texas A&M University Calvin Young, Department of Ecology and Conservation Biology, Texas A&M University James VanKley, Department of Biology, Stephen F. Austin State University Donald B. Burt, Department of Biology, Stephen F. Austin State University Leslie Winemiller, Department of Ecology and Conservation Biology, Texas A&M University Kirk Winemiller, Department of Ecology and Conservation Biology, Texas A&M University Chelbie Gilkes, Department of Biology, University of Guyana Akeem Sinclair, Department of Biology, University of Guyana Carmen G. Montaña, Department of Biology, Stephen F. Austin State University

Abstract: Rivers within the Guiana Shield in South America possess a rich freshwater biodiversity with a high degree of endemism. The Rupununi region, situated in the Central Rupununi savannas, is influenced by hydrological seasonality, with flooding during the wet season that creates aquatic habitat connectivity between the Rupununi River (Essequibo

Basin) and the Branco River (Amazon Basin). This connectivity facilitates potential exchange of fish and other aquatic organisms between these river basins. In May 2023, we surveyed fish assemblages in littoral habitats at sites within the Rupununi River and associated floodplain lakes near Yupukari Village during the early phase of the annual flood pulse. The river channel was characterized by sandy substrates with low total dissolved suspended solids (TDS), and moderate to rapid water velocity; whereas floodplain lakes had substrates dominated by detritus, leaf litter, and woody debris, higher TDS, and no flow. Surveys using multiple fishing gears yielded a total of 139 fish species (847 individual fish), with more species in floodplain lakes (90 spp.) compared to the river channel (73 spp.), and an overlap of 22 spp. between the two habitat types. Most species were contained in two species-rich taxonomic orders: Characiformes (e.g., characids and tetras) and Siluriformes (e.g., catfishes). Eleven trophic guilds were identified, with omnivore and carnivore guilds being most common in both habitats. The parasitic guild (trichomycterid catfishes) was more common in the river channel, and detritivores were common in floodplain lakes. Our results fill knowledge gaps concerning fish diversity in the Central Rupununi Region during the rising water season. Future research will use stable isotope analysis to estimate trophic niche diversity among major taxa and infer basal production sources supporting fish biomass in river channel and floodplain habitats.

Title: Analysis of South American Characiform species between river and floodplain lake littoral habitats

Presenting author: Calvin Young

Affiliation: Texas A&M University, Department of Ecology and Conservation Biology

Coauthors: Kendall Hastings, Department of Ecology and Conservation Biology, Texas A&M University Takiya Jackson, Department of Ecology and Conservation Biology, Texas A&M University Kirk Winemiller, Department of Ecology and Conservation Biology, Texas A&M University Leslie Winemiller, Department of Ecology and Conservation Biology, Texas A&M University Sophie Scott, Department of Biology, Stephen F. Austin State University Megan Beeksmma, Department of Biology, Stephen F. Austin State University Lily Williams, Department of Biology, Stephen F. Austin State University Carmen Montaña, Department of Biology, Stephen F. Austin State University Donald Burt, Department of Biology, Stephen F. Austin State University James VanKley, Department of Biology, Stephen F. Austin State University

Abstract: The Guiana Shield region of South America has one of the richest freshwater fish faunas on Earth. We surveyed fishes in several littoral habitats of the Rupununi River channel and its surrounding floodplain lakes in southwestern Guyana. Using multiple collection methods, we documented 35 species in the hyper-diverse order Characiformes (tetras, piranhas and related species). Specimens were measured for standard length. Species were classified into trophic guilds, and the size structure and guild structure of assemblages were compared between channel and floodplain habitats. On average, characiform fishes were larger in the littoral habitats of floodplain lakes. The river channel and floodplain lake samples were both dominated by omnivores, but samples from

floodplain lakes also had many piscivores and detritivores. Further surveys and analysis of other fish taxa will further our knowledge of fish biodiversity in this tropical region.

General Poster Session

Title: Contrast of diel activity patterns versus body mass in Asian Euungulates: ecological, evolutionary, and conservation implications.

Presenting author: Namrata Bhandari

Affiliation: Biology Department, Texas State University

Coauthors: Ivan Castro-Arellano, Biology Department, Texas State University

Abstract: Ungulates are relevant for ecosystem dynamics through herbivory, seed dispersal, seed predation, and being important prey for large carnivores. But anthropogenic factors are causing widespread loss of ungulates worldwide. Understanding the behavioral ecology of daily activity patterns of ungulates can not only aid their conservation but also provide an opportunity to get insight into mammalian temporal niches. The tendency of species and clades to use similar diel activity patterns over time (i.e., temporal niche conservatism) could be relevant for ecological processes. Animal activity patterns are dependent on body mass through metabolic and thermoregulatory processes and thus our expectation is that body mass will affect diel patterns of ungulates: Large herbivores require higher energy, so they will spend longer time foraging, are tolerant to low nutritional food, and tend towards being cathemeral (low directionality), whereas small herbivores likely spend less time foraging, feed on high nutritional food and will tend to be time specialists (high directionality). This study will evaluate these relationships using data from sites in Asia and Texas ranches (i.e., exotic populations). We will use time-stamped camera trap data from freely available data repositories plus fieldwork in Texas. Data will be analyzed using R statistical programming (Activity and Overlap packages), Oriana circular statistical software, and ROSARIO to determine Kernel density estimation and daily activity overlaps among and within species. Findings from this study will show the influence of body mass of different ungulates on activity patterns from local and global scales, which aids in making informed decisions for their management and conservation.

Title: Evaluating Small Mammal Biodiversity using Camera Traps

Presenting author: Amanda Laboy

Affiliation: Texas A&M Department of Rangeland, Wildlife, and Fisheries Management

Coauthors: Ty Werdel, Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M

Abstract:

The small mammal community within the Post Oak Savanna Ecoregion of the Ecological and Natural Resource Teaching Area at Texas A&M University has been historically

understudied. Despite the forthcoming management interventions aimed at combating woody encroachment through techniques like fire, herbicide, and mechanical removal, little is known about the composition of this small mammal community. Our research aims to fill this gap by establishing an efficient survey method for small mammal richness and diversity. In our pilot study, we deployed ten modified bucket camera traps, each equipped with two cameras: one facing downward and the other outward. Half of these traps were baited to investigate potential increases in detection compared to un-baited sites. Preliminary findings indicate a greater detection rate for baited sites among species such as white-footed mice, armadillos, fox squirrels, and opossums. By extending the duration of our study and expanding the number of baited camera trap sites, we aim to comprehensively assess small mammal richness and diversity before and after the implementation of management practices. Through this approach, we expect to observe changes within site occupancy, richness, and diversity of small mammal communities in this Post Oak Savanna and how the small mammal community responds to woody encroachment management, offering contributions to the ecological understanding and conservation strategies in similar ecosystems.

Title: The influence of a novel immune challenge on immune cell proliferation in the purple sea urchin, *Strongylocentrotus purpuratus*, based on disease state

Presenting author: Imogen Southerland

Affiliation: Texas A&M Biology Department

Coauthors: Dr. Amy Tan, Department of Biology, Texas A&M University; Dr. Marie Strader, Department of Biology, Texas A&M University

Abstract: Purple sea urchins, *Strongylocentrotus purpuratus*, are a keystone species in kelp forests along the Pacific coast of North America, maintaining a delicate balance between kelp overgrowth and overgrazing that causes urchin barrens. Elevated marine temperatures have the potential to disrupt this balance by increasing the transmission of pathogens such as black spot disease that causes softening and erosion of the internal skeleton. The echinoderm innate immune system primarily functions through recognition of non-self cells and responds with phagocytic defenses. The immune cells—coelomocytes—are usually found dispersed throughout the coelomic fluid but activate, proliferate, and migrate to infection sites when injury or pathogens are detected. There is limited information about the production and differentiation of new coelomocytes, how they are produced, or how quickly they activate following pathogen exposure. Therefore, in this experiment, we exposed animals with conspicuous black spot lesions and those without lesions to a novel immune challenge and compared their immune responses. Urchins were injected with sheep erythrocytes (a novel immune challenge) and coelomocyte numbers were counted 1, 6, and 24 hours after injection to assess whether immune response was enhanced or compromised by immunoquiescence (urchins housed in the lab aquarium for 4 months), disease (urchins with black spot lesions), or baseline immune activation (urchins in the lab aquarium for <1.5 months). These results reveal how *S. purpuratus* could be impacted by, and combat, increased exposure to disease.

Title: Space Use, Movement, and Survival of Translocated Desert Bighorn Sheep in Sonora, Mexico

Presenting author: Dylan Stewart

Affiliation: Texas A&M University, Department of Rangeland, Wildlife, and Fisheries Management

Coauthors: E. Alejandro Lozano-Cavazos, Departamento de Recursos Naturales Renovables, Universidad Autónoma Agraria Antonio Narro; Stephen Webb, Texas A&M Natural Resources Institute, and Department of Rangeland, Wildlife and Fisheries Management, Texas A&M University

Abstract: Mountain sheep abundance across North America has declined >60% from historic times. In response, state and federal agencies have conducted >1,000 reintroduction projects, translocating >21,000 bighorn sheep. Despite these efforts, ~50% of reintroductions are considered unsuccessful, leading researchers to stress the importance of post-release monitoring on the overall success of future reintroductions. Our objectives were to quantify space use, movement, and survival of translocated desert bighorn sheep (*Ovis canadensis mexicana*). We conducted our research in the Sierra El Alamo Mountains, ~45 km W of Caborca, in northwestern Sonora, Mexico. We captured and fitted 16 bighorn sheep (9 females, 7 male) with GPS collars, which collected 1 GPS fix every 3 hours starting in November 2023. We created monthly 95% Brownian bridge movement models (BBMM), calculated monthly distance travelled, and used the Kaplan-Meier methods to estimate survival. Monthly home range size for females was greatest in April (1,319 ha) and least in September (291 ha). Similarly, for males, home range size was greatest in February (1,533 ha) and least in October (513 ha). Cumulatively, movement was greatest from April through June (~49 km) for females and from February through April (~52 km) for males; movement was least in October and December for both sexes. Annual survival (November 2023 to November 2024) was 81% (13/16) for both sexes. Early post-monitoring data suggest the reintroduction effort was successful because annual survival was high, and reintroduced sheep joined herds with native sheep and settled into the study area quickly.

