



ECOLOGICAL INTEGRATION SYMPOSIUM 2023

Ecology through time:
perspectives from the past, present, and
future

March 30th - 31st, 2023

Texas A&M University, College Station, Texas

PROGRAM BOOK¹



Welcome to the 23rd annual Ecological Integration Symposium!

Texas A&M University's Ecological Integration Symposium (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.

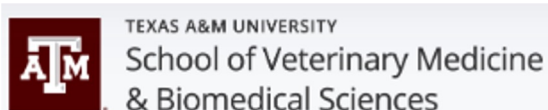
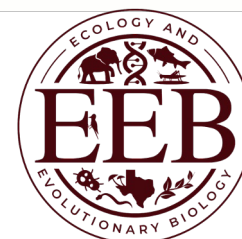
Continuing the tradition of EIS since its inception in 2000, we are a graduate student-run event that is open to the public and free to attend.

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.

Special Thanks to Our Sponsors:



Schubot Center

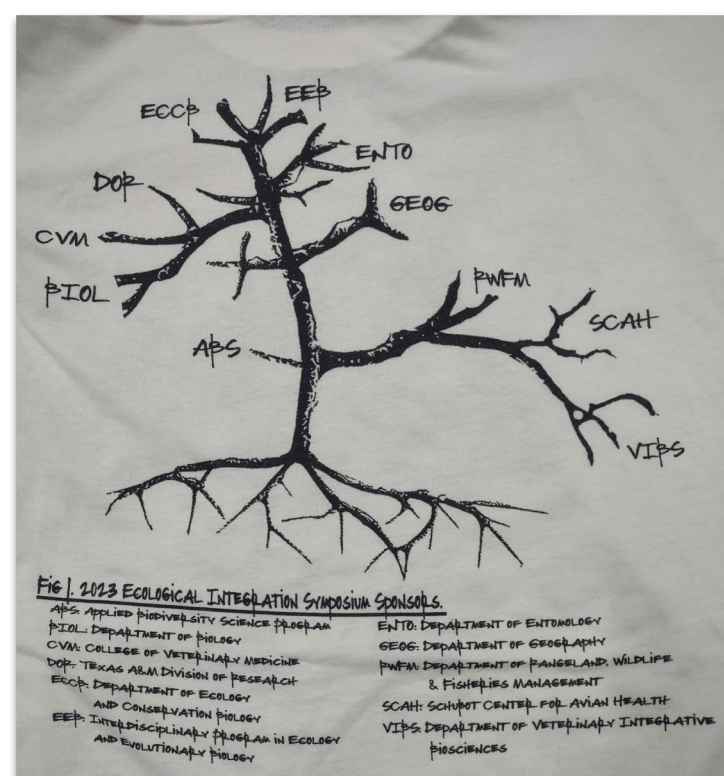
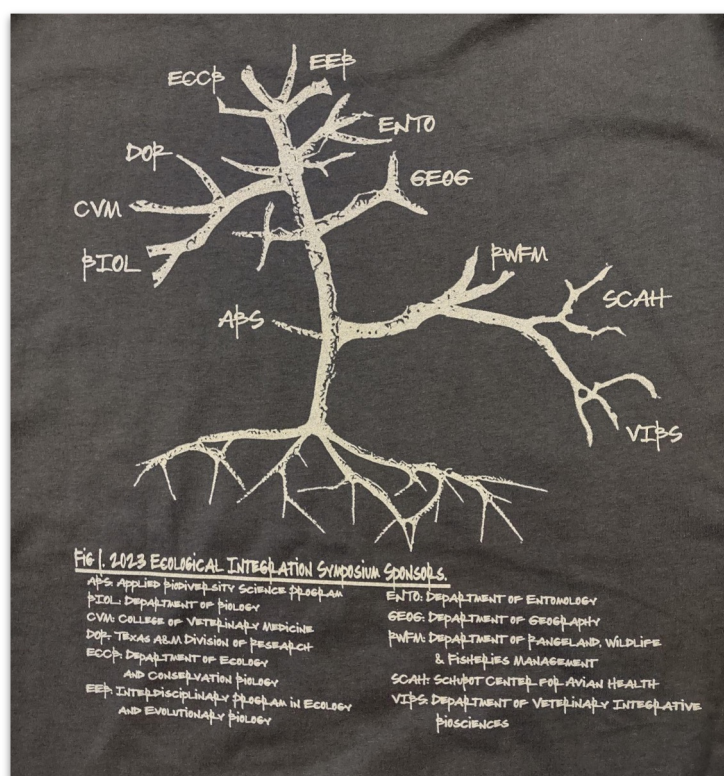


TEXAS A&M UNIVERSITY
Biology

EIS Merchandise



The new 2023 EIS merchandise along with limited edition vintage merchandise are available for [pre-order](#)! There are shirts, mugs, and hats for sale!



Symposium Schedule



Thursday, March 30th
Annenberg Presidential Conference Center

Time	Event	Location
8:00 AM - 4:00 PM	Registration	APCC Lobby
8:45 - 9:00 AM	Welcoming Remarks	APCC Frymire Auditorium
9:00 - 10:00 AM	Kelly Zamudio	APCC Frymire Auditorium
10:00 - 10:10 AM	Break	APCC Lobby
10:10 - 11:10 AM	Walter Jetz	APCC Frymire Auditorium
11:10 - 11:20 AM	Break	APCC Lobby
11:20 AM - 12:20 PM	Emília Martins	APCC Frymire Auditorium
12:30 - 1:45 PM	Lunch	Leach Teaching Gardens
2:00 - 3:00 PM	Daniel Simberloff	APCC Frymire Auditorium
3:00 - 3:15 PM	Break	APCC Lobby
3:20 - 4:20 PM	Rodrigo Medellín	APCC Frymire Auditorium
4:20 - 4:30 PM	Break	APCC Lobby
4:30 - 5:30 PM	Speaker Panel	APCC Frymire Auditorium
5:30 - 8:00 PM	Announcements & Happy Hour	Carney's Pub and Grill 3410 S College Ave Bryan, TX 77801

Symposium Schedule



Friday, March 31st
Rudder Tower

Time	Event	Location
8:00 AM - 3:00 PM	Registration	Rudder Tower Lobby
8:00 - 9:00 AM	Poster check-In	Rudder Tower Lobby
9:00 - 10:00 AM	Student Oral Presentations	Rudder Tower 401, 410, 501
10:00 - 10:20 AM	Break	Rudder Tower 407
10:20 - 11:20 AM	Student Oral Presentations	Rudder Tower 401, 410, 501
11:20 AM - 2:00 PM	Lunch	Rudder Tower 601
12:00 - 2:00 PM	Student Poster Session	Rudder Exhibit Hall
2:00 PM - 3:00 PM	Student Oral Presentations	Rudder Tower 401, 410, 501
3:15 PM - 3:30 PM	Awards & Closing Remarks	Rudder Exhibit Hall
6:00 PM	Social (Food & Drinks Provided)	Off-campus



Thursday morning's talks will be in the Annenberg Presidential Conference Center from 9:00 AM -12:20 PM, with lunch from 12:30-1:45 PM in the Leach Teaching Gardens. The Gardens takes 18 minutes by foot or 5 minutes by bus from Annenberg. **Bus 5** arrives at the Bush School stop every 7 minutes and arrives at The Gardens (bus stop: AgriLife Center Building). Any campus parking pass can be used to park in lot 43 outside Annenberg.

Talks resume at 2:00. You can take **Bus 5** back to the Bush School from the stop across the street from the AgriLife Center. If you do not have a TAMU parking pass, a limited number of paper parking passes are available at the registration desk.

Getting Around Campus

Interactive Campus Map:

<https://www.tamu.edu/map/index.html>

Daily Bus Schedules:

<https://transport.tamu.edu/busroutes/>

Hourly Parking Lot Information:

<https://transport.tamu.edu/Parking/pbp.aspx>

Additional TAMU Transportation Information:

<https://transport.tamu.edu/>



Welcoming Remarks from Dr. Brendan Roark

Associate Vice President for Research

Thursday, March 30th at 8:45 AM

Annenberg Presidential Conference Center, Frymire Auditorium

Dr. Roark is the Associate Vice President for Research and the Director of the Environmental Programs in Geosciences. His research interests focus primarily on understanding natural and anthropogenic climate variability over the last 50,000 years emphasizing biogeochemical cycling and paleoceanographic reconstructions in marine and estuarine environments. His research employs a diverse analytical toolbox using environmentally sensitive isotopic ($\delta^{13}\text{C}$, $\delta^{18}\text{O}$ and $\delta^{15}\text{N}$) and trace element proxies (Sr, Mg, and Cd) to reconstruct environmental variables such as temperature, ocean circulation, salinity, river inflow, and nutrient utilization in different natural archives. He also employs a variety of geochronology methods (^{14}C , U/Th, and skeletochronology) in order to develop high-resolution chronologies in marine archives. Finally, he runs a well developed and diverse field program ranging from small boat coral drilling operations to blue water oceanography cruises with ROVs, submersibles, and AUVs as a critical part of his research program.