Title: Towards a temporal theory of ecology; The role of body mass activity budgets of North American Artiodactyls

Presenting author: Brian McElligott

Affiliation: Texas State University, Biology Department

Coauthors: Ivan Castro-Arellano, Department of Biology, Texas State University

Abstract: Energy dynamics can shape ecological patterns and impact the evolutionary trajectory of a species. The metabolic theory of ecology links body mass to multiple ecological traits. This study seeks to extend these insights to activity patterns at a macroecological scale, using the large repository of camera trap dataset to explore the relationship between body mass and diel patterns of activity of North American artiodactyls. Artiodactyla, a diverse mammalian order, reflects episodes of rapid evolution

driven by climate volatility, resulting in a wide range of body sizes and morphologies. Investigating phylogenetic niche conservatism and intraspecific diel temporal niche conservatism will help us understand the evolutionary drivers of activity patterns. We predict that as the strength of niche conservatism increases, the directionality of activity will decrease in artiodactyls. Concurrently, as we compare a gradient of body masses of artiodactyl species, we expect the directionality of activity will decrease. Larger species will tend to be time generalist, while smaller species will tend to be time specialists. This would then help support the hypothesis of a positive relationship between body mass and temporal niche conservatism. This study contributes to a previously unexplored aspect of macroecology relationships at a continental-scale approach by addressing the relationship between body mass and activity patterns in North American artiodactyls within the context of temporal niche conservatism

Title: Mesohabitat and macroecological correlates of Blue Sucker occurrence in regulated rivers

Presenting author: Hannah Evans

Affiliation: Texas A&M University - Rangeland, Wildlife, and Fisheries Management

Coauthors: Meghan Booknis - Department of Ecology and Conservation Biology, Texas A&M University
Rebecca Mangold - Department of Ecology and Conservation Biology, Texas A&M University
Johnathan Ellard - Department of Ecology and Conservation Biology, Texas A&M University
Joshuah Perkin - Department of Ecology and Conservation Biology, Texas A&M University
Hayden Roberts - Department of Ecology and Conservation Biology, Texas A&M University
Noah Santee - Department of Ecology and Conservation Biology, Texas A&M University
Jacob Wolff - Department of Ecology and Conservation Biology, Texas A&M University
David.L.Smith@erdc.dren.mil - U.S. Army Corp of Engineers

Abstract: Blue sucker (*Cypleptus elongatus*) populations occur in the Mississippi River and Gulf of Mexico drainages of North America and are negatively affected by habitat fragmentation and flow regime alteration caused by dams. During fish assemblage surveys in August of 2022, we collected five juvenile blue suckers (312–428 mm total length) in the Angelina River upstream of Sam Rayburn Reservoir in East Texas (46,335 ha surface area) where the occurrence of the species was previously unconfirmed. Given this unexpected finding, we (1) analyzed mesohabitat associations to compare habitats we sampled with reports in the literature and (2) reviewed blue sucker occurrences in state, national, and global databases across historical (1950–1980) and contemporary (1981–2022) time periods to assess occurrence across gradients of habitat fragmentation and streamflow regulation. The blue sucker population in the Angelina River upstream of Sam Rayburn Reservoir was previously unconfirmed but is within the native range. Mesohabitats occupied by blue suckers were consistent with literature reports, including fast velocity, shallow depth, and coarse substrates. The low degree of regulation (19% of natural runoff stored by upstream reservoirs) and a high degree of habitat connectivity (287 rkm of unfragmented mainstem habitat) for the Angelina River upstream of Sam Rayburn Reservoir matched range-wide patterns of persistence within relatively intact (unfragmented and unregulated) or remnant (fragmented but unregulated) riverscapes.

Our review reveals that blue sucker populations might persist (1) in remnant river fragments where local habitat conditions are appropriate and (2) where effects of habitat fragmentation and flow regulation are not coupled.

Title: Integrating stream ecosystem theories into spatial modelling of fish richness and assemblage structure

Presenting author: Lucas Stevens

Affiliation: Texas A&M University Ecology and Conservation Biology

Coauthors: Lucas Stevens, Lauren E. Yancy, Noah S. Santee, Emily B. Parker, Jake Madewell, Fernando E. Chavez, Hannah Evans, Jacob P. Wolff, and Joshua S. Perkin (All Department of Ecology and Conservation Biology)

Abstract: Freshwater streams are frequently fragmented by dams, road crossings, and flood control infrastructure that have the potential to significantly affect stream fish assemblages. Separating natural versus anthropogenically-derived assemblage structuring mechanisms within fragmented riverscapes is challenging. Riverscape concepts such as the river continuum concept (RCC), serial discontinuity concept (SDC), and network dynamics hypothesis (NDH) conceptualize the roles of natural and anthropogenic regulators of assemblage structure along longitudinal gradients in streams. We surveyed fish assemblages and habitat variables across three years from 40 sites along the longitudinal dimension of White Creek, a headwater stream in College Station, Texas, to test theory-based hypotheses regarding the structuring of fish metacommunities. To achieve this goal, we constructed asymmetric eigenvector maps (AEMs) that integrated aspects of RCC, NDH, and SDC theories and used these AEMs to test three hypotheses. We hypothesized that: (H1) fish species richness would increase in a downstream direction but fragmentation by road-stream crossings would disrupt this increase, (H2) spatial contexts based on the RCC, SDC, and NDH would explain more variation in metacommunity structure compared to a neutral model, and (H3) distinct fish assemblages would exist within fragments of stream created by impassable road-stream crossings. Competing generalized additive models based on stream theories revealed the SDC was the top-ranked model for predicting longitudinal increase in species richness, supporting H1. Spatial variables based on AEMs integrating stream ecosystem theories (particularly the SDC) explained more variation in assemblage structure relative to the neutral model, supporting H2. Assemblage clustering and ordination showed unique assemblage structure in three of the four fragments, providing partial support for H3. Our results help to bridge the gap between theory and conservation of stream fishes by revealing that integration of stream ecosystem theories provides insight to origins of spatial processes that regulate assemblage structure.

Title: Investigating variation in cave habitat use among mammal species in response to soft tick abundance

Presenting author: Brianna Mena

Affiliation: Department of Biology, Texas State University

Coauthors: Ivan Castro-Arellano, Department of Biology, Texas State University

Abstract: Ticks are relevant vectors that play a crucial role in zoonotic pathogenic cycles. With a rise in tick-borne diseases (TBDs) in North America, it is imperative to identify reservoir hosts where certain TBDs are endemic. While the soft tick *Ornithodoros turicata* is recognized as one of the primary vector species for *Borrelia turicatae*, the agent of Tick-borne Relapsing Fever (TBRF) in the United States, potential vertebrate reservoirs that are relevant for the sylvan cycle of this pathogen remains largely unknown. In this ongoing study, the aim is to quantify the exposure of different mammal species to *O. turicata* in cave habitats within San Marcos and San Antonio, Texas, USA, and narrow down the list of species that maintain and potentially disperse the pathogen at local scales. As part of the expected results, small to medium-sized mammals (i.e. raccoons, opossums, and porcupines) will likely be the species most frequently visiting caves, as suggested in other studies. A second part of the study aims to relate cave vertebrate use with soft tick abundance. We expect that low-tick abundance sites will show increased mammal use against high tick abundance sites, showing potential evidence of vector or pathogen avoidance by determining ecological patterns and interactions between vectors and reservoir hosts at fine spatial scales, the intensity of pathogen spread among wild mammals can be identified, also revealing the risk of potential spillover to humans. Understanding the distribution of reservoir hosts for a pathogen within a wildlife community is crucial to understand the potential risks of human zoonotic infections.

Title: Development of genomic resources for the gecko tapeworm, *Oochoristica javaensis*

Presenting author: Chelsea Thorn

Affiliation: Texas A&M University, Biology

Coauthors: Charles D. Criscione, Department of Biology, Texas A&M University

Abstract: Most genomic resources for parasitic platyhelminths are restricted to fish or mammalian host systems. The development of genomic resources for helminths that infect reptiles is necessary to provide a comparative basis for understanding the evolutionary dynamics of helminths across vertebrate taxa. We aim to develop genomic resources for a reptile-helminth system to fill this gap. Such a system can be further used to study the evolutionary interactions of vertebrate immunology and helminth counter-defense. To this end, we are developing genomic resources for the gecko tapeworm *Oochoristica javaensis*, a cyclophyllidean tapeworm native to southeast Asia that uses gekkonid lizards as definitive hosts. We chose this tapeworm for several reasons. First, it is commonly found infecting the invasive Mediterranean gecko, *Hemidactylus turcicus*, in the southern U.S., and thus is amenable to field-based studies. Second, genomic resources are available for several mammalian cyclophyllideans of human or economic importance. Hence, *O. javaensis* can serve the role of a comparative base as a flatworm parasite of reptiles. We used short-read sequences, long-read sequences, optical mapping, and transcriptome data from several individuals to assemble and annotate a draft genome of *O. javaensis*. The draft genome is 87.12 megabases with 8,498 protein coding genes. Benchmarking Universal Single-Copy Orthologs (BUSCO) scores were similar to or better than genome assemblies for other cyclophyllidean tapeworms. Orthologous cluster analysis of *O. javaensis* and

related parasitic flatworm taxa protein coding genes identified 7,759 shared clusters between taxa. Mitochondrial annotation identified 12 protein coding genes, 22 transfer RNA genes, and 2 rRNA genes, consistent with other tapeworm taxa. We also identified 2 distinct mitochondrial haplotypes. Phylogenetic analysis of mitochondrial protein coding genes supports the placement of *O. javaensis* in Cyclophyllidea. Future work in this system will address virulence and the evolution of parasite counter-defense interactions between the gecko host and its parasite.

Title: Characterization of the major histocompatibility complex (MHC) in the invasive gecko species, *Hemidactylus turcicus*.

Presenting author: Ryne Maness

Affiliation: Texas A&M University, Biology Dept.

Coauthors: Charles Criscione, Department of Biology, Texas A&M University

Abstract: Being the only ectothermic amniote clade, reptiles can serve as an effective evolutionary “bridge”; in our understanding between the basal fish immune system and the mammalian system. Yet, studies on reptile immune defense in relation to helminth infections are virtually non-existent. As such, the development of resources in a reptile system amenable to study host-helminth interactions is necessary. To this end, we are developing genomic and transcriptomic resources for the invasive Mediterranean house gecko (*Hemidactylus turcicus*) because this reptile presents opportunities in studying vertebrate-parasite coevolution. First, the Mediterranean gecko is infected with several helminth parasites, some of which have high prevalence. Thus, the system has potential as a field-based model to study the evolution of vertebrate immune defense and helminth counter-defense. Second, because helminth infections in the gecko vary across locations in easily accessible locations (e.g., human habitation) across the southern U.S., the system can be used to test the role of parasite-mediated selection and spatial variation on the evolution of allelic variation at immune-related genes such as the major histocompatibility region (MHC). Currently, little is known about the MHC among gecko species. Here, we report on a draft assembly of *H. turcicus*. Using short and long-read data (i.e., Illumina and Nanopore reads, respectively), we generated a high-quality reference genome. We then searched this assembly to locate potential loci associated with the MHC region. Future work will utilize newer genomics tools (e.g., Hi-C) to fully characterize the MHC region. With such genomic resources at hand, we will be well poised to use the Mediterranean gecko as a model to address various aspects of vertebrate-helminth coevolution.

Title: Hydrodynamics and Fish Assemblage Fluxes in a Forested Riverscape

Presenting author: Blake Elzi

Affiliation: Texas A&M University, Ecology and Conservation Biology

Coauthors: Lucas Stevens, Department of Ecology and Conservation Biology, Joshua Perkin, Department of Ecology and Conservation Biology

Abstract: Abiotic factors such as hydrologic variability in rivers, streams, and floodplains affect fish abundance and distribution. Fish assemblage variability is strongly tied to hydrologic fluctuations in channel- floodplain ecosystems where hydrologic connectivity (i.e., water-mediated connections during floods) between a channel and a floodplain allows for fish immigration and emigration. Understanding how flow variability affects hydrologic connectivity and thus fish movement is therefore important for understanding how channel-floodplain ecosystems might be managed and preserved. We tracked water mediated connectivity between creek channels and floodplains and associated changes in fish assemblage composition in Lick Creek Park near College Station, TX. We surveyed fish assemblages and measured environmental variables across two paired channel-floodplain sets of sites during fall of 2023. Floodplain habitats were relatively shallow compared to creek channel sites and largely devoid of fishes following extreme drought during summer 2023. Wetland fish assemblages were dominated by phytophilic species (spawning over vegetation) while creek fish assemblages represented a mixture of spawning strategies, including vegetation spawners, nest spawners, substrate spawners, and broadcast spawners. These results provide baseline data for tracking fish assemblage development in wetlands following the return of high water and highlight the importance of hydrologic connectivity between channel and floodplain habitats.

Title: Examining phosphorus output at endangered Atlantic Salmon hatchery

Presenting author: Claire Legaspi

Affiliation: Texas A&M University, Ecology and Conservation Biology

Coauthors: Oliver Cox - USFWS, Peter LaMothe - USFWS

Abstract: Craig Brook National Fish Hatchery (CBNFH), located in East Orland, Maine, supports some of the last native Atlantic salmon (*Salmo salar*) populations. CBNFH specifically supports the Maine Distinct Population Segment of Atlantic salmon, producing over 3 million eggs every year. CBNFH's wastewater phosphorus output is currently above Environmental Protection Agency (EPA) limits. CBNFH is interested in investigating methods for reducing phosphorus output to align with EPA standards. Phosphorus output is directly linked to feed use; only 20-30% of phosphorus in feed is absorbed by fish, the rest is excreted as waste.

Unlike other species of salmon, Atlantic salmon can spawn several times within their lifetime. It takes 3 years for an Atlantic salmon to reach maturity– CBNFH keeps spawners that are 3, 4, and 5 years old. 5 year spawners produce the most eggs per female, which is actually undesirable for genetic diversity reasons, so more spawning emphasis is placed on younger fish. Subsequently, 5 year spawners produce the least amount of eggs, but occupy the most biomass and consume the most feed. Reducing or eliminating the 5 year age class would lead to a reduction in feed use, which could lead to a reduction in overall phosphorus output

Title: Temporal and Spatial Variability of Fish Assemblages in Harmon Creek: The Influence of Habitat Complexity and Environmental Drivers

Presenting author: Erica Hagemeyer

Affiliation: Sam Houston State University

Coauthors: Dr. Jeffrey R. Wozniak, Department of Biological Sciences, Sam Houston State University, Huntsville, Texas, 77341

Abstract: Habitat heterogeneity and environmental factors can be key drivers of fish diversity in pristine headwater stream systems. Monitoring how these parameters change through time and space can provide insight into shifts in fish community dynamics. This research project, set in Harmon Creek, a second order stream in the Trinity River Basin, seeks to explore how fish assemblages vary amongst the stream's various habitat types (e.g., pools, riffles, and runs) and how key environmental drivers (e.g., temperature, dissolved oxygen, and turbidity) influence the fish community composition. Previous assessments of the fish community indicate that the Blacktail Shiner (*Cyprinella venusta*) and Western Mosquitofish (*Gambusia affinis*) are the most dominant species with the total community diversity including 16 species. Blacktail shiner (*Cyprinella venusta*) ranks 1st in overall abundance in this stream system with estimates of over 15,000 individual species. We hypothesize that habitat complexity (e.g., habitat type) will have a strong influence on fish diversity. We also hypothesize that fish diversity will be highest in areas/sampling events when temperature is moderate, turbidity is low, and dissolved oxygen is high. To test these hypotheses, we will conduct monthly fish surveys at 5 locations, for the period of one year, along the Harmon Creek ecosystem. Water column temperature, dissolved oxygen and turbidity will also be recorded. Temporal data is essential in understanding how the ecosystem responds to change. Our goal is that this study will help habitat managers better understand how streams, and more specifically the fish that inhabit them, respond to fluctuations in key environmental variables through time. The relationship between biotic and abiotic drivers is fundamental to maintaining fish biodiversity, and it is expected that the results of this study will provide a thorough understanding of this relationship.

Title: Southern Pine Forest restoration implications for small mammal diversity

Presenting author: Gage Grantham

Affiliation: Stephen F. Austin State University- Arthur Temple College of Forestry and Agriculture

Coauthors: Christopher M. Schalk, PH.D. Research Ecologist, Forest Service- Southern Research Station, Nacogdoches, TX, 75965, USA

Kathryn R. Kidd, PH.D., Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University, Nacogdoches, TX, 75965, USA

Reuber Antoniazzi, PH.D., Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University, Nacogdoches, TX, 75965, USA

John L. Willis, PH.D. Research Forester, Forest Service- Southern Research Station, Auburn, AL, 36849, USA

Jessica L. Glasscock, PH.D., Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University, Nacogdoches, TX, 75965, USA

Abstract: Industrial forest management practices converted historic native pine species forests (e.g., shortleaf pine [*Pinus echinata*]) to homogenous, high-density plantations consisting of native off-site species (e.g., loblolly pine [*Pinus taeda*]). Restoration efforts have been aimed at converting these sites back to historical upland pine forests utilizing species that were more commonly found in the site, which typically integrates one of two approaches: 1) a conversion strategy, which involves replacing off-site species with preferred historic pine species, but this approach can be fairly intensive and costly, or 2) the retention strategy which emphasizes forest structure over species identity and is more gradual and less intrusive on the landscape. However, the impact of each of these restoration strategies on small mammal diversity is not well understood. We sought to determine the relative strengths of two factors (pine species identity vs. forest structural characteristics) on an ecosystem service (support of biodiversity). Specifically, using Hunt camera traps, we recorded small mammal occurrences across six treatments that differed in tree species composition (monoculture forests of loblolly pine, monoculture forests of shortleaf pine, or mixed shortleaf-loblolly pine forests) and covariates that measure forest structure from two treatments (understory mulched or unmulched). We found that covariates describing forest structure was a stronger predictor of small mammal community composition (species richness and structure) as compared to pine species identity. These results suggest a retention, rather than a conversion, approach to restoration can still support biodiversity in forest ecosystems while achieving restoration objectives.

Title: The Suckermouth Minnow (*Phenacobius mirabilis*): An imperiled and rare fish species in east Texas streams

Presenting author: Magdalene Moses

Affiliation: Stephen F. Austin State University

Coauthors: Anastasia Simpson, Stephen F. Austin State University Rebecca Mangold, Texas A&M University Johnathan Ellard, Texas A&M University Joshua S. Perkin, Texas A&M University Kevin Conway, Texas A&M University Kole Kubicek, Lamar University Carmen Montana, Stephen F. Austin State University

Abstract: The decline of biodiversity and increase in the number of endangered and imperiled species is a worldwide issue. These trends are especially concerning in global hotspots where the diversity of species is the greatest. The Southeast of the United States is considered a hotspot for freshwater biodiversity. In Texas, the eastern portion of the state, supports a high fish diversity compared to other regions in Texas. However, rapid changes in land use associated with rapid urbanization, channelization, impoundments, and agriculture have affected richness, abundance, and distribution of fish species in eastern Texas streams. The Suckermouth Minnow, *Phenacobius mirabilis*, is one of many fish

species considered a Species of Greatest Conservation Need (SGCN) in Texas. In 2020, this minnow was listed as “Apparently Secure” in rivers of Texas. However, information in its abundance and distribution in east Texas streams is still lacking. Given that *P. mirabilis* is considered a rare species within its own range of distribution, qualitative and quantitative assessment of its population is needed to fill information gaps concerning trends over time in streams of Texas. Here, we sought to fill gaps in the distribution of *P. mirabilis* based on historical records compiled from online databases (e.g., FoTX) and contemporary surveys from field collections conducted in summer of 2023 in three river basins in east Texas including the Sabine River, Neches River, and Big Cypress River. Historical records suggest that *P. mirabilis* is indeed a rare fish species in east Texas streams. Contemporary surveys also indicated that this minnow is rare and its presence in east Texas streams correlates with streams having low turbidity and substrates consisting of sand, gravel, or rock, with limited silt. Future research focused on historical and contemporary data using an ecological niche model will help to predict potential habitat for *P. mirabilis* and provide a baseline assessment for species’ distribution in east Texas streams.

Title: Conservation status of the threatened Red River Pupfish (*Cyprinodon rubrofluviatilis*) in the upper Brazos River, Texas.

Presenting author: Lily DiFrank

Affiliation: Stephen F. Austin State University

Coauthors: Chase Nimee, Department of Biology Stephen F. Austin State University Mike Curtis, Department of Biological Sciences, University of North Texas Kaley Cave, Department of Biological Sciences, University of North Texas David Hoeinghaus, Department of Biological Sciences, University of North Texas Zacchaeus Compson, Department of Biological Sciences, University of North Texas Carmen Montaña, Department of Biology Stephen F. Austin State University

Abstract: The Red River Pupfish (*Cyprinodon rubrofluviatilis*) is an endemic fish inhabiting saline environments in the reaches of the upper Red River and Brazos River systems of Texas and Oklahoma. The Red River Pupfish is listed as threatened in Texas due to habitat alteration and introduction of nonnative species. To better understand how local fish assemblages and environmental variables influence the abundance and distribution of the pupfish, we measured local fish species richness and instream habitat variables at three sites with different environmental conditions in the Salt Fork of the Brazos River, Texas. We measured fourteen local environmental conditions that may influence the pupfish abundance across the sites including parameters associated with water quality, water flows, and general stream habitat conditions. The fish assemblage associated with the threatened pupfish was quantified in terms of species richness and abundance. In addition, we asked if high abundance of a native shiner (Red Shiner, *Cyprinella lutrensis*) could influence the population structure of the pupfish via predation of larval pupfish. Overall, our results suggest that the stream site with higher abundance of pupfish contained low abundance of Red Shiner. This site was also characterized by high conductivity and salinity, constant flow throughout the year, and substrates with traces of oil. The other two sites, which had lower abundance of pupfish, had wider channels and more isolated pools, with

one of the sites relatively less saline, but with greater species richness. Given the conservation concerns of the threatened pupfish in the Brazos River, our findings suggest that threatened pupfish persists as 'fugitive species' that are tolerant of environmental conditions that exceed tolerances of other fish species inhabiting these harsh saline waters of the upper Brazos River, but unable to maintain populations in less extreme habitats where potential predators and competitors (e.g., Red Shiner) are present in higher densities. Additional research is needed to understand the relative importance and interactions of whole fish assemblages and environmental factors affecting Red River Pupfish distribution and abundance in the upper Brazos River of Texas.

Title: Mapping Epigenetic Divergence in a Migratory Divide between Songbirds

Presenting author: Sope Adeniji

Affiliation: Department of Biology, Texas A&M University

Coauthors: Hannah Justen, Department of Biology, Texas A&M University; Kira Delmore, Department of Biology, Texas A&M University

Abstract: Seasonal migration in animals is a remarkable navigational feat that is controlled by both genetic and environmental factors. The Swainson's thrush, a Nearctic migrating songbird, has two main subspecies - a coastal form that migrates along the Pacific Coast of North America, wintering in Central America, and an inland form that migrates along an eastern route, wintering primarily in South America. The objective of this study was to identify epigenetic mechanisms underlying the divergence in migratory orientation between these two subspecies of Swainson's thrushes. We used direct tracking data and whole genome resequencing data to select birds from the hybrid zone with the most extreme latitudinal bearings on the fall migration and ancestries (coastal vs. inland). We used Enzymatic Methyl-seq to identify 5mC and 5hmC throughout the entire genome. We identified differences in genome-wide methylation between the two subspecies and linked differentially methylated genes to key biological processes with a focus on genes related to migration. The results of our study enhance the existing body of knowledge on the role of epigenetics in not only generating variation in migratory behavior but also maintaining reproductive isolation among species.

Title: Characterizing the gut microbiomes of damselflies and mayflies.

Presenting author: Liz Reed

Affiliation: University of Texas at Austin

Coauthors: Dr. Jo-anne Holley, Department of Integrative Biology, University of Texas at Austin

Annie Le, University of Texas at Austin Lane Morgan, University of Texas at Austin Chia-Hsuan Ho, University of Texas at Austin

Abstract: Many insects depend on their gut microbiomes for essential functions, including nutrient supplementation, digestion, development, and immunity. Alteration of the gut microbial composition can cause insects to develop susceptibility to stressors and

pathogens. The gut microbiome may be altered through environmental influences like pollutive runoff. Aquatic insect gut microbiomes can be particularly vulnerable to these changes because the insects are in constant contact with their environment. Such insects are ubiquitous in aquatic ecosystems and are crucial food sources for fish, insects, and other organisms. Aquatic insects also have important applications to humans as biological indicators in environmental research. The biodiversity of aquatic insects in a stream can describe the health of that particular habitat, potentially reflecting the impacts of pollution. Biological contaminants and chemical pollutants have been long standing concerns for aquatic habitats and their organisms. However, even with these documented concerns, there is limited research on how pollution impacts the gut microbiome of aquatic insects. Our research has focused on characterizing the gut microbiomes of aquatic mayfly and damselfly nymphs collected from six Austin creeks with different levels of human-associated degradation (polluted, moderate, and pristine). Using sequences of the V4 region of the 16s rRNA gene, we compared the relative abundance of bacteria found in each insect species and statistically determined if their gut microbiomes differ between each creek location associated with varying pollution levels.