Plenary Speaker Line-Up

Thursday Morning, March 30th



Dr. Kelly Zamudio

9:00 - 10:00 AM

Professor at the University of Texas at Austin and an Endowed Fellow of the Doherty Regents Chair in Molecular Biology

TBA



Dr. Walter Jetz

10:10 - 11:10 AM

Professor of ecology and evolutionary biology in the School of the Environment at Yale University

“Assessment and monitoring of global biodiversity change”



Dr. Emília Martins

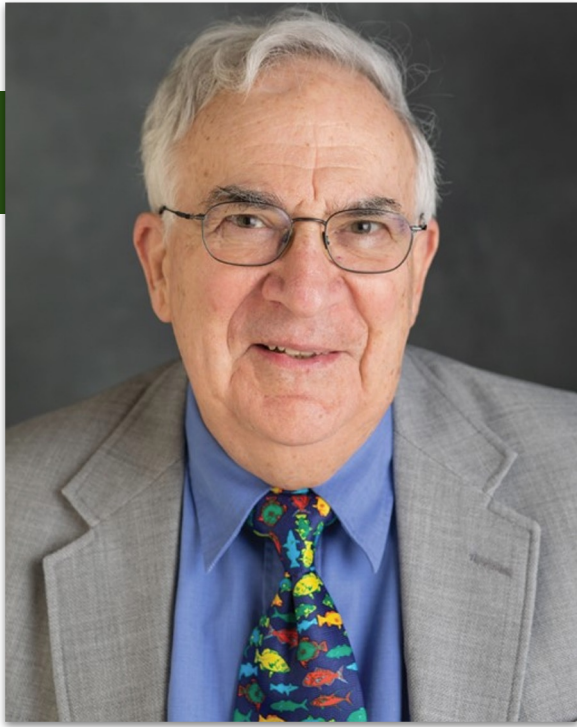
11:20 AM - 12:20 PM

Professor at the School of Life Sciences at Arizona State University

“Predicting behavior and sensory resilience in a changing world”

Plenary Speaker Line-Up

Thursday Afternoon, March 30th



Dr. Daniel Simberloff

2:00 - 3:00 PM

Nancy Gore Hunger Professor of Environmental Studies at the University of Tennessee

“The past, present, and future of invasion science”

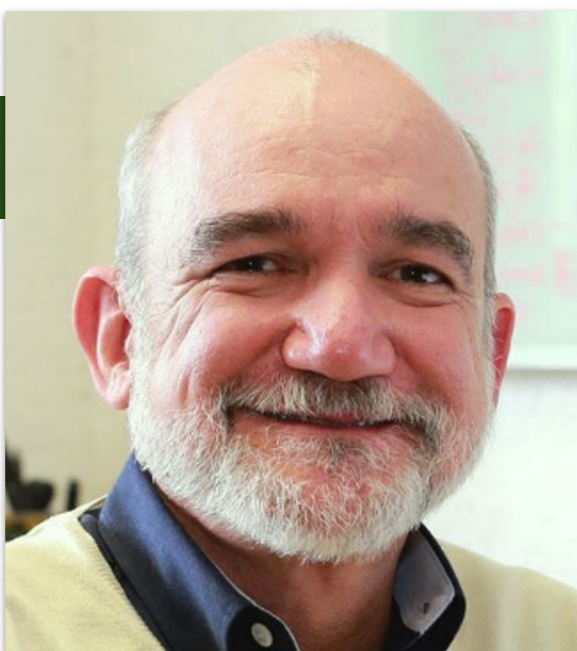


Dr. Nancy Grimm

Cancelled

Virginia M. Ullman Regents Professor of Ecology at Arizona State University

“Nature-based solutions for cities to adapt and transform in response to climate change”



Dr. Rodrigo Medellín

3:20 - 4:20 PM

Senior Professor of Ecology at the Universidad Nacional Autónoma de México

“How to do conservation science, implement it, and not die trying”



Speaker Panel

5:30 PM

Please join us at 4:30 on Thursday, 3/30/23, for an engaging discussion with our plenary speakers where you will have the opportunity to ask questions to researchers leading their respective fields!

To submit your questions for the plenary speakers, click this [link](#) or scan the QR code!



Student Oral Presentations



Friday, March 31st | 9:00 - 10:00 AM

Start Time	Room 401	Room 410	Room 501
9:00 AM	<p>Katie Sanbonmatsu The Evolution of Sexual Systems in Mosses</p>	<p>Johnathan Ellard A multiscale conceptual framework to predict movement and habitat associations of an imperiled megafish, the Alligator Gar (<i>Atractosteus spatula</i>)</p>	<p>Miriam Catalan Winter Heatwaves: Understanding the Lasting Effects of Record-breaking December Temperatures on Stand Transpiration in a Loblolly Pine Forest</p>
9:15 AM	<p>Lydia Morley Turnover importance: Quantifying generalism in terms of spatial heterogeneity</p>	<p>Yasmin Quintana High dominance of invasive armor catfish linked with isotopic space shift and niche compression of native species in Guatemala</p>	<p>Justinn J. Jones Estimating Biophysical Parameters of Urban Trees on Texas A&M University Campus using Mobile Lidar</p>
9:30 AM	<p>Gage Strozier, Jayda Arriaga, Jack Bradford, and Rachel Kurian Plant Talk: Belowground Herbivory Enhances Aboveground Plant Volatile Emission and Increases Neighboring Plant Antiherbivore Defenses</p>	<p>Rose Blanchard Predictability and conceptual repeatability of the predator associated burst speed body shape in independently evolved populations of western mosquitofish</p>	<p>Marisa Collura Scaling up the Ladder: Estimating Tree Water Use by Integrating LiDAR in the Pineywoods</p>
9:45 AM	<p>Jorge Medina-Duran The revision of the eugregarines (<i>Apicomplexa</i>) of crickets and allies (Orthoptera: <i>Grylloidea</i>)</p>	<p>Hayden Roberts River Carpsucker versus Llano River Carpsucker: Morphological divergence of an undescribed catostomid</p>	<p>Sekinat Atobiloye Ecological Risk Assessment of Heavy Metals in Surface Water and Sediments of Urban Watersheds in Greater Houston</p>

Student Oral Presentations

Friday, March 31st | 10:20 - 11:20 AM



Start Time	Room 401	Room 410	Room 501
10:20 AM		Noah Santee Testing responsiveness of stream fish functional traits to anthropogenic riverscape alterations	Nikunj Goel A predictive theory of human mediated biological invasions
10:35 AM	Seema Rana Differential responses to double-stranded RNA (dsRNA) injection and feeding in orthopteran insect pests	Christopher Peterson Intergenerational heritability of methylation in stony corals	Dohee Kim Decoupled seasonality of carbon allocation in above and belowground activities
10:50 AM	Ali Lira-Olguin Molecular phylogenetics of the ectoparasitic sucking louse genera <i>Hoplopleura</i> and <i>Polyplax</i> (<i>Phthiraptera: Anoplura, Hoplopleuridae, and Polyplacidae</i>)	Maria A. Hurtado-Materon What trait-environment relationships can tell us about ecological and evolutionary dynamics	Nicole Havrilchak Gas exchange responses of diverse C4 grass species to drought
11:05 AM	Jenna Hulke Testing key tenants of the mating system model of complex life cycle evolution: does the trematode <i>Alloglossidium renale</i> show evidence of inbreeding depression?	Kasuni Daundasekara Identifying serpentine adaptation genes by tracing evolutionary-genomic history of <i>Streptanthus</i> , <i>Caulanthus</i> and their allied genera (<i>Brassicaceae</i>)	Austin Kelly Juniper's Legacy: Soil Infiltrability 10+ Years After Tree Death