Title: Exploring thermal tolerance limits of the upsidedown jellyfish

Presenting author: Edgardo Rivera

Affiliation: Biology

Coauthors: Edgardo Rivera¹, Ziyu Wang¹, Marie Strader¹ ¹Texas A&M University, Department of Biology

Abstract: *Cassiopea xamachana* is an epibenthic Scyphozoan that undergoes a complex life cycle, which includes a juvenile stage called the ephyra. *Cassiopea* are mainly found in shallow lagoons or mangroves throughout the Florida Keys and the Caribbean. *C. xamachana* adults are highly tolerant to various temperatures, but the thermal limits to which early life-history stages can survive and maintain homeostasis is unknown. We investigated the cold and heat tolerance limits of *C. xamachana* ephyrae and their response to gradual temperature drop and rise, respectively. We identified the critical thermal minimum and maximum temperature by measuring pulsation rate (pulse/minute), total bell diameter (TBD), and tissue integrity. We found that ephyrae tolerated cold temperatures as low as 9°C, while pulsation rate steadily decreased as the temperature decreased. TBD decreased from 3.8 mm to 2.5 mm when the temperature dropped from 28°C to 26°C but stayed constant until ephyrae stopped feeding at 18°C. When the temperature dropped close to 9°C, ephyrae started to lose their tissue integrity or disintegrate. For the heat tolerance experiment, ephyrae tolerated heat up to 39°C. Bell pulsation stayed constant until 36°C and then it started to dramatically decrease. TBD stayed relatively the same around 5 mm to 4 mm but began to decrease at 36°C. When the temperature was close to 38°C many of the ephyrae had begun to disintegrate. Overall, we find that *C. xamachana* ephyra are highly tolerant of temperature, with a range from 9°C to 36°C, which may help explain their ability to inhabit a wider variety of tropical coastal habitats. This data on the thermal limits of early-life history stages of *C. xamachana* is

critical for understanding their resilience and adaptability amid global temperature change, especially as they expand their ranges as climates shift.

Title: EGFR Over-Expression in ERBB2 Independent Colorectal Cancer

Presenting author: Megan Thomas

Affiliation: Texas A&M University Department of Biology

Abstract: Colorectal cancer (CRC) remains the second leading cause of cancer-related deaths in the United States. ERBB2, a transmembrane growth factor receptor, serves as a negative predictive biomarker for human CRC. Our investigation revolves around understanding the role of ERBB2 deficiency in CRC and evaluating its potential as a target for clinical therapies. Previous research, employing Ingenuity Pathways Analysis (IPA) and Gene Set Enrichment Analysis (GSEA), revealed the upregulation of genes associated with the EGFR signaling pathway in ERBB2 deficient murine colon tissue. This suggests a potential direct connection between EGFR upregulation and ERBB2 deficient tumors. I hypothesize that in ERBB2 deficient tumors, EGFR overexpression will be observed, indicated by higher EGFR protein concentration levels and reduced levels of apoptosis. I investigated this hypothesis by utilizing a Western blot assay analysis to characterize protein concentrations and a cleaved caspase-3 assay to quantify the levels of apoptosis in murine colon tissue samples.

Title: Diel Activity: Exploring Temporal Niche Conservatism in African Euungulates and its Ecological Consequences

Presenting author: Brier Klossing

Affiliation: Texas State University, Biology Department

Coauthors: Ivan Castro-Arellano, Department of Biology, Texas State University

Abstract: Mammalian activity patterns have been of research interest but proved difficult to study. Recent technological advances have made it possible to address big questions in this area. Activity patterns are likely influenced by body mass, which directly impacts species through metabolic and thermoregulatory processes. For example, large herbivores tend to forage more on abundant items of low nutritional value, often having a trend towards cathemeral activity (i.e., low activity directionality). While small herbivores tend to forage on rarer items of high nutritional value, achieving their foraging requirements within a shorter time span and thus tending to be time specialists (i.e., high activity directionality). If body masses are similar among closely related mammalian taxa, then species should tend to retain temporal niches over evolutionary time (i.e., temporal niche conservatism). We aim to investigate how body mass influences the activity patterns of African Euungulates across multiple sites within Africa and in non-native sites within Texas game ranches. To accomplish our study, we will utilize open-source trail camera data from online data repositories and deploy trail cameras at game ranches to analyze activity patterns across these datasets. We will use R statistical programming utilizing Activity and Overlap packages, Oriana a circular statistical software, and a null model approach (i.e., ROSARIO algorithm). We predict large mammals will show longer foraging activities during

a diel cycle, and consistent activity patterns across sites (i.e., intraspecific niche conservatism, Intra-NC), while small mammals will show high activity directionality during a diel cycle, and activity pattern variation across sites (i.e., absence of Intra-NC). Our findings can inform if body mass influences activity patterns at continental scales.

Title: Is fragmentation affecting the Bat-Plant interaction networks?

Presenting author: Tatiana Velasquez-Roa

Affiliation: Texas State University, Biology department

Coauthors: Oscar E. Murillo-Garcia, Department of Biology, Universidad del Valle, Colombia.

Abstract: Anthropogenically driven fragmentation reduces species diversity and changes species compositions within tropical forests, causing changes in the structure of interaction networks, which could trigger effects in important processes related to plant reproduction and forest maintenance. Currently there is a need to characterize the effects of fragmentation on the structure of plant-animal interaction networks in threatened ecosystems such as the tropical dry forest (TDF). For this purpose, information on the interactions between bat species and the plants consumed by them was collected in ten remnants of TDF in Colombia. In addition, a characterization of each remnant was done using landscape metrics, and it was related to structural properties of the interaction networks (nestedness, modularity, and robustness). In addition, for the purpose of including the effects of spatial variation in the interaction bat-plant on the modularity and robustness, the multilayer interaction network focus was used. Finally, we calculated the beta diversity of interactions between remnants, decomposed it into species and interaction turnover components, and assessed whether it was associated with remnant distance. We captured 1,142 bat individuals grouped into 36 species (28 phyllostomids/19 frugivorous) and collected more than 19,600 seeds from their droppings. Our results suggest fragmentation influences nestedness and robustness at the different scales studied (remnant, 2.5 km buffer and 5 km buffer). We find that species and interaction composition became similar in the nearby remnants. Our results prove that the different types of approaches used in this study gave us an integrative view of the bat-plant interaction behaviour and how they are related to landscape characteristics. The previous statement is key and fundamental because this study focused on the most threatened ecosystem of Colombia, and its outcomes can aid restoration actions in the tropical dry forest.

Title: Symbiont communities of juvenile *Acropora hyacinthus* remain stable following a mass mortality event in Mo'orea but contribute to bleaching severity

Presenting author: Stephanie Hendricks

Affiliation: TAMU Biology

Coauthors: Stephanie Hendricks, Department of Biology, Texas A&M University James Fifer, Department of Biology, Texas A&M University, Department of Ecology, Evolution, and Marine Biology, University of California San Diego, Department of Biology, Boston University Marie Strader, Department of Biology, Texas A&M University

Abstract: Coral reefs are highly biodiverse ecosystems that support up to 25% of marine life, reduce shoreline erosion, contribute to tourism, and serve as resources for food and fishing. These important and valuable ecosystems experience extreme stress from marine heatwaves (MHWs), which are projected to increase in the next century. Prolonged heat stress can lead to a process where corals lose their obligate algal symbionts (family Symbiodinaceae), otherwise known as coral bleaching. In 2019, corals in Mo'orea, French Polynesia, experienced a MHW that resulted in severe bleaching and mortality. Symbiont communities from colonies of *Acropora hyacinthus* were assessed through ITS2 sequencing: 1) during the height of bleaching in May 2019, 2) after bleaching in October 2019, and 3) in November 2021, when a new cohort of juvenile recruits naïve to the 2019 bleaching event were observed. We found no change in symbiont community composition between timepoints, where C3ae/C3/C3g (genus *Cladocopium*) was the dominant ITS2 type profile found in most adults and was maintained in juveniles. However, additional whole genome sequencing at specific reef zones found that an increased abundance of *Cladocopium* reads was associated with lower bleaching susceptibility ($p < 0.0001$; $r = 0.57$), while an increased abundance of *Symbiodinium* reads was associated with higher bleaching susceptibility. Thus, bleaching and mortality are largely driven by interactions between environment and the genus of symbiont. Taken together, symbiont communities drive physiological responses to MHWs, but remain stable through time, potentially reflecting either host adaptations or environmental specificity.

Title: Apparent Self Fertilizing Boulder Brain Coral and Implications for Reef Restoration

Presenting author: Elizabeth Suh

Affiliation: Department of Integrative Biology, The University of Texas at Austin

Coauthors: Daisy Flores, Department of Integrative Biology, The University of Texas at Austin Alexa Huzar, Department of Integrative Biology, The University of Texas at Austin Mikhail Matz, Department of Integrative Biology, The University of Texas at Austin Mark Vermeij, CARMABI Foundation Kristen Marhaver, CARMABI Foundation Emily Nixon, Scripps Institute of Oceanography Joaquin Yus, University of Illinois Urbana-Champaign

Abstract: Reef-building corals reproduce once a year in a mass spawning event that is vital for maintaining genetic variation. Having diverse genetic variation is vastly important for corals to survive in an increasingly changing environment. In order to better understand this reproductive phenomenon, we collected eggs, sperm, and adult coral samples in 2022 from boulder brain corals, *Colpophyllia natans*, in Curacao, and performed crosses to study variation in genetic inheritance. Interestingly, during this reciprocal cross experiment we observed a case of apparent self fertilization in one of the three *Colpophyllia natans* adults, with a fertilization rate of 27%. We designed the experiment with checks to monitor and prevent cross-contamination, so it is unlikely that this result is due to error. Corals are not normally able to self fertilize, so this result could indicate that this coral is a chimera or a mosaic organism. To better understand the self-fertilization that was observed, we took multiple samples of the adult colony across its surface area. We are extracting DNA from the eggs, sperm, larvae, and adult polyps, which we will then use to perform a genomic

analysis using 2bRAD libraries and Illumina sequencing. We expect the results to show either genotype differences to indicate that this coral is a chimera or a gradient of mutations across the coral to indicate that it is a mosaic organism. By sequencing and analyzing the other parents that did not self-fertilize, we can determine whether there was contamination or reveal significant differences between the putative chimera. Further research is needed to fully understand this phenomenon, but it is relevant because the apparent self fertilizing *Colpophyllia natans* coral has died since the samples were collected in 2022. Results will provide a clearer understanding of coral reproduction and give more knowledge on how to better preserve coral reefs.

Poster Session 2

Title: Investigating the Barriers and Opportunities to Creating Wildlife Corridors on Agricultural Lands

Presenting author: Shelby Bork

Affiliation: Department of Biology, Texas State University

Coauthors: Dr. Christopher Serenari, Department of Biology, Texas State University

Abstract: Habitat fragmentation occurs when a large area of natural habitat is broken up into smaller patches and isolated from one another, degrading ecosystems and leading to significant biodiversity loss. This problem is expected to worsen for wildlife as climate change progresses and organisms are forced to relocate to more suitable habitats. Agricultural lands, especially within the Great Plains region of the U.S., are a major contributor to fragmentation. Wildlife corridor creation, linkages that reconnect pieces of habitat, is a promising and effective policy tool to mitigate the negative effects of fragmentation. However, for various understudied reasons, formulation and implementation of wildlife corridor policies has been slow or non-existent in most states. The goal of this research is to aid the development of wildlife corridor policy in the U.S. To accomplish this goal, this masters project will identify the primary policy barriers that prevent creation of wildlife corridors in the Great Plains. Professionals in 12 states with experience working on a wildlife corridor project within the Great Plains region will be surveyed to identify factors that encumber the various stages of the policy process. Findings will help researchers and decision-makers identify where and how the design, completion, and monitoring of wildlife corridor projects is most and least productive, and which stages of the policy process require the most resources.

Title: Behavioral Syndromes in *Podarcis siculus*: Insights into Invasion Success

Presenting author: Jade Bach

Affiliation: TAMU- Biology

Coauthors: Breann Richey- Department of Ecology and Conservation Biology, Texas A&M University Dr. Michelle Lawing- Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Invasive species can outcompete native species for resources such as food, water, and habitat, leading to declines or even extirpations of native flora and fauna. This disruption to ecosystem balance can have cascading effects, impacting other species and altering entire habitats. This research focuses on the behavior of the Italian wall lizard (*Podarcis siculus*), aiming to explore the prevalence of invasion syndrome behaviors across native and non-native populations. Here, we conduct a behavioral analysis using a specifically tailored ethogram and analyze behavioral data using the Behavioral Observation Research Interactive Software (BORIS). We analyzed video recordings showcasing various behaviors of *P. siculus* which are related to invasion success, including boldness, neophilia, aggression, and exploration. Each phase of behavioral analysis and video assessment involved at least two individuals to minimize subjectivity and ensure consistency in our observations. While initial analyses have been done by undergraduate researchers, the conclusive findings and complex statistical analysis are currently underway. Through this research we aim to highlight behavioral differences between native and non-native populations of lizards. These insights will increase our understanding of invasion dynamics and give conservationists insight into how to safeguard species vulnerable to invasion pressures.

Title: Diet of Introduced Mongoose in St. Croix, USVI

Presenting author: Nicole Stevens

Affiliation: EEB/ECCB

Coauthors: Doris Olenkiewicz, Biomedical Sciences Major, Texas A&M University Taylee Sankey, Animal Science Major, Texas A&M University Lee Fitzgerald, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Invasive species are one of the largest threats to biodiversity worldwide and have a disproportionately harmful ecological impact in island ecosystems. Small Indian Mongoose (*Urva auropunctata*) are voracious predators native to southeast Asia that have been introduced to a number of Caribbean islands, resulting in the decline, extirpation, and extinction of many species. For example, mongoose introduction is linked to the complete extirpation of the St. Croix ground lizard (*Pholidoscelis polops*) from St. Croix. Therefore, understanding more about mongoose diet will be useful for predicting success of ongoing repatriation efforts for *P. polops*. The most recent published assessment of mongoose diet on St. Croix is from 1953, before much of the landscape had reverted back to its historical land cover. Our goal was to update our understanding of mongoose diet on St. Croix, specifically at sites where *P. polops* translocations are planned. To do so, we trapped mongoose at four sites in a 5x8 grid with 30m trap spacing. Traps were set out for four nights and checked daily for a total of 640 total trapping nights. Each captured mongoose was humanely euthanized and stomach contents were removed and sorted. In total, we captured 76 mongoose and have found remains of insects, centipedes, crustaceans, rodents, reptiles, and plant materials. Notably, we have found substantially fewer remains of *Anolis* lizards than Wolcott (1953) despite their continued presence on the island, indicating that reptiles are not an integral part of the current mongoose diet on St. Croix. Quantification of

stomach contents is still ongoing, but our preliminary results indicate that mongoose diet is varied and may be conducive to coexistence with *P. polops*.

Title: Chromosome Number and Sex Chromosome Evolution in Scarabaeidae

Presenting author: Sean Chien

Affiliation: Texas A&M University. Department of Biology

Coauthors: Max Chin, Department of Evolution and Ecology, University of California, Davis, CA, USA; Heath Blackmon, Department of Biology, Texas A&M University, College Station, TX, USA

Abstract: A karyotype is one of the simplest descriptions of a genome. It reveals the sex chromosome system and chromosome number, which have important roles in evolutionary change. Chromosome number evolution has been hypothesized to play a role in several speciation processes. Differences in chromosome number and sex chromosome system may cause intrinsic barriers to gene flow. Coleoptera is an excellent group to use as a model in studying chromosome number and sex chromosome systems. Haploid chromosome number ranges from 4 to 18 in the Coleoptera clade Scarabaeidae. Sex chromosome systems are equally variable in this group with XO, XY, Xyp, Xyr, and NeoXY systems. To understand the mode and tempo of karyotype evolution in Scarabaeidae, we built a time-calibrated phylogeny using sequences from 245 species and four genes. We then fit probabilistic models of chromosome number and sex chromosome system evolution. We also estimated the ancestral character states by reconstructing phylogeny and simulating stochastic character maps. The results indicate that Scarabaeidae has a lower rate of fusion and fission, and fusion plays a dominant role in chromosome evolution.

Title: The Effects of Multiple Herbivores on Sorghum Defenses

Presenting author: Nathan Kincaid

Affiliation: Texas A&M University, Department of Geography

Coauthors: Emily Russavage, Department of Entomology, Texas A&M University. Zoe Farmer, Department of Entomology, Texas A&M University. Thea Alonzo, Department of Plant Pathology and Microbiology, Texas A&M University. Micky D. Eubanks, Department of Agricultural Biology, Colorado State University.

Abstract: Plants contend with many different stressors, including insect herbivory. When plants are attacked by a single insect herbivore, specific plant defenses are activated - for example, plants can produce and emit a blend of herbivore-induced plant volatiles (HIPVs). HIPVs are odorous chemicals released by plants to attract insect predators and parasitoids to kill the herbivore. However, plants in natural conditions are rarely attacked by a single herbivorous insect species. Previous studies have shown that attack by one herbivore (e.g., an aphid) can decrease or dampen a plant's ability to defend against a new, different herbivore (e.g., a caterpillar). In the present study, we wanted to investigate the effects of two herbivore species on HIPV emissions from sorghum plants. We collected HIPVs from plants that: 1) had no herbivore present, 2) were infested with 100 sorghum aphids (SA;

Melanaphis sorghi), 3) were infested with 1 fall armyworm (FAW; Spodoptera frugiperda), or 4) were infested with both SA and FAW. HIPVs were collected using dynamic headspace sampling techniques. Compounds were identified and quantified using GC-MS. Here, we found a total of 46 different compounds emitted by plants across treatments. Total volatile emissions did not differ amongst treatments ($F_{3,8}=0.28$, $p=0.83$). However, random forest analysis indicated that the compounds heptadecane, methyl salicylate (MeSA), 2,6-dimethyl-undecane, and hexadecane all differed amongst treatments. Heptadecane and MeSA were present in all herbivore-treated plants. Interestingly, plants infested with both herbivores produced, on average, over 3,000 ng/g of hexadecane, but FAW-only plants produced 0 ng/g. The results of this study suggest that crop breeders and entomologists searching for crop plant defense traits should investigate the effects of multiple herbivores on these defenses to maximize the effectiveness of this pest management strategy.

Title: Cophylogeny Across Geographic Barriers: Using Genetic Markers to Explore the Coevolution between *Geomys pinetis* Pocket Gophers and their Chewing Lice.

Presenting author: Abby Jensen

Affiliation: Ecology and Conservation Biology and Texas A&M University

Coauthors: Danielle Dillard, Ayomiposi Abraham, Oluwaseun Ajileye, Jessica E. Light

Everybody is Ecology and Conservation Biology and Texas A&M University

Abstract: Pocket gophers (Rodentia: Geomyidae) are solitary, fossorial rodents, known to have long-term ecological and evolutionary associations with their parasites, especially their chewing lice (Psocodea: Phthiraptera: Ischnocera). These relationships are believed to be influenced by the behavior and distribution of the pocket gopher, as well as the behavior of the chewing lice. Understanding the evolutionary dynamics within this system can offer insight into the historical biogeography and speciation processes of both the pocket gophers and their chewing lice. *Geomys pinetis*, the Southeastern pocket gopher, is distributed throughout Alabama, Georgia, and Florida and is known to be parasitized by two species of chewing lice depending on the location: *Geomydoecus scleritus* or *Geomydoecus mobilensis*. Previous research has found that geographic barriers can influence these associations, potentially leading to divergence in both hosts and parasites. In fact, genetic differentiation has been found in *Geomys pinetis* due to natural barriers within their range presented by the Apalachicola, Suwannee, and St. Johns Rivers. Through molecular phylogenetic analysis, we will explore the relationship that *Geomys pinetis* has with its chewing lice and investigate whether geographic barriers influencing the host also directly shape the host associations, genetic differentiation, and distribution of the parasites. We expect the lice will exhibit patterns of mirroring their hosts in response to geographic breaks, reflecting a similar evolutionary history and dispersal pattern to the Southeastern pocket gopher. This study has the ambition to shed light on the coevolutionary dynamics between these species, providing valuable insights into their ecological and evolutionary interactions.

Title: Exploitative competition: An invasion mechanism of the invasive lacertid lizard *Podarcis siculus*

Presenting author: Paige Hudson

Affiliation: Texas A&M University, Ecology and Conservation Biology, Psychological Brain Sciences

Coauthors: Breann Richey, Dr. Michelle Lawing, Department of Ecology and Conservation Biology, TAMU

Abstract: Invasive species pose a significant threat to biodiversity by disrupting habitats, monopolizing resources, and displacing native species. Understanding the mechanisms behind the success of invasive species is crucial for predicting population dynamics and devising effective conservation management strategies. The Italian wall lizard, *Podarcis siculus*, is a globally invasive lacertid native to the Italian Peninsula. As *Podarcis siculus* continues to increase its native and near-native range it has displaced multiple populations of endemic lizard species. Affected native lizards are typically completely eradicated or forced into less optimal habitats. By measuring competitive exclusion through resource use and guarding, this study aims to understand the direct mechanisms through which *Podarcis siculus* successfully outcompetes native lizards. This research employs observational and experimental methods to assess the interactions between *P. siculus* and resources such as heat, food, and shelter, when in isolation versus in sympatry with *Sceloporus consobrinus*, the Prairie lizard, a similarly-sized lizard which is sympatric in *P. siculus*'s invasive range. Through this study we will quantify the magnitude of heterospecific species interactions between the Italian wall lizard and affected native species, as well as identify the behaviors that contribute to a successful invasion and exclusion of native species. Results from this study have the potential to provide critical information about resource acquisition that could be utilized in implementing proactive and sustainable conservation practices.

Title: Sexual dimorphism in an invasive population of suckermouth armored catfish: Implications for management

Presenting author: Wesley Arend

Affiliation: Texas A&M - Ecology and Conservation Biology

Coauthors: Rebecca D. Mangold, Department of Ecology and Conservation Biology, Texas A&M University; Christopher L. Riggins, Meadows Center for Water and the Environment, Texas State University; Collin Garoutte, Meadows Center for Water and the Environment, Texas State University; Yeyetzi Rodriguez, Meadows Center for Water and the Environment, Texas State University; Thomas C. Heard, Meadows Center for Water and the Environment, Texas State University; Nick Menchaca, Atlas Environmental; Janaye Williamson, Atlas Environmental; Dusty McDonald, Texas Parks and Wildlife Department, Inland Fisheries Division, Corpus Christi Fisheries Management District; Daniel Daugherty, Texas Parks and Wildlife Department, Inland Fisheries Division, Heart of the Hills Fisheries Science Center; Monica McGarrity, Texas Parks and Wildlife Department, Inland Fisheries Division; Kevin W. Conway, Department of Ecology and Conservation Biology & the Texas A&M Biodiversity Research and Teaching Collections; Joshua S. Perkin, Department of Ecology and Conservation Biology, Texas A&M University.

Abstract: Objective: Suckermouth armored catfishes (SACs; Loricariidae) have invaded water bodies outside their native range globally. Population control methods, including removals and genetic biocontrols, may be enhanced through greater knowledge of sex discrimination, sex ratios, and potential sex bias among control methods. Methods: We investigated sexual dimorphism and population sex ratio for an invasive SAC population of *Hypostomus* sp. in the upper San Marcos River, Texas, USA, as a means of advancing ongoing management of the population. Result: Among 385 specimens obtained at random during a planned dewatering of a 100-m reach of the river, the sex ratio was biased toward females (proportion of females = 0.60). Morphometric analyses of 105 females and 108 males based on a generalized boosted classification model revealed elongated dorsal and anal fins in males correctly classified sex for 83% of individuals (95% CI = 77–88%). Seven independent observers used results from the generalized boosted classification model to assign sex to 30 fish, with average accuracy of 72% (range = 43–83%). The accuracy of the model and validation exercises were highest for fish >240 mm total length, the estimated length of reproductive maturity. Conclusion: Morphometrics based on dorsal- and anal-fin sizes can be used to infer sex externally from hundreds of SACs removed per year to evaluate long-term population management success.