Student Oral Presentations



Friday, March 31st | 2:00 - 3:00 PM

Start Time	Room 401	Room 410	Room 501
2:00 PM	<p>Griffin Nicholson Conspecific oophagy by tadpoles: importance as a source of anuran egg mortality and conditions for occurrence</p>	<p>Katelyn Sanchez Population genetic structure of Townsend's big-eared bats in the western United States</p>	<p>Lee May The production of destruction: How society invented the flammable Lost Pines "Forest" of Texas</p>
2:15 PM	<p>Nicole Stevens Occupancy and dispersal in a recently established population of the endangered St. Croix ground lizard (<i>Pholidoscelis polops</i>) and implications for conservation</p>	<p>Austen Ehrie Measuring Mantled Howler Monkey (<i>Alouatta palliata</i>) Testes via Parallel Laser Photogrammetry: Expanding the use of Non-Invasive Methodologies</p>	<p>Mariana Dairel How does fire history affect plant communities' regeneration in tropical savannas?</p>
2:30 PM	<p>Katrina Keith Functional Diversity in Songbirds of Concern</p>	<p>Colton Watts The eco-evolutionary dynamics of sexual traits that increase mate encounter rates</p>	<p>Stefanie Bergmans Activity related to lunar brightness and diel activity patterns of <i>Tapiridae</i> and <i>Felidae</i> species across Neotropical sites</p>
2:45 PM	<p>Madeleine Barham Nest Survival of White-tailed Hawks in South Texas During the 2021-2022 Breeding Season</p>	<p>Shannon Jarratt-Harris Aggression and Parental Care of <i>Nicrophorus orbicollis</i></p>	<p>Jodie M. McVane Fiber Hemp Agronomy for South Central Texas</p>

Student Poster Session

Friday, March 31st, 12 - 2 PM



Number	Presenter	Title
1	Elizabeth Elkins	Characterize urban tree attributes using terrestrial LiDAR and quantitative structure model
2	Miranda Peterson	Microhabitat estimation for the sedge wren in a south Texas wildlife refuge
3	Nicole Dautreppe	Seeking to mitigate avian malaria in Texas: The Grasshopper Sparrow
4	McKenna Sanchez and Katelyn Sanchez	Influence of Pesticide Usage on Avian Malaria Prevalence
5	Jordyn B. Walborn and Caitlin A. Clark	Parental Budgets and Feeding Behavior of Nesting White-Tailed Hawks
6	Mycha A. Van Allen	Lights Out Texas: A novel pipeline for detection of highly pathogenic avian influenza and ticks in wild passerines
7	Keegan Nichols	Improving disease resistance and queen quality of managed <i>Apis mellifera jemenitica</i> Rutter colonies in Saudi Arabia
8	Ashyaa Brown	Differences in Africanized and European honey bees (<i>Apis mellifera</i>): visitation of larval cells by nurses
9	Sydney Martinez	Pesticide residues in wax lead to premature self-removal behavior in honey bees (<i>Apis mellifera</i>)
10	MacKenzie Hoffman	Activity Patterns and Potential Interactions Among Cattle, White-tailed Deer and Wild Pigs
11	Chelsea Thorn	The complete mitochondrial genome of the gecko tapeworm, <i>Oochoristica javaensis</i> .
12	Isaac Brown	Carnassial relative blade length (RBL) as an indicator of carnivoran dietary ecology
13	Anthony Gomez	Evidence for temporal niche partitioning between two wild Suidae species in the Neotropics
14	Kaitlyn Romoser	Survey of Vulnerable Amazonian Manatees Using Environmental DNA (eDNA): Methods for Surveys in Remote Field Settings
15	Jennifer Berry	SARS- Cov-2 in Mammal Species
16	Peter Dorn	Direct fire is a potential agent of selection on animals

Student Poster Session

Friday, March 31st, 12 - 2 PM



Number	Presenter	Title
17	Javier Garcia Saldana	Impacts of Roads in Biodiversity, A Study of Roadkill of The Florida Panther (<i>Puma concolor coryi</i>)
18	Breann Richey	Behavior, constraints, and morphological response of a rapidly evolving invader, <i>Podarcis siculus</i>
19	Anni Wu	The Role of Behavior in Invasion Success: Using Behavioral Syndromes to Identify Behaviors that Aid in Species Invasions
20	Audra Hicks	Determining the Role of Neophilic Behavior in the Invasion Success of the Italian Wall Lizard
21	Sim Khemani	Boldness in the Italian Wall Lizard (<i>Podarcis siculus</i>) and its Invasion Success
22	Ryan Frazier	Diet of the Invasive American Bullfrog (<i>Lithobates catesbeianus</i>) in Western New Mexico
23	Madison Clark	Anuran Acapella: Variation of mating calls for <i>Leptodactylus fuscus</i> in Toco, Trinidad
24	Erica Hagmeyer	Assessing the Impact of Environmental Drivers on Fish Community Dynamics in a Headwater Stream
25	Chase Nimee	Biotic and abiotic factors influencing population dynamics of two endangered fish species (Smalleye Shiner <i>Notropis buccula</i> and Sharpnose Shiner <i>N. oxyrinchus</i>) in a Great Plains River in Texas
26	Cameron Olsen	Anatomical Survey of the Olfactory Apparatus in the Walking Catfishes (<i>Siluriformes: Clariidae</i>)
27	Caroline Crisp	Population Structure of Red River Pupfish (<i>Cyprinodon rubrofluviatilis</i>) in Three River Segments of the Upper Brazos River, Texas
28	Emilee Holderness	Morphological adaptations of the Western Mosquitofish, <i>Gambusia affinis</i> , in relation to naiad predation
29	Lucas Stevens	Quantifying Movement of Seven Imperiled Pelagic-Broadcast Spawning Fishes in Three Great Plains Rivers
30	Meghan Booknis	Mesohabitat and macroecological correlations for blue sucker (<i>Cycleptus elongatus</i>) occurrence in regulated rivers
31	Eli Torrez	Coexistence of three stream dwelling cyprinid fishes: Implications for conservation of urban streams in east Texas