Title: Habitat selection coefficients decrease in a transient population of *Podarcis siculus*

Presenting author: Audra Hicks

Affiliation: Texas A&M University

Coauthors: Audra E. Hicks^{1*}, Breann M. S. Richey¹, Loris Di Vozzo², Mirko Guasconi², Marco A. L. Zuffi², & A. Michelle Lawing¹

¹ Department of Ecology and Conservation Biology, Texas A&M University, 77843, College Station, TX, United States ² Natural History Museum, University of Pisa, I-56011 Calci, PI, Italy

Abstract: Invasive species are a leading cause of biodiversity loss. An important stage in the invasion cycle is the transient stage. Transient populations are populations that blip in and out of existence through propagule pressures. Outcomes associated with transient populations are: the population will become established with high propagule pressure, or a lack of resources will not lead to establishment regardless of propagule pressure. From there, transient populations may lead to local extinction, establishment, or rapid expansion. Here, we test whether there are differences in habitat selection between a transient population of *Podarcis siculus* compared to its mainland counterpart. Transient populations in general have been poorly studied in the context of invasion biology, especially in lizards. Habitat selection is a vital factor in the establishment process because areas with high resource availability will provide a better opportunity for establishment. *P. siculus* is a great species to study for this question because there are well-documented populations considered native, invasive, and native invasive, and because they threaten local endemic congeners. Knowledge of how exactly habitat use may shift is important in monitoring recently invaded areas and islands. We conducted habitat surveys and visual encounter surveys on the island of Elba in the Tuscan Archipelago to estimate habitat use

and availability along 45 transects and 5 different land types to quantify habitat selection. We compared those to transects from the mainland population of provenance in Livorno, Tuscany, Italy. We found a shift in quantified habitat selection coefficients, with mainland populations exhibiting higher levels of habitat selection. Leaf litter and path types were the most disproportionately used perch categories in the mainland and transient island populations, respectively. Habitat selection in established versus transient populations is valuable to study because it provides the opportunity to better understand how ecological processes like invasion manifest at different stages.

Title: How increasing ocean temperatures and microbe content impact sea urchin development

Presenting author: Elliana Carter

Affiliation: Texas A&M University- Biology

Coauthors: Amy L. Tan, Department of Biology, Texas A&M University, Marie Strader, Department of Biology, Texas A&M University

Abstract: Marine environments are threatened by rapid anthropogenic change, leading to questions concerning how marine organisms can successfully adapt at a sufficient rate. Purple sea urchins (*Strongylocentrotus purpuratus*) are a keystone species in kelp forests along the Pacific coast of North America. These kelp forests rely on a delicate balance between urchins and kelp to maintain this important habitat. As a marine invertebrate with external fertilization and development, environmental conditions have the potential to alter the early growth and development of purple sea urchins. Elevated ocean temperatures increase the spread of pathogens and could compromise larval development due to stress. In order to study the effects of elevated temperatures and early microbe exposure, *S. purpuratus* larvae were reared in four water conditions: combinations of temperature (14°C vs. 18°C) and microbial content (sterilized artificial seawater vs filtered water from an adult tank). We analyzed larval body size and immune cell numbers in pluteus larvae (5 days post fertilization) to see how their phenotype was affected by environmental conditions. We found that larvae reared in warmer temperatures or sterile water were larger and also had more pigment cells (one type of immune cell). The decreased pigment cell count in larvae raised exposed to the adult microbiome could be caused by activation of those cells in response to bacteria in the water. Although warmer water may accelerate larval growth, it is possible that the higher temperature could stress larvae and compromise immune function when challenged with a pathogen. These results suggest that urchin development can be impacted by elevated temperatures and increased pathogen spread that may occur as a result of global change.

Title: Effects of ectopic expression of Spiroplasma RIP toxin genes in Drosophila to determine the mechanistic basis of a defensive mutualism

Presenting author: Shannon Jarratt-Harris

Affiliation: Texas A&M University, Ecology and Evolutionary Biology

Coauthors: Chanwoo Kim, Chelsea Chanheng, Emily Lubrich, Mariana Mateos

Abstract: Associations between arthropods and heritable endosymbiotic bacteria are widespread, taxonomically, and mechanistically diverse, and have a strong influence on the evolutionary ecology of their hosts. An emerging model system for the study of insect-bacteria interactions is the association between *Drosophila* and *Spiroplasma*. Certain *Drosophila*-*Spiroplasma* interactions involve defense benefits for the host against natural enemies (parasitic wasps and nematodes). The mechanism is not fully understood, but a *Spiroplasma*-encoded toxin (Ribosome Inactivating Protein; RIP) appears to be involved. Whether this toxin is sufficient to cause wasp death has not been determined. Here we assess the role of specific genes in this interaction by ectopically expressing them in *Drosophila*. In preparation, we conducted several assays with four previously developed transgenic fly lines designed to ectopically express one of two *Spiroplasma* RIP genes (RIP1 and RIP2) via the UAS/GAL4 system. We used the GAL4 driver lines Da-GAL III and Hml Δ GAL-4>UAS-GFP to ectopically express each of the following transgenes: UAS-RIP1, UAS-BIP-RIP1, UAS-RIP2, UAS-BIP-RIP2, where BIP is a *Drosophila* secretion signal. The UAS parents are heterozygous for the corresponding transgene and the CyO balancer chromosome. We evaluated embryo-to-adult lethality by comparing the proportion of adult offspring with curly wings (not expressing RIP) vs. straight wings (inherited the UAS-RIP chromosome). Lethality was detected in all four responder lines when crossed with Da-GAL III driver line in which most/all our offspring had curly wings. In a similar study conducted by Garcia-Arreaez and colleagues, proportion of embryo mortality produced similar but not identical outcomes with Da-GAL4. Lethality was not detected in any of the responder lines when crossed with the Hml Δ GAL-4>UAS-GFP driver line as the F1 curly and straight phenotypes occurred in equal proportions. We did not observe a significant difference in sex ratio survivorship. We additionally performed a validation step to determine the identity of the vector used as this was not disclosed in the Garcia-Arreaez study. UAS-RIP1 was constructed using the PUASP vector and UAS-RIP2, UAS-BIP-RIP1, UAS-BIP-RIP2 uses the PUASt vector. Our next step is to choose the appropriate driver line that most accurately recapitulates RIP activity in flies to evaluate its effect on various species of parasitoid wasps.

Title: Hydrological modeling using artificial neural networks for flood event forecasting

Presenting author: Rennan Dias

Affiliation: Ecology & Conservation Biology

Coauthors: Wagner Rambaldi Telles, Instituto do Noroeste Fluminense de Educação Superior, Universidade Federal Fluminense, Brazil; Antônio José da Silva Neto, Instituto Politécnico, Universidade do Estado do Rio de Janeiro, Brazil.

Abstract: Flood prediction through hydrological modeling of watersheds remains an emerging need in society, particularly in regions highly affected by these extreme events. Models based on artificial neural networks have demonstrated significant potential for addressing this issue due to their simplicity and agility. In this study, a model was developed using a multilayer perceptron network for predicting river discharge and water

level based on the previous day's river state and precipitation forecast. The Pomba River in the city of Santo Antônio de Pádua-RJ was investigated due to its regular occurrence of flood events that impact the entire population. Metric and graphical results showed the model's strong ability to estimate discharge and water levels at a station with limited data throughout the year. On the other hand, the model encountered difficulties in accurately estimating peak values.

Title: Habitat depth drives bleaching tolerance variation in lineages of a Caribbean coral, *Montastrea cavernosa*

Presenting author: Camille Brown

Affiliation: Department of Integrative Biology, The University of Texas at Austin

Coauthors: Dominique N. Gallery, Department of Integrative Biology, The University of Texas at Austin; Evelyn A. Abbott, Department of Integrative Biology, The University of Texas at Austin; Mikhail V. Matz, Department of Integrative Biology, The University of Texas at Austin

Abstract: *Montastrea cavernosa*, or great star coral, is a large reef-building coral prolific in Caribbean reef systems. Curiously, along the Florida Keys reef tract, four genetically distinct lineages of this species have been found – two deep water (>20 m) and two shallow water (3-10 m) – each nearly exactly relegated to reefs of their preferred depth. Each lineage appears to be specialized to its habitat, having adapted to the sunlight, nutrient availability, turbidity, and temperature changes characteristic of the environment. Surprisingly, these differential adaptations (described by patterns in gene expression) are not well explained by the coral's genetic lineage, and instead are highly correlated with the depth at which the colony is living. That is to say that the genetic differences between the four lineages does not seem to have evolved via local selective pressures, nor do the adaptations to specific depths arise from genetic differences between the lineages. This project further investigates physiological differentiation between *M. cavernosa* depth variants in response to a particularly relevant ecological stressor: heat-induced loss of zooxanthellae symbionts, also known as bleaching. As ocean waters warm globally, devastating bleaching events have increased in frequency across reef systems, threatening tropical species worldwide. We aimed to determine how different lineages from the aforementioned habitats respond to bleaching stress by conducting a common garden experiment. We induced bleaching in previously genotyped samples from nearshore, offshore, and deep habitats by gradually increasing the tank's water temperature. Analysis of photographic data revealed that a sample's habitat of origin is a significant predictor of its resistance to heat-driven bleaching. Advancing understanding of complex interactions between genetic diversity and species resilience to environmental changes is essential to informing responsible and effective coral conservation and restoration practices.

Title: Sexual Antagonistic Selection Detected within One Generation of Stickleback Fish

Presenting author: Jordan Engstrom

Affiliation: University of Texas at Austin, Department of Integrative Biology

Coauthors: Alexa Huzar, Department of Integrative Biology, University of Texas at Austin Coral Loockerman, Department of Integrative Biology, University of Texas at Austin Matt Ming, Department of Integrative Biology, University of Texas at Austin Mikhail Matz, Department of Integrative Biology, University of Texas at Austin Daniel I. Bolnick, Department of Ecology & Evolutionary Biology, University of Connecticut Mark Kirkpatrick, Department of Integrative Biology, University of Texas at Austin

Abstract: Understanding the role of sexually antagonistic selection (SAS) in species is vital to understanding the evolutionary processes that drive sexual dimorphism and the origins of new species. SAS occurs when an allele that is beneficial to one sex is detrimental to the other and can be driven by sex-biased expression. Despite its importance for evolution, studying SAS remains challenging because the classical tools of molecular evolution cannot detect it. However, previous work has developed methods to detect SAS acting within a generation. Using a previous dataset of threespine stickleback fish (*Gasterosteus aculeatus*), we found some evidence for patterns of SAS in Sticklebacks. Unfortunately, that dataset had confounding variables that prevented the measurement of the strength of SAS, and was limited in its ability to detect when SAS is acting and in what tissues. Therefore, we designed a study using stickleback populations in 5 lakes across Vancouver Island. 250 samples from three age groups, fry, juveniles and adults, were collected from each lake. We also collected tissue samples from the spleen, gonads, and brain, for expression level analysis. After extracting DNA and RNA from the stickleback fish samples, we identified the sex of each individual by amplifying the IDH gene which has two copies in males but only one copy in females. DNA samples were then pooled by sex, age, and lake and whole-genome sequencing by pool-seq is currently ongoing, as well as expression level quantification by RNA-seq. When the sequencing is complete, we will determine at what life stage SAS acts, its targets on the genome, and the impact on the viability of males and females. We further believe this methodology could become generalized beyond sticklebacks and establish itself as the standard procedure for identifying SAS within a single generation.

Title: How will Climate Change Affect Rangeland Management Practices?