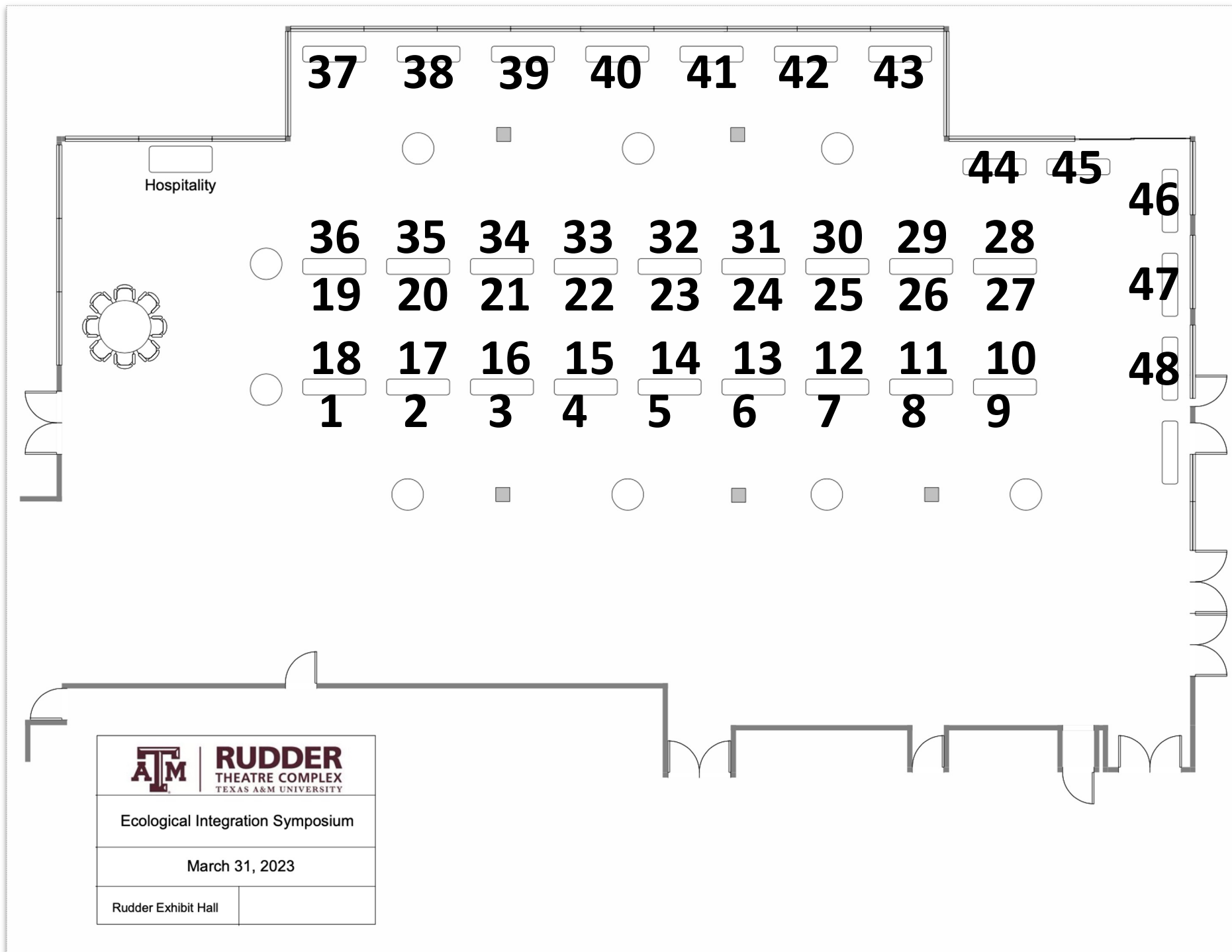
Student Poster Session

Friday, March 31st, 12 - 2 PM



Number	Presenter	Title
32	Claire Legaspi	Do Living Shorelines Enhance Fish Habitats?
33	Rebecca Mangold	Multiscale stream fish species-discharge relationships: The relative roles of evenness, density, and spatial aggregation
34	Brooke Torjman	Erosion-control structures enhance fauna but decrease microphytobenthic productivity in restored salt marshes in Galveston Bay
35	Norely Faz	Microbial Activity and Response to Temporal and Chemical Gradients in the Gulf of Mexico.
36	Joelle A. Roman	Bacteria and archaeal composition on the Texas coast following hurricane Harvey
37	Siena Stassi	Microplastic abundance and diversity in East Texas stream food webs
38	Sofia Oliveira	Squash defense response to striped cucumber beetles aggregation pheromone
39	Luis Hurtado	Niche Divergence in bryophytes with extreme sex-based segregation
40	Nicholas Chow	Photostimulating the ER-chloroplast junction, but not only the ER, results in immediate cytosolic calcium release in <i>Arabidopsis hypocotyl</i> cells
41	Leonardo Collazos	The seasonally dry forests of Peru: a re-analysis of their diversity patterns and floristic relationships
42	Analisa Flores	Spatial and temporal variation in orchid-insect communities: Insights from motion capture field cameras
43	Lydia Morley	Machine learning and motion capture field cameras: Can computers help us organize our raw observational data?
44	Ryne Maness	The complete mitochondrial genome of the invasive Mediterranean house gecko (<i>Hemidactylus turcicus</i>).
45	Richie Rasulis	The first recombination map for the blue whale, <i>Balaenoptera musculus</i>
46	Ashrafou Ouro-Djobo	Genetic Diversity of Viruses associated with Texas wheat fields
47	Elyssa Garza	Loci underlying plant tolerance to harsh serpentine soils
48	Megan Copeland	Genome assembly of an expanding forest pest: <i>Dendroctonus frontalis</i> (southern pine beetle)

Poster Session Layout





ORAL PRESENTATION ABSTRACTS

Session 1
Friday, March 31st 9 - 10 am

Oral Presentations

9:00 AM - 10:00 AM Session
Rudder Tower, Room 401

Bold name(s) indicates presenting author(s)

9:00 AM – The Evolution of Sexual Systems in Mosses

Katie Sanbonmatsu, Daniel Spalink
Ecology and Conservation Biology, Texas A&M University
katie.sanbonmatsu@tamu.edu

The frequency with which bryophytes transition between sexual states is unmatched by their vascular plant relatives, and mosses reign supreme in this regard. Yet, the ecological and evolutionary mechanisms that drive the evolution of separate and combined sexes in mosses remain somewhat obscure. Here, aim to re-evaluate the evolutionary ecology of sex in mosses. To do so, we use the largest sexual state database of mosses to date, the most comprehensive species-level phylogeny of mosses, and a massive geographic database to uncover the patterns and processes governing moss reproduction. We employed several methods and models, including HiSSE, ChromEvol v2.0, and Generalized Dissimilarity modeling to test important hypotheses about the evolution of sexual systems in this enigmatic group of plants.

We found that the ancestral state in mosses is dioicy, as demonstrated by previous studies. We also verify using the most modern techniques that monoicy is associated with higher rate of diversification, but our results suggest a much higher value than those previously reported in mosses. Most importantly, we demonstrate that monoicous lineages do not have larger range sizes, but instead have smaller ranges with low range overlap between closely related species. We interpret this as a phenomenon in which monoicous species likely experience a ‘sweet-spot’ in the frequency of long-distance dispersal of spores. Here, LDD contributes to the formation of nascent selfing populations, but is insufficient to maintain gene flow between daughter and parent populations, resulting in many incipient lineages that diverge allopatrically.

9:15 AM – Turnover importance: Quantifying generalism in terms of spatial heterogeneity

Lydia Morley, Daniel Spalink
Texas A&M University
lydia.morley@tamu.edu

Research surrounding plant-pollinator relationships has focused on highly specialized associations, largely ignoring the interesting phenomena guiding the history, biogeography, and ecology of more generalized systems, which predominate among native North American orchids. Compared to specialization, generalization is difficult to quantify, and many alternative classifications exist. Using a beta diversity framework to quantify generalism enables us to establish a standardized, numeric measure of generalist tendencies that jointly describes many important features of generalist relationships.

We formulated a novel index for assessing spatial variation in generalized relationships, which we termed “turnover importance”: T . We then used T to explore patterns underlying native North American orchid-insect relationships: After constructing a nearly comprehensive native North American orchid phylogeny and collecting occurrence records for both orchids and their pollinators, we tested for phylogenetic signal in T . Then, we tested for correlations between turnover importance, eco-geographic variables, and conservation status. To illuminate how turnover importance can be used to guide conservation efforts and eco-evolutionary studies, we performed case studies that characterize high, low, and intermediate values of T . We found that turnover importance is evolutionarily labile across the native North American orchid phylogeny. Further, orchids with higher turnover importance scores occupy larger ranges and broader climatic niches.

Oral Presentations

9:00 AM - 10:00 AM Session
Rudder Tower, Room 401

9:30 AM – Plant Talk: Belowground Herbivory Enhances Aboveground Plant Volatile Emission and Increases Neighboring Plant Antiherbivore Defenses

Gage Strozier, Rachel Kurian, Jack Bradford, Jayda Arriaga, Morgan Thompson, Anjel Helms
Entomology, Texas A&M University
gages@tamu.edu

When attacked by insect herbivores, plants emit specific blends of volatile chemical cues called herbivore-induced plant volatiles (HIPVs). Plants can detect HIPVs emitted by neighboring plants and prepare a faster or stronger defense response following herbivory, a phenomenon known as plant defense priming. Belowground root herbivory can also induce changes in aboveground HIPVs, but it remains unknown if neighboring plants can detect and respond to these HIPVs. Therefore, we investigated whether exposure to aboveground HIPVs from belowground herbivore-damaged plants influences the defense response of neighboring plants challenged by aboveground herbivores. We exposed zucchini squash (*Cucurbita pepo*) plants to aboveground volatiles from undamaged control plants or plants with herbivory by belowground striped cucumber beetle (*Acalymma vittatum*) larvae. Following 24 hours of HIPV exposure, we challenged plants to herbivory by an aboveground-feeding herbivore, squash bug (*Anasa tristis*) nymphs. We discovered that squash bugs gained significantly less mass and punctured the squash plant leaves fewer times when feeding on zucchini squash exposed to HIPVs from plants with root herbivory. We also collected the volatiles emitted by both larvae-damaged plants and undamaged plants over a period of 24 hours and observed a greater emission of the compound (E)- β -ocimene from larvae-damaged plants than the control plants. These results indicate that exposing neighboring plants to volatiles from larvae-damaged plants diminished squash bug performance on the neighboring plants, suggesting defense priming and revealing a new form of interplant communication.

9:45 AM – The revision of the eugregarines (Apicomplexa) of crickets and allies (Orthoptera: Grylloidea)

Jorge Medina-Duran, Jordan Moore, Hojun Song
Ecology and Evolutionary Biology, Texas A&M University
jorgemedinad@tamu.edu

Eugregarines are a diverse group of obligate parasites within the phylum Apicomplexa, known to infect various invertebrate hosts, including insects. We have undertaken a comprehensive revision of eugregarines in Orthoptera, focusing on crickets and their allies in the Grylloidea superfamily. By gathering existing linear morphometric data, qualitative traits, and molecular data for various life stages of described species, we aim to assess the validity of the current taxonomical classification, clarify species boundaries, and evaluate the diagnostic value of morphological traits. These quantitative methods will offer insights into the biology, host specificity, and geographical distribution of this highly diverse group, enhancing our understanding of eugregarine taxonomy and enabling more accurate species delineation. Our comprehensive study lays the groundwork for future research on the ecology and evolution of eugregarines and their hosts within Grylloidea and serves as a model for future research on other gregarine species, ultimately contributing to a more complete understanding of host-gregarine interactions.