Presenting author: Kelley Mundy

Affiliation: TAMU - Rangeland, Wildlife, and Fisheries Management

Coauthors: Kelley Mundy, Hannah Moreno, Garrison Trichel, Humberto L. Perotto-Baldivieso

Evan P. Tanner

1 Texas A&M University, College Station, TX 77843, USA 2 Texas A&M University-Kingsville, Kingsville, TX 78363, USA

Abstract: Climate Change is affecting changes in cover dynamics in rangelands. Herbicides are valuable tools for rangeland management for controlling undesirable species and opening grazeable areas. Post-emergent herbicides should be applied between

temperatures of 18.3 and 29.4 °C. We used 30-year average data from 1990- 2019 and ensemble models with projections to 2040. Temperature data was used to model changes in the application ranges for herbicides. Our data shows that the number of counties above the application threshold increased from 7 to 25 in June, 22 to 77 in July, and 29 to 95 in August. With most post-emergent herbicides having an application range, temperature is projected to be a limiting factor, especially during the summer and winter seasons, which can reduce the ability to use herbicide as a management strategy by 2040.

Title: Using Drone Imagery to Evaluate Post-Grazing Herbaceous Vegetation Structure

Presenting author: Shanna Gleason

Affiliation: TAMU Rangeland, Wildlife & Fisheries Management

Coauthors: Humberto L. Perotto-Baldivieso, Department of Rangeland, Wildlife, & Fisheries Management, Texas A&M University Michael T. Page, Compass Environmental Solutions Jose Silverio Avila-Sanchez, Borderlands Research Institute, Sul Ross State University

Abstract: Grazing has traditionally been used primarily to promote forage growth for livestock. For many Texas landscapes, there is an increasing focus on wildlife and multi-use management. The ability to use grazing to manipulate habitat is becoming increasingly valuable to land managers. One game species important to Texas, the northern bobwhite (*Colinus virginianus*), require variation in vegetation structure to fulfill cover needs and to facilitate movement and feeding. Quantifying the spatial heterogeneity of a grazed landscape is useful for evaluating the habitat available to northern bobwhite, and to assess the effectiveness of grazing. To measure heterogeneity, traditionally on-the-ground sampling would be used. Drone imagery however, provides quicker, more accurate data collection with increased sampling coverage. The specific objective of this study was to use drones to collect herbaceous plant height data to quantify spatial heterogeneity following a grazing event. Seven 27-ha drone flights were conducted in a grazed pasture in Duval Co., TX in 2021. Using structure-from-motion technology, the plant heights were derived from the imagery. These heights were classified into four categories: < 5cm (representing bare ground), 5-30cm (representing optimal herbaceous height for northern bobwhite), 30-40cm (representing target grazing height), and >40cm (representing herbaceous vegetation too tall/dense for northern bobwhite). The class and patch data were then used to compute relevant landscape metrics. The 5-30cm category has the highest mean patch area, while the 30-40cm category had the highest patch density. The Euclidean Nearest Neighbor distance was lowest for the 5-30cm and 30-40cm categories. These results indicate a very heterogenous landscape in terms of herbaceous structure. Patches of optimal heights are close enough for ease of movement, and they take up most of the landscape, providing abundant habitat opportunities. These results provide useful insight for future management decisions, and offer new techniques for gathering and assessing vegetative data.

Title: Comparison of morphological diversity of catfishes in channel and floodplain habitats of the Rupununi River, Guyana.

Presenting author: Kendall Hastings

Affiliation: Texas A&M University Department of Ecology and Conservation Biology

Coauthors: Takiya Jackson, Department of Ecology and Conservation Biology, Texas A&M University Calvin Young, Department of Ecology and Conservation Biology, Texas A&M University Kirk Winemiller, Department of Ecology and Conservation Biology, Texas A&M University Leslie Winemiller, Department of Ecology and Conservation Biology, Texas A&M University Megan Beeksmas, Stephen F. Austin University Sophie Scott, Stephen F. Austin University Lily Williams, Stephen F. Austin University Donald B. Burt, Stephen F. Austin University Carmen Montaña, Stephen F. Austin University James VanKley, Stephen F. Austin University

Abstract: In the Neotropics, catfishes (Siluriformes) span diverse habitats, feeding behaviors, and trophic niches, making them an ideal group to study and compare ecomorphological diversity. We surveyed catfish diversity in the Rupununi River, Guyana, South America during the end of the low-water season in 2023. We collected 22 genera and 28 species from river channel and floodplain habitats. Twenty-eight morphological characteristics were measured, including total length, standard length, head length, head height, gape width, interorbital distance, eye position, eye diameter, snout length, snout protrusion, body depth, caudal peduncle length, depth, and width, depth below midline, dorsal fin height and length, anal fin height and length, caudal fin depth and length, pelvic fin length and height, and adipose fin height and length. Species were ordinated and morphological spaces in the channel vs. floodplain were analyzed using principal components analysis. There was broad overlap in morphological space between floodplain and river-channel assemblages; however, there was greater diversity of morphotypes in the river channel. We infer from these results that catfishes occupying habitats in the Rupununi River channel have greater niche diversity that may be associated with higher habitat heterogeneity and more complex species interactions.

Title: Unveiling the Microbial Tapestry: Probing Protistan Abundance and Diversity in Hydrothermal Vent Plumes of the NE Pacific

Presenting author: Alexis Adams

Affiliation: A&M Oceanography

Coauthors: Kayla Knedd and Dr. Sarah Hu (Department of Oceanography, Texas A&M University) and Dr. Julie Huber (Department of Marine Chemistry and Geochemistry at Woods Hole Oceanographic Institution)

Abstract: Hydrothermal vents have emerged as crucial centers of primary productivity in the dark ocean. The nutrient rich diffuse vent fluid creates a unique ecological niche for single-celled eukaryotes, or protists. Two notable hydrothermal vents fields in the NE Pacific off the Juan de Fuca Ridge, Axial Seamount and Gorda Ridge, were analyzed to see if there is greater protistan abundance and diversity within the hydrothermal vent plume compared to diffuse vent fluid. Prokaryotic cell counts from the 2023 Axial Seamount research expedition indicated an increased presence of prokaryotes, relative to background

seawater. This means the plume environment includes an abundance of microbial food, one capable of supporting larger protist communities. Research was further supplemented with 18S rRNA gene amplicon sequencing and used to analyze protistan diversity and abundance within the plume, background, and vent. Specifically, elevated ASV presence within the plume and vent indicated greater species richness compared to the background seawater alongside additional analysis to indicate presence of increased protistan diversity at the phylum level.

Title: Meta-Analysis of Threats to Freshwater Fish of North America

Presenting author: Dylan Kim

Affiliation: Department of Biology, Baylor University

Coauthors: Mark Lueders, Department of Environmental Sciences; Dr. Ryan McManamay, Department of Environmental Science, Baylor University

Abstract: Over 800 freshwater fish species reside in North America, with each facing varying levels of imperilment from any number of sources. The categorization and analysis of these sources is vital, not only for understanding the distinct ways in which these species are affected by threats, but also to assist in organizing efforts to preserve them—and by extension, the freshwater ecosystems they inhabit. Herein, we categorize and condense compiled threat data in a concise but informative meta-analysis. The analysis builds on existing broad categorization of threats, with subsequent division into subcategories and keywords for increased specificity. Utilizing these keywords allows for large quantities of text to be parsed for relevant information and is an essential tool in our threat analysis. We use prevalence of threats, threat subcategories, and keywords to provide insight into the trends in not only threats to North American fish species, but also their descriptions among conservation scientists.

Title: Who Reigns Supreme in the Mid-Cayman Rise Deep-sea Hydrothermal Vents?

Presenting author: Kayla Nedd

Affiliation: Texas A&M University, Department of Oceanography

Coauthors: Alexis Adams (Texas A&M University, Department of Oceanography), Dr. Julie Huber (Woods Hole Oceanographic Institution, Department of Marine and Geochemistry), and Dr. Sarah Hu (Texas A&M University, Department of Oceanography)

Abstract: Deep sea hydrothermal vents play a critical role in nutrient cycling in the deep ocean. Their food web dynamics support a plethora of organisms both on the micro and macro level. Most research has been centered around bacterial and archaeal organisms. Historically, protists have been excluded from this conversation, despite their direct impact on deep-sea food web dynamics. Understanding the role protists play in nutrient cycling and prokaryotic mortality is imperative, especially in an aphotic zone, where chemosynthesis is prevalent. Vent samples taken from Mid-Cayman Rise have been found to have three putative endemic taxa. However, the species level abundance is unknown. This information will provide a glimpse into the microbial composition of these vent sites.

Using the R programming language, a statistical analysis will be run on the amplicon sequence variants of these putative endemic taxa to determine their species diversity.

Title: When, where, and what was dinner? Capturing dietary niche variation in North American mammals.

Presenting author: Dana Reuter

Affiliation: Department of Ecology and Conservation Biology, Texas A&M

Coauthors: Varun Chapa Department of Ecology and Conservation Biology, Texas A&M , Helen Hunter Department of Ecology and Conservation Biology, Texas A&M , Amanda Fleming, Mathis Wilson Department of Ecology and Conservation Biology, Texas A&M , Rayyan Zulfiqar Department of Ecology and Conservation Biology, Texas A&M , Taylor Speier, Anish Ravi, Gabriel Alexander Department of Ecology and Conservation Biology, Texas A&M , Robert Guralnick Florida Museum of Natural History, A. Michelle Lawing Department of Ecology and Conservation Biology, Texas A&M

Abstract: The way organisms obtain energy from their surroundings drives a cascade of adaptations, both physical and behavioral. Currently, few resources allow for the study of within-species (intraspecific) variation in mammalian diets. Limited knowledge of diet variation across spatiotemporal scales also leads to less robust between-species (interspecific) comparisons. Knowledge of individual, temporal, and geographic diet variation is essential for understanding the conservation, ecology, and evolution of mammals. Our aim is to create a database of quantitative North American mammalian diet data which captures geographic and temporal diet variation. We purposefully sought to improve data access without losing metadata from the primary sources. Through literature searches, we aggregated diet data from primary research papers and previously published databases. Each record includes detailed taxonomic information for the predator, the prey item, the fraction of the predator's diet that the prey represents, sampling methods, quantification protocols, and detailed spatiotemporal information. We collected over 230 references and 3,858 dietary records for 28 species. Most of the current dataset constitutes carnivoran predators and includes 166 unique families of consumed plant and prey items. We found that there is not even representation in the literature with Puma concolor having 58 references and others, such as some bats, having none. Dietary records for many mammals span a wide number of localities and years making our data valuable for understanding human impacts on species diets through time and across geographic space.

Title: Hemi-parasitic mistletoes in a Madagascar rainforest show highly skewed host tree associations based on ecology and phylogenetic relationships

Presenting author: Julieanne Montaquila

Affiliation: Rice University

Coauthors:

Elena Siemens, Rice University; Divya Saikumar, Rice University

Abstract: Mistletoes encompass a polyphyletic group of hemi-parasitic plants that grow on trees and other woody hosts from which they steal water and minerals. In Madagascar, the endemic mistletoe genus *Bakerella* is a staple food source for wildlife, including multiple endemic lemurs such as the brown mouse lemur, *Microcebus rufus*. We analyzed data from Ranomafana National Park (RNP) on *Bakerella* infestation of surveyed trees to evaluate patterns of host-association and better understand the ecology of this unique yet understudied parasitic plant. We hypothesized that *Bakerella* will be most common on trees pollinated by *Microcebus rufus*, a small lemur that also disperses *Bakerella* seeds in the canopy. We expected to see physiological traits of trees, such as wood density, correlated with infestation rates as well. We analyzed about 4,500 observations of individual trees of 207 distinct species surveyed in RNP for *Bakerella*. We found that the generalist/specialist index (G) for *Bakerella* is 0.21, indicating *Bakerella* is less of a generalist than assumed observationally. Additionally, when we analyzed the Manly Index for preference of hosts, we found that there was significant bias for *Bakerella* to over-infest some tree species and underinfest others. Twenty percent of *Weinmannia bojeriana* individuals were infested with *Bakerella* despite making up only about 2.5% of the overall tree community and being relatively spatially dispersed in the forest. Surprisingly, wood density was not correlated with *Bakerella* infestation. We will additionally be examining phenology and phylogenetic relatedness as a potential underlying variable, which could point to traits for coevolution with mistletoe in high-affinity clades or the evolution of anti-mistletoe defenses in low-affinity clades. By developing a greater comprehension of the parasite-host ecology of *Bakerella* we can better understand the complex ecological interactions of a highly biodiverse rainforest and help conserve wildlife that depend on *Bakerella* mistletoe.