Oral Presentations

9:00 AM - 10:00 AM Session
Rudder Tower, Room 410

9:00 AM – A multiscale conceptual framework to predict movement and habitat associations of an imperiled megafish, the Alligator Gar (*Atractosteus spatula*)

Johnathan Ellard, Hayden Roberts, Dan Daugherty, Paul Fleming, and Josh Perkin
Texas A&M University
jellard@tamu.edu

Increasing popularity of Alligator Gar as a sportfish combined with changes to the riverscapes they inhabit create a need for greater information on the ecology of the species to enhance management. Ecological theory predicts that movement by riverine fishes at the population level is characterized by heterogeneous mixtures of stationary and mobile individuals that together contribute to a leptokurtic (i.e., high peak, long tails) distribution of movement distances. We evaluated movement and habitat associations of Alligator Gar in the Brazos River of Texas at fine (every 2 hours for 24 hours) and coarse (every month for 16 months) temporal scales to test for (1) the presence of leptokurtosis and (2) relationships between movement distance and habitat dissimilarity or the amount of time fish were at large. Dispersal by Alligator Gar with >8 relocations at coarse (n = 13 fish) and fine (n = 5) scales revealed leptokurtosis at the coarse but not fine scale. There was no relationship between dispersal distance and habitat at the fine scale, but dispersal was positively correlated with time. Movements by fish with >2 relocations at the coarse scale (n = 43) revealed highly mobile fish moved longer distances over longer time periods to access novel habitats. Our results revealed that Alligator Gar moved nearly constantly without strong habitat associations over short time periods (hours to days), but highly mobile members of the population moved long distances to novel habitats (e.g., from river mainstems to inundated floodplains) over longer time periods (seasons to years).

9:15 AM – High dominance of invasive armor catfish linked with isotopic space shift and niche compression of native species in Guatemala.

Yasmin Quintana, Friedrich Wolfgang Keppeler, Kirk O. Winemiller
Texas A&M University
yquintana@tamu.edu

The Usumacinta River Basin is a globally important center for freshwater fish. Armored catfishes from South America (*Pterygoplichthys* spp.) invaded the Usumacinta River ~20 years ago and have become highly abundant through the basin. This invasive catfish can deplete basal resources (e.g., periphyton and detritus), with potential negative effects for native fauna. We explored isotopic space ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) overlap between armored catfish and native species, as well as the potential effect of armored catfish abundance on native fishes at a similar trophic level. The study was conducted in the tributaries San Pedro River (SPR; low invasion) and La Pasion River (LPR; high invasion) in the dry season. Moreover, we evaluated relationships of environmental factors and invasive catfish biomass, with $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ signatures, and species trophic position. Overall, *Pterygoplichthys* had lower isotopic overlap with native species in LPR (except for *Poecilia mexicana*), with native fish showing compressed isotopic spaces and higher trophic position relative to SPR. *Pterygoplichthys* biomass, conductivity, and water flow velocity were significantly associated with native fish $\delta^{13}\text{C}$; and water depth and sedimentation had a significant association with native fish $\delta^{15}\text{N}$. *Pterygoplichthys* mainly relied on benthic food resources in both rivers, and water-column resources had greater relative importance for native species in LPR. Findings provide evidence that invasive *Pterygoplichthys* and some environmental factors impact native fishes trophic ecology. Further research is needed to distinguish between the direct influence food resource depletion versus indirect effects via food web pathways or habitat alteration.

Oral Presentations

9:00 AM - 10:00 AM Session Rudder Tower, Room 410

9:30 AM – Predictability and conceptual repeatability of the predator associated burst speed body shape in independently evolved populations of western mosquitofish

Rose Blanchard, Joshua Perkin
Texas A&M University
Rose.blanchard@tamu.edu

Predation is a driver of evolution and is often studied in freshwater fishes. A common morphological adaptation found in populations rich with pursuit predators is the predator associated burst speed (PABS) body shape. This body shape, which includes a smaller head, smaller body, and larger caudal region has been noted in many species of small freshwater fishes, including Western Mosquitofish (*Gambusia affinis*). The PABS body shape is predictive of fish morphology among populations with and without pursuit predators. However, the repeatability and transferability of the PABS has not been rigorously tested and the current literature provides vague methodological descriptions. This study focuses on testing the repeatability of tests of the PABS body shape and aims to develop a streamlined process that could be widely used by others. We studied 13 populations of Western Mosquitofish, including six populations included in previous studies of the PABS and seven new populations not previously studied. We collected and photographed fish from the wild, created 10 homologous landmarks representing body shape, and used Procrustes transformation of landmarks to correct differences in fish orientation and size. We used principal components analysis to produce latent shape factors representing linear combinations of landmark coordinates, used multivariate analysis of variance to test for differences in shape factors among populations with two predator status levels (i.e., centrarchid predators present or absent), and used linear discriminant function analysis (DFA) to test whether shape factors were predictive of predator status across previously studied and recently studied populations. The DFA results revealed that predator status was correctly classified for 92% of fish from the newly studied populations. Differences in body shape among the two predator statuses included shorter total length, smaller head, and larger caudal region when predators were present, supporting repeated observation of the basic tenets of the PABS body shape paradigm.

9:45 AM – River Carpsucker versus Llano River Carpsucker: Morphological divergence of an undescribed *Catostomid*

Hayden Roberts, Joshua Perkin, Preston Bean, Gary Voelker, Kevin Conway, Henry Bart
Ecology and Conservation Biology, Texas A&M University
hcr@tamu.edu

Within Texas, there is evidence of an undescribed species of carpsucker, the Llano River Carpsucker (*Carpoides* sp. cf. *carpio*). The Llano River Carpsucker is thought to possess a more slender body, have a different mouth morphology, and occur sympatrically with the more broadly distributed River Carpsucker (*Carpoides carpio*). The objective of this study was to assess morphological variation among members of the genus *Carpoides* inhabiting the Colorado River basin of Texas. Sampling during the summer of 2022 resulted in the capture and preservation of 197 adult specimens. Photographs of specimens were digitized with 17 homologous landmarks and used to perform a morphological analysis investigating spatial gradients of body shape variation. A principal component analysis was performed on specimens pooled across the waterbodies to determine shape features that best explained morphological variation. Dorsal and pelvic fin position were the most important variables explaining the morphological variation where shape variation was driven by a gradient in body depth across the waterbodies sampled. Specimens collected from the Llano and San Saba Rivers were the most slender, while specimens from the Concho and Colorado Rivers exhibited deeper bodies. Unexpectedly, a mixture of slender, broad, and intermediate bodied specimens were observed in the Pedernales River. This study provides insight into the morphological variation among members of *Carpoides* within the Colorado River basin. Further research investigating covariance between morphological and genetic variation of these populations is planned and could provide evidence for multiple species of *Carpoides* within the basin.

Oral Presentations

9:00 AM - 10:00 AM Session Rudder Tower, Room 501

9:00 AM – Winter Heatwaves: Understanding the Lasting Effects of Record-breaking December Temperatures on Stand Transpiration in a Loblolly Pine Forest

Miriam Catalan, Marisa L. Collura, Peter Caldwell, and Georgianne W. Moore
Department of Ecology and Conservation Biology, Texas A&M University
mmorua_0206@tamu.edu

There is a need to investigate the vulnerability of evergreen forests to winter heatwaves in the southeastern USA due to climate change. In 2021, Texas experienced unseasonably warm late fall and winter temperatures, reaching record maximums of 29°C in December for seven consecutive days. This was followed by a summer heatwave with both record-breaking daytime and nighttime temperatures in June and July of 2022. The purpose of this study was to compare transpiration rates on record-breaking winter temperatures to the growing season to evaluate the impact on forest health. The study was conducted in a mature naturally regenerated mixed pine forest in Cook's Branch Conservancy located in Montgomery, Texas. To estimate stand transpiration (mm/day-1), five loblolly pine trees (*Pinus taeda*) were instrumented with sap flow sensors (n=10) from October 2021 to October 2022. Climate data was also collected from a nearby weather station. Stand transpiration in December 2021 (64 mm month-1, 25°C) approached 90% of July 2022 transpiration rates (58 mm month-1, 38°C). Transpiration followed maximum temperatures most of the year until the summer heatwave and drought triggered a precipitous decline in water use due to loss of conductivity. During this time, temperatures reached a consecutive 37°C to 41°C. This suggests that the observed water stress during the summer was exacerbated by the prior warmer winter temperatures, resulting in a lasting effect on tree health. Future research should focus on assessing the impact of excessive transpiration during the winter season on loblolly pine forest growth and water balance.

9:15 AM – Estimating Biophysical Parameters of Urban Trees on Texas A&M University Campus using Mobile Lidar

Justinn J. Jones, Sorin C. Popescu
Texas A&M University
justinn.j.jones@tamu.edu

Urban trees are an easily overlooked component of the built environment, providing numerous benefits such as improved air and water quality, carbon sequestration, and providing shade, mitigating urban heat island effect. To better understand the importance of the various ecosystem services provided by urban trees, we must be able to map, identify, and measure individual trees as accurately and efficiently as possible.

The overall goal of this project is to map urban trees on a portion of the Texas A&M University campus and estimate their biophysical parameters, such as tree height, diameter at breast height, basal area, and crown diameter, using mobile lidar. The specific objectives will be to: develop the methodologies of mobile lidar data collection and analysis, and compare direct and derived biophysical parameters against field-collected forest inventory data.

Mobile lidar data were collected in the winter of 2023 using a GeoSLAM ZEB Horizon laser scanner mounted to a backpack while riding an electric scooter. GPS reference data were collected using a Trimble Geo7x concurrent to the lidar scan. The forest inventory was conducted in the winter of 2023. Within the scan area, n=50 trees were randomly selected and measured for diameter at breast height (DBH), total tree height (h), and identified by species. DBH measurements were collected using a steel diameter tape, and tree heights were collected using a TruPulse 200 laser rangefinder.

Preliminary results for field vs lidar-derived DBH and height measurements show an $R^2=0.87$ and $R^2=0.985$, respectively.

Oral Presentations

9:00 AM - 10:00 AM Session
Rudder Tower, Room 501

9:30 AM – Scaling up the Ladder: Estimating Tree Water Use by Integrating LiDAR in the Pineywoods

Marisa Collura, Miriam M. Catalan, Justinn J. Jones, Peter Caldwell, Sorin Popescu, and Georgianne W. Moore
Ecology and Conservation Biology, Texas A&M University
mcollura95@tamu.edu

Quantification of stand transpiration at the regional scale is labor intensive, time consuming, and has poor scalability. To improve the understanding of the linkages between individual trees, forest stands, and watersheds accurate models are needed to estimate transpiration. The aim of this study is to improve the upscaling of stand transpiration at two different age pine-dominated forests in East Texas by integrating remote sensing techniques with mobile LiDAR scanning (MLS) and sap flow sensors. The specific objectives are: (1) to quantify stand transpiration (mm/day-1) across two pine-dominated stands using in-situ measurements; (2) and establish a prediction model to estimate stand transpiration using tree metrics from the MLS. Site one is a mature naturally regenerated forest dominated by loblolly pine (*Pinus taeda*) (n=5). Site two is a young, planted forest dominated by shortleaf pine (*Pinus echinata*) (n=10), with sparsely distributed mature loblolly pine trees (n=3). Sap flow sensors were installed in both sites (n=31) to estimate tree water-use (L/day-1) and calculate stand transpiration. For each instrumented tree, the metrics were estimated using MLS. A general linear regression model was used to compare MLS and in-situ tree metrics to the tree water use. We found tree water use was positively correlated with DBH, tree height, and crown height. This shows that lidar can accurately estimate tree metrics, reducing the time and cost of labor.

9:45 AM – Ecological Risk Assessment of Heavy Metals in Surface Water and Sediments of Urban Watersheds in Greater Houston

Sekinat Atobiloye, Yakubu, Momoh, Adedoyin, Folasade, Bukunmi-Omidiran, Titilope
Environmental and Interdisciplinary Sciences, Texas Southern University
sekinat.atobiloye@tsu.edu

Greater Houston is a metropolitan area located in southeastern Texas. The area is home to numerous industries, including oil and gas, manufacturing, and petrochemicals. These industries have contributed to the growth of the region but have also resulted in environmental pollution. The area has several watersheds that are important for the region's water supply and recreational activities. These watersheds are under constant threat from pollution due to the intense urbanization, industrialization, and agricultural practices in the area. This study aimed to evaluate the ecological risk posed by heavy metals in surface water and sediments of four urban watersheds in Greater Houston. The potential ecological risk index (PERI) and the heavy metal pollution index (HPI) were used to assess the ecological risk and the degree of pollution, respectively. The results revealed that Cu, Ni, and Zn were at levels that can pose a threat to aquatic organisms in all water samples. In the sediment samples from downstream Clear Creek, Pb exceeded the screening level. The PERI values indicated that the sediments and water posed a low and moderate ecological risk, respectively, to the aquatic ecosystem. The HPI values showed that the water samples were polluted with heavy metals, and the severity of pollution varied along each watershed. Overall, this study highlights the need for continuous monitoring and management of heavy metal pollution in urban watersheds to protect the health of the aquatic ecosystem and human populations that depend on it.



ORAL PRESENTATION ABSTRACTS

Session 2

Friday, March 31st 10:20 - 11:20 am

Oral Presentations

10:20 AM - 11:20 AM Session
Rudder Tower, Room 401

10:20 AM – Cancelled

10:35 AM – Differential responses to double-stranded RNA (dsRNA) injection and feeding in orthopteran insect pests

Seema Rana, Changsun Kang, Julianne Allred, Derek A. Woller, Dongin Kim, and Hojun Song
Department of Entomology, Texas A&M University
seema.rana@ag.tamu.edu

Orthopteran insect pests, specifically the Mormon cricket, *Anabrus simplex* (Orthoptera: Tettigoniidae) and desert locust, *Schistocerca gregaria*, (Orthoptera: Acrididae), are known to cause significant economic losses to the rangeland forage and agricultural crops due to their destructive migratory behavior during their sudden and periodic outbreaks. Currently, the management methods rely heavily on broad-spectrum chemical insecticides, which can be toxic to the non-targets and may eventually develop resistance in the targeted species. Therefore, we aimed to assess the potential of RNA interference (RNAi)-based alternative strategies which could supplement the current methods. In insects, RNAi efficiency varies with the method of dsRNA delivery, so we tested two different methods of dsRNA delivery— injection and oral feeding of dsRNA in both species. Our results showed that both species are sensitive to the injection but not to the oral feeding of dsRNA, likely due to high nuclease activity in the insect midgut. To overcome this, we encapsulated dsRNA in poly lactic-co-glycolic acid (PLGA) nanoparticles and studied its release kinetics and RNAi efficiency by oral feeding. However, we found that while the PLGA nanoparticle permeates from the insect digestive system to the hemolymph, it failed to induce an efficient RNAi response of the targeted genes. Therefore, further research is necessary to investigate the stability of dsRNA and its uptake mechanism in these species to devise RNAi as a viable alternative management strategy.

Oral Presentations

10:20 AM - 11:20 AM Session
Rudder Tower, Room 401

10:50 AM – Molecular phylogenetics of the ectoparasitic sucking louse genera *Hoplopleura* and *Polyplax* (Phthiraptera: Anoplura, Hoplopleuridae, and Polyplacidae)

Ali Z. Lira-Olguin, Nina du Toit-Heuis, Sonja Matthee, Conrad A. Matthee, Lance A. Durden, and Jessica Light
Ecology and Evolutionary Biology, Texas A&M University
alizeltzin@tamu.edu

Sucking lice (Phthiraptera: Anoplura) are obligate and permanent hematophagous ectoparasites of placental mammals. Globally, more than 550 valid species of sucking lice have been recognized belonging to 50 genera and 15 families, where almost 60% of them are ectoparasites of rodents. Traditionally, morphology-based phylogenies have been used to describe the relationships among the groups inside Anoplura, however, a recent molecular phylogenetic analysis demonstrates that some clades of sucking lice are not monophyletic. The discrepancy between these two datasets indicates that further studies are needed to reevaluate the phylogenetic relationships across the group. Within Anoplura, the genera *Hoplopleura* and *Polyplax* are the most diverse genera of sucking lice, with 164 species and 82 species, respectively. Historically, these genera have undergone several taxonomic changes and their limits have been only tested in a morphological framework, neither their monophyly nor internal relationships have been analyzed in a molecular phylogenetic context. Consequently, the purpose of this project was to test the monophyly of the genera *Hoplopleura* and *Polyplax* using a molecular approach. We used two molecular markers (COI, and EF-1 α) broadly used in Hexapoda systematics and we placed our resulting hypotheses in the context of the previously reported phylogenies of anoplurans to determine the internal relationships and their position within the Anoplura as well as to analyze their host associations by incorporating the phylogenies of their hosts.