Title: Using Geographic Information Systems to examine the potential Impact of Wind Turbines on Grassland Birds

Presenting author: Drew Berdo

Affiliation: Texas State University- Biology

Coauthors: Joe Veech, Department of Biology, Texas State University

Abstract: While wind energy is a known way for humans to reduce emissions from fossil fuels, there is limited public discourse on how wind energy impacts wildlife. Grassland birds are one of the most threatened bird groups in the world and much of their habitat overlaps with the majority of current and future wind energy capacity in the United States. I am using data collected from the North American Breeding Bird Survey (BBS) and wind turbine data from the United States Geological Survey to examine the potential impact of wind turbines on how grassland birds utilize available habitat. I created a Turbine Proximity Index (TPI) that quantifies the potential impact of wind turbines on grassland birds through spatial analysis in ArcGIS Pro. The index quantitatively assesses BBS routes across grasslands of North America based on how they are potentially impacted by turbines. This index takes into account the number of turbines within a set distance of the route. Through statistical analysis, I will use a Before-After Control Impact (BACI) analysis to assess the relationship between the TPI and bird abundance and species richness along a selection of BBS routes.

Title: Anglers and Spotted Seatrout: Using Participation Preferences to Understand Angler Diversity

Presenting author: Danial Nayeri

Affiliation: Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University

Coauthors:

Daniel G. Pilgreen, Gerard T. Kyle, William E. Smith (Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University)

Zack Thomas (Texas Parks and Wildlife Department)

Steve Sutton (Community Outreach and Engagement, Atlantic Salmon Federation)

Abstract: Recreational fishing represents a prominent human use of coastal resources. Managing diverse motivations and preferences is a consistent challenge for natural resource managers. Recreation specialization is a process in which participants become more specialized and exhibit preferences for participation style as they gain experience. These specific styles of participation (SOP) serve as a useful tool for fisheries managers to understand the preferences and needs of their diverse users by meaningfully segmenting the population. Previous studies have developed a SOP self-classification measure to classify fishing guides on context-specific SOP attributes such as tackle and bait type, casting tactic, and targeted species. While previous research has examined SOP's utility in angler segmentation, this study aims to broaden it to general recreational anglers and investigate its utility for resource management. Data were collected from 846 licensed anglers in Texas, including recreational anglers (n = 491) and fishing guides (n = 355). The survey, developed with the Texas Parks and Wildlife Department, was administered online through email using a modified Dillman method in fall 2023. The survey included items assessing spotted seatrout angling satisfaction, management preferences, and demographics alongside the SOP self-classification measure. Statistical analyses, including chi-squares and t-tests were conducted to investigate the differences in SOP, satisfaction, and management preferences across guides and recreational anglers. Analysis of variance (ANOVA) was used to examine differences in satisfaction and slot regulation preferences across SOP in anglers. Findings support the extended use of the SOP self-classification measure in populations that exhibit diverse levels of specialization. Additionally, significant differences were observed in preferences for management across SOP. Although prescribing regulations to meet the needs of diverse constituents is a challenging task, the SOP self-classification measure offers fisheries managers a user-friendly approach to classify their diverse constituents and leverage SOP to identify common management preferences across users.

Title: Stealth Democracy and Exotic Wildlife Ranching in Texas

Presenting author: Consuelo Azuaje

Affiliation: Texas State University - Biology Dept

Coauthors: Dr. Chris Serenari, Department of Biology at Texas State University

Abstract: Humanity is engaged in an era of societal norm renegotiation wherein behaviors, values, and ideas once treated as axioms are becoming increasingly challenged. At the same time, life on Earth is experiencing an increasingly sharp crisis of biodiversity loss that is transforming ecosystems around the globe for all organisms that depend on them. The nexus of norm renegotiation and biodiversity loss complicates wildlife governance and highlights a need to examine evolving nature conservation norms. One major debate is over the commodification of wildlife movement which fundamentally challenges the normative social construct of nature conservation. Exotic wildlife ranching serves as an example of society's struggles to reconcile nature conservation norms with economic goals in an increasingly polarized social and political atmosphere. Without proper management, sociopolitical conflict divides segments of society and stalls policy innovation and success. Nevertheless, exotic wildlife ranching is experiencing a global boom and is worth several billion dollars. However, beliefs about how exotic wildlife governance should work is under-explored. Specifically industry members' views on the industry's effects ecosystems and how the industry should relate to society are unknown. To address these information gaps, we applied stealth democracy theory to a Texas context. Texas is estimated to have the largest concentration of exotics of any geopolitical space in the world. We surveyed 3,258 industry members using a list obtained from the Texas Parks and Wildlife Department. Regression analysis of 416 total responses will provide insight into industry members' motivation for participating in their industry, to what degree society should influence their industry, and what governance arrangements are acceptable.

Title: Examining Trends in Body Mass of Endemic Madagascar Shrews

Presenting author: Alexia Engel

Affiliation: Department of Biology

Coauthors: Maria A. Hurtado-Materon. Ecology and Evolutionary Biology Program, Texas A&M University, College Station, TX 77843. A. Michelle Lawing. Department of Ecology and Conservation Biology, Texas A&M University, College Station, TX 77843

Abstract: Sexual dimorphism is the visual morphological differences in sexes. These differences can include size, color, ornaments, or anatomically supplied weapons. The purpose of having these differences are typically for sexual selection indicating various fitnesses to an environment. For that reason studies of dimorphism provide insight into the evolutionary mechanisms that can drive phenotypes. Body mass data and sexual dimorphism data on Malagasy mammals all within the Tenrecidae family in Madagascar was utilized. This data includes subfamilies Oryzorictinae, Tenrecinae, Geogalinae, and Nesomyinae. Although in this family it is been found that males are larger than females, this trend is not general to the entire family. In the Oryzorictinae subfamily females are primarily larger, but in the Tenrecinae, Geogalinae, and Nesomyinae subfamilies the male is larger than the female. Data on Lemuriformes, the largest group of mammals without male-based sexual dimorphism, is compared to the data of the Oryzorictinae. The environmental factors affecting both the Lemuriformes and the Oryzorictinae is explored as a possible explanation as to why females are larger than males in both of these subfamilies.

Title: Effects of Microplastic Uptake on Amphibian Growth & Development

Presenting author: Andre Felton

Affiliation: University of Texas at San Antonio, Department of Integrative Biology

Coauthors: Daniela Cortez, Oscar Hernandez, Cristina Mendez, Meredith Slimp, Brianna Zamarripa, and Jeffrey Hutchinson - Department of Integrative Biology, University of Texas at San Antonio

Abstract: Global declines of amphibian populations have primarily focused on classic chemical contaminants and compounds (i.e., pesticides, fertilizers, salts, etc.), but there is a paucity in research addressing the role of emerging pollutants such as microplastics and nanoplastics on amphibian health and contributory role to global declines. Microplastic pollution has been shown to be ubiquitous across freshwater systems yet our understanding of exposure routes and interactions within ephemeral fluvial systems that exhibit high spatiotemporal variability in MP concentrations on co-occurring amphibians that utilize ephemeral pools for reproductive and development purposes is limited. In this study, the effect of chronic microplastic exposure on amphibian growth and development throughout larval and metamorphic stages was examined using *Xenopus laevis*. Tadpoles across four treatment concentrations were exposed to secondary generated polyethylene microplastic fragments throughout pre- and pro-metamorphic development. Results regarding impacts on growth and developmental stages are currently being processed and analyses will be reported during the poster presentation. Amphibians are among the most threatened taxa globally and have served as effective models for other ecotoxicological studies, yet less than 1% of all studies investigating the effects of MP on biota have used amphibians. As global plastic production is expected to continue and increase, understanding MP exposure routes and effects of chronic exposure on amphibian health can provide insight to effective mitigative practices in conservation efforts.

Title: What Does the Puma Like for Dinner?; Taxonomic, temporal, and geographic variation in the diet of the Mountain Lion.

Presenting author: Amanda Fleming

Affiliation: Department of Biology, Texas State University

Coauthors: Varun Chapa, Department of Veterinary Medicine and Biomedical Sciences, Texas A&M University; Anish Ravi, Department of Ecology and Conservation Biology, Texas A&M University; Robert Guralnick, Florida Museum of Natural History; Michelle Lawing, Department of Ecology and Conservation Biology, Texas A&M University; Dana Reuter, Department of Ecology and Conservation Biology, Texas A&M University

Abstract: Puma concolor is a keystone species that contributes to top-down ecosystem regulation across both the American continents. Analyzing the diet of *P. concolor* is crucial to understanding what regulates their populations, as many have been displaced by human activities. Our goal for this project was to analyze diet variation of *P. concolor* over time and by location. We collected detailed data on the diet of *P. concolor* from previously published scat analyses to reveal patterns in diet variation. We averaged prey items by

family to make the diet records comparable across the numerous studies. Additionally, we identified biases that arose from differences in primary quantification method. We found that the most commonly recorded families with the highest diet percentage are Cervidae, Dasypodidae, Leporidae, and Tayassuidae. We used those four prey families to investigate trends through time. We then plotted those families by latitude and longitude. . We found that both Cervidae and Leporidae decreased in diet proportion in the references over time while Dasypodidae and Tayassuidae increased. Leporidae is more frequently consumed below -38 degrees latitude, Dasypodidae between -45 and -55 latitude, and Cervidae above the equator. The most variation was observed in the top prey family between 0 and -23 degrees latitude. Our study shows that *P. concolor*'s diet varies across its distribution in patterns that should be further analyzed to determine ecosystem effect. This insight has conservation implications for the diverse communities the puma inhabits across its range.

Title: The Human Dimensions of the Big Bend

Presenting author: MK Futrell

Affiliation: Human Dimensions of Natural Resources lab, RWFM, TAMU

Coauthors: Gerard Kyle, Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University, Daniel Pilgreen, Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University

Abstract: Understanding the human dimensions of natural resource management is crucial to create intersectional conservation efforts. One way we can do this is through the use of visitor data to better inform park and protected area management. Through the Visit Big Bend Initiative, we surveyed nearly 900 visitors to five sites in Texas' Big Bend region in 2022.

We collected zip code data, routing data, economic data, and recreation data, all of which were processed in R and visualized in QGIS to produce maps that help us understand who is visiting the Big Bend, how they get there, where they are coming from, and what they are doing while they are there. Making data like these accessible and usable to local governments and ecologists alike is crucial for the advancement of ecotourism and helping local government agencies to protect the native wildlife and beautiful landscape in the Big Bend region.

In summary, our work reveals the human side of managing the Big Bend region. Understanding how and why people interact with natural spaces enriches our understanding and supports better, collaborative ways to take care of this diverse place.

Title: Using genomic tools to enhance biodiversity assessments in karst subterranean estuaries

Presenting author: Muntadher Mashaan

Affiliation: Texas A&M University-San Antonio

Coauthors: Muntadher Mashaan, Danielle Bragg, Fernando Calderon Gutierrez, and Elizabeth Borda

Abstract: Aquifers of the Yucatan Peninsula and Cozumel Island are characterized by an extensive fresh or brackish water layer converging into karst subterranean estuaries along karstic coastlines, exhibiting salinity stratified water layers separated by a halocline. These systems host distinct faunal communities influenced by historical and present-day hydrogeological changes and are considered hotspots for stygobionts (i.e., aquatic cave adapted fauna). Most studies have focused on macrofauna living in the water column, with limited attention given to benthic faunal communities. This study employs low pass whole genome sequencing, also known as genome skimming, from sediment samples from cave systems El Aerolito (Cozumel), and Crustacea (Caribbean Coast of the Yucatan Peninsula). This method potentially allows for simultaneous biodiversity assessments of macro-, meio- and micro-fauna. These caves were selected due to their unusually high macrofaunal species richness (El Aerolito) and high densities (El Aerolito and Crustacea). As several species from these aquifers are federally listed as vulnerable to endangered, the use of genomic assessments is expected to improve biodiversity estimates at the community level and characterize poorly known and studied taxa.