11:05 AM – Using demographic estimates of selfing to test for inbreeding depression in a progenetic trematode

Jenna Hulke, Charles Criscione
Department of Biology, Texas A&M University
jhulke@tamu.edu

Three-host life cycles have evolved among trematodes, but subsequently several species in these lineages have evolved precociousness (i.e., sexually mature in their second intermediate host). The question has been raised as to why precociousness is not more common given studies have found few constraints to truncating the third host from a life cycle. The mating system model of Brown et al (2001) argues that complex life cycles preclude inbreeding and thus, its costs (i.e., inbreeding depression) by concentrating potential mating partners. The model assumes a shorter life cycle results in inbreeding and predicts a shorter life cycle can only evolve if there is no inbreeding depression. We tested this assumption and prediction in the hermaphroditic trematode *Alloglossidium renale*, which has an obligate 2-host life-cycle with sexual reproduction occurring within the paired antennal glands of grass shrimp. We evaluated the mating system of *A. renale* from 3 different populations with one temporal replication. Using genetic estimates based on deviations from Hardy-Weinberg equilibrium and identity disequilibrium, all population samples had high levels of inbreeding. We provide a novel approach by estimating a lower-bound selfing rate using infection intensities. If this demographic estimate exceeds the genetic estimate of inbreeding, there would be evidence of inbreeding depression. The genetic estimates were on par or greater than levels of inbreeding based on the demographics estimates. We found no evidence of inbreeding depression from field-based data and the lack of inbreeding depression in this species fits both the assumption and prediction of the mating system model.

Oral Presentations

10:20 AM - 11:20 AM Session Rudder Tower, Room 410

10:20 AM – Testing responsiveness of stream fish functional traits to anthropogenic riverscape alterations

Noah Santee, Kevin Conway, Weston Nowlin, David Smith, Joshua Perkin
Ecology and Conservation Biology, Texas A&M University
noahthelefty22@tamu.edu

Natural environmental filters that regulate the distribution of fish functional traits across riverscapes are affected by anthropogenic alterations. These alterations can include water quality degradation, flow regime homogenization, flow depletion, and stream dewatering. The objective of this study was to conduct exploratory analyses to identify the traits most responsive to anthropogenic environmental changes using fish assemblage data from three case studies. We used fish community data and widely available categorical trait data to calculate the richness of trait strategist responses to environmental change documented in three case studies. We hypothesized that (1) fishes intolerant to anoxic conditions would be most responsive to improved water quality (Trinity River, Texas); (2) fishes that utilize the opportunistic life history strategy would be most responsive to flow regime homogenization (lower Sabine River, Texas); (3) fishes considered to inhabit large rivers would be most responsive to groundwater overdraft (Republican River in Colorado, Kansas, and Nebraska). We used random forest models, variable importance plots, and partial dependence plots to determine trait-environmental relationships. Results from the models provided partial support for H2 and little to none for H1 and H3. However, our inclusion of multiple traits in each case study allowed us to identify several traits that respond similarly to anthropogenic alterations. The traits commonly associated with fish responsiveness to these anthropogenic riverscape change were herbivory, cruiser swimming, preference for run habitats in mainstem rivers, a preference for gravel substrate, and periodic-opportunistic life strategies.

10:35 AM – Intergenerational heritability of methylation in stony corals

Christopher Peterson, Mikhail Matz
Integrative Biology, University of Texas at Austin
Christopher.r.peterson@gmail.com

DNA methylation is a widespread epigenetic modification in eukaryotes that is a hypothesized mediator of phenotypic plasticity; understanding its dynamics could improve predictions about responses to environmental change. Within corals, higher gene body methylation is associated with more stable gene expression across different environments, while less methylated genes are more dynamically regulated. The intergenerational transmission of methylation varies greatly among taxa; methylated sites are generally inherited in plants and insects, but not in mammals. We investigated methylation heritability in *Acropora*, a stony reef-building coral. Two *A. millepora* and two *A. selago* adults were crossed, producing eight offspring crosses (four hybrid, two of each species). For each sample, we used whole-genome bisulfite sequencing to identify methylated loci and allele-specific alignments to quantify inheritance at each locus. If methylation is heritable, differential methylation between the parents and between the two offspring alleles should be the same at a given locus. We found a mixture heritable and non-heritable loci, with heritable portions ranging from 44% to 90% among crosses. Heritability was more consistent among crosses in gene body loci than other genomic regions (i.e., the deviation between differential methylation in parents and offspring were of similar magnitude and direction), although the average degree of heritability at each locus did not differ among genomic regions. Our results provide evidence that methylation heritability is variable throughout the genome, although further investigations is needed to understand how this may impact gene expression or plasticity.

Oral Presentations

10:20 AM - 11:20 AM Session
Rudder Tower, Room 410

10:50 AM – What trait-environment relationships can tell us about ecological and evolutionary dynamics?

Maria A. Hurtado-Materon, Jenny McGuire, Rachel A. Short, NSF-NERC Grant team and A Michelle Lawing
Texas A&M University
maria.h.m_1995@tamu.edu

Understanding the evolutionary and ecological processes that drive global biodiversity patterns at temporal and spatial scales is key to increasing our ability to predict the effects of disturbances in natural ecosystems. Environmental factors that impact the performance of community members are likely to affect the distribution of traits and species across space and through time. Functional traits can play an important role in community assembly by sorting organisms with similar traits into similar environments. Given that communities respond to changing environments through functional traits, we can use that relationship to evaluate the biological processes that affect biodiversity patterns. In particular, an ecometric trait is a quantitative trait that has a functional relationship with one or more environmental or climatic factors, especially when measured at the community level at regional or continental scales. This study aims to propose a new framework including phylogenetic patterns combined with ecometrics to answer the question of why some ecological and evolutionary processes drive trait-environment relationships at community level. We used phylogenetic and trait null models to determine the distribution of the evolutionary relationship and trait in mammal communities at the global scale. We found a general pattern of underdispersion in phylogenetic diversity and a random pattern in trait distribution.

11:05 AM – Identifying serpentine adaptation genes by tracing evolutionary-genomic history of *Streptanthus*, *Caulanthus* and their allied genera (Brassicaceae)

Kasuni Daundasekara, Elyssa R. Garza, and Alan E. Pepper
Department of Biology, Texas A&M University
kdaundasekara@bio.tamu.edu

Adaptation to extreme environments is an important problem in ecology and evolutionary biology. Serpentine soil, which has high concentrations of toxic heavy metals and low concentrations of essential plant nutrients, is an excellent model environment to study plant adaptations to harsh environments. The annual mustard, *Caulanthus amplexicaulis* var *barbarae* (CAB), which is serpentine tolerant, and its sister taxon, *Caulanthus amplexicaulis* var *amplexicaulis* (CAA), which is serpentine intolerant is a superb model to study genetic mechanisms underlying serpentine tolerance. Several approaches (QTL analysis, coding sequence evolution, RNAseq) are being used in our laboratory to identify candidate genes for serpentine tolerance in CAB. In this study, we are using the gene ancestry of CAB and CAA as an additional tool to prioritize candidate genes. To trace the ancestry of CAB and CAA, we are using ~30 species within the genera *Caulanthus*, *Streptanthus*, and related genera. Elucidation of the phylogenetic history of CAB and CAA is challenging due to at least one known episode of recent introgression. Here, we are determining the evolutionary history of CAB and CAA by comparing highly resolved phylogenies from both organellar (chloroplast and mitochondria) and nuclear genomes. Comparison of plastid genomes has led to identification of natural selection in this phylogenetic group. Results from chloroplast and mitochondrial phylogenies show that the maternal lineage of CAB and CAA clade is likely a serpentine intolerant *Caulanthus* lineage. We are using gene-tree discordance between organellar and nuclear phylogenies to identify nuclear loci with paternal inheritance and explore the potential of using this information to prioritize candidate serpentine tolerance genes and test using synthetic biology and CRISPR/CAS9 mutagenesis approaches.

Oral Presentations

10:20 AM - 11:20 AM Session Rudder Tower, Room 501

10:20 AM – A predictive theory of human mediated biological invasions

Nikunj Goel

University of Texas at Austin

nikunj410@gmail.com

We face an invasion crisis. The globalization of trade has accelerated the introduction of species beyond their native range, costing enormous economic and ecological losses. Therefore, we need a predictive theory of human mediated invasions to safeguard ecosystem services. However, predictions from current models are unreliable because they make incorrect assumptions about propagule dispersal. Classical diffusion models assume that propagules disperse locally in random directions. In contrast, dispersal patterns of human-assisted invasive species are characterized by long-distance directional jumps. Because of this fundamental mismatch between reality and model assumptions, predictions of diffusion models are unreliable. For example, diffusion models predict radially expanding patterns, even though the radial distance from the origin is a poor predictor of species arrival. We propose an age-structured metapopulation model to describe the spread patterns of human-mediated invasions. Next, using a bayesian framework, we explicitly incorporate the above model to analyze the spread of zebra mussels in the inland USA by commercial shipping network. Model: Our analysis suggests that although a species can take multiple paths to reach the destination, it will take the path with the least resistance. To understand this idea, let us define network distances between patches such that when transportation flux is high, patches are effectively close even though the patches might be geographically far apart. Now one can define many ordered paths from origin to destination. Of these paths, the invasion route corresponds to the path for which the sum of network distances along the ordered path is the smallest. Consequently, the species' arrival time to the destination is proportional to the sum of network distances. Surprisingly, species spread on the network space yield radial spread patterns reminiscent of diffusion models, even though invasion patterns are spatially incoherent on the geographical space. Data analysis: (a) We find that zebra mussels were likely introduced in Lake Erie before 1982, five years before the first detection in 1987 near Leamington. (b) However, there are only one in three chances it was introduced at Leamington. (c) Elasticity analysis suggests that arrival time is most sensitive to transition probability from age class 1 to 2 (S1) and fecundity in age class 2 (F2), which suggests that targeted strategies to reduce S1 and F2 could potentially slow the spread of zebra mussels. (d) Not all age groups contribute equally to zebra mussel dispersal—age class 2 is the major contributor to the species' spread.

10:35 AM – Decoupled seasonality of carbon allocation in above and belowground activities

Dohee Kim, Benju Baniya, Malik Nkrumah, and Asko Noormets

Ecology and Conservation Biology, Texas A&M University

doheekim@tamu.edu

The carbon allocation, the growth dynamics between above- and belowground tissues, can impact a forest's resilience to environmental factors. Although aboveground growth dynamics have been well documented, belowground growth, growth efficiency, and the relationship to aboveground dynamics are still poorly understood. In this study, we used monthly diameter increment and partitioned soil CO₂ efflux to assess the growth patterns of above- and belowground elements in a shortleaf pine forest in east Texas, and global FLUXNET and COSORE datasets for biome comparisons. The seasonal divergences between above- (BPa) and belowground productivity (BPb) were observed by the repeated hysteresis. BPa increased from April through June, while BPb of root activity increased from June through September. Heterotrophic activity was continued with about 2-fold greater magnitude than rhizosphere activity. Comparable trends of asynchrony between gross primary productivity and soil respiration were also found in a global dataset, particularly in the evergreen needleleaf forest. The sequential growth of above- and belowground components is aligned with prior findings, sink-driven allocation models and the "surplus carbon" hypothesis. As the transitions between phases of BPa and BPb seem to correlate with moisture availability with a monthly delay, the step decline of moisture availability in June may have terminated BPa and shifted the transport of photoassimilates to the belowground. This is consistent with previous studies on the restriction of tree stem growth under moisture deficits in summer. Future studies will explicate the mechanisms of coupling between above- and belowground C use.

Oral Presentations

10:20 AM - 11:20 AM Session
Rudder Tower, Room 501

10:50 AM – Gas exchange responses of diverse C4 grass species to drought

Nicole Havrilchak, Jason B. West
Ecology and Conservation Biology, Texas A&M University
nhavrilchak@tamu.edu

Identifying functional responses of grasses to drought will be increasingly important under future climate change scenarios. The distribution of C4 grass subtypes and lineages have been observed to be associated with precipitation gradients, however the mechanistic basis of this distribution is not yet well understood. Stomatal strategy likely plays an important role when water is limiting, with past studies demonstrating that C4 grass species from drier areas have more responsive stomata and higher water use efficiencies. Both strategies act to conserve water and maintain physiological functioning. We conducted a greenhouse experiment with 24 C4 grass species of diverse lineages and subtypes in order to assess physiological strategies in response to drought. Species differed in their response to drought and in their photosynthetic C gain under well-watered conditions ($p < 0.01$ and $p < 0.001$). Panicoideae species generally performed better than Chloridoideae and Aristidoideae species under well-watered conditions, with photosynthesis averaging 20.0 and 18.4-18.5 $\mu\text{mol CO}_2 \text{ m}^{-2} \text{ s}^{-1}$, respectively. Panicoideae species also generally had greater declines in net photosynthesis, stomatal conductance, transpiration, and instantaneous water use efficiency under drought, with the Chloridoideae species having only a slight photosynthetic advantage under drought. Stomatal conductance declined by twice as much for Panicoideae species as compared to Chloridoideae. However, Panicoideae species typically had the highest water use efficiency under both drought and well-watered conditions. Generally, stomatal conductance was less responsive to drought for PCK subtype species. Our results suggest that species-level coordination of traits, lineage, and subtype all determine gas exchange response to drought.

11:05 AM – Juniper's Legacy: Soil Infiltrability 10+ Years After Tree Death

Austin Kelly, Pedro Leite, Bradford Wilcox
Texas A&M University
austink1185@tamu.edu

Woody encroachment has predominated rangelands across North America causing significant changes in biological, chemical, and hydrological characteristics. Junipers (*Juniperus* spp.) are some of the most prevalent encroachers across the Great Plains, converting acres of grasslands into closed-canopy woodlands due to lack of fire and historical overgrazing. Prior research has documented the impact that living trees have on their surroundings, such as increases in soil infiltration and organic matter, but much less has been documented about the legacy that these trees leave after death or removal. In this study, juniper trees at the Sonora Experiment Station, which were determined to have been killed in 2011, presumably by drought, were chosen as our target plants. Data collection points were chosen both under the canopy of the dead plants and in the herbaceous intercanopy, where no trees have been known to grow. Infiltrability and penetration resistance (a parameter of soil compaction) were measured at these points. Our findings determined that topsoil infiltrability was significantly higher under canopies of dead trees than that of the herbaceous intercanopies. Soil penetration resistance was significantly higher in the intercanopies than under the dead trees' canopies. These results suggest that even 10 years after a juniper's death, the positive influences on soil health properties of decreased soil compaction and increased soil infiltrability stay prevalent, and even rival the rates of living trees. In turn, the process of juniper encroaching and being killed through management practices may be a method of soil health improvement, particularly soil water infiltrability.



ORAL PRESENTATION ABSTRACTS

Session 3

Friday, March 31st 2:00 - 3:00 pm

Oral Presentations

2:00 PM - 3:00 PM Session
Rudder Tower, Room 401

2:00 PM – Conspecific oophagy by tadpoles: importance as a source of anuran egg mortality and conditions for occurrence

Griffin Nicholson, Alberth Humberto Rojas Carranza, Gregory Brown, Lee A. Fitzgerald
Ecology and Evolutionary Biology, Texas A&M University
gnicholson@tamu.edu

The Chiricahua Leopard Frog (*Rana chiricahuensis*), a species of conservation concern in the American Southwest, was previously unknown to exhibit conspecific oophagy as tadpoles. My research team observed the first record of this behavior in the species, which I present here. We subsequently hypothesized conspecific oophagy by tadpoles is the most important source of *R. chiricahuensis* egg mortality at our research site. Additionally, based on previous hypotheses on behavioral occurrence, it was unexpected to find this behavior in *R. chiricahuensis*. We thus hypothesized, counter to previous reasonings, that conspecific oophagy by tadpoles broadly occurs across anurans and is only conditional on the encounter rate between tadpoles of late development and conspecific egg masses. We conducted logistic regressions to determine how characteristics of local conspecific tadpoles and the riverscape predict *R. chiricahuensis* egg mass survival. We found abundance of tadpoles locally to an egg mass was a significant predictor of egg mass mortality, but factors of tadpole size distribution (average size and number of tadpoles at different size classes) had higher significance and were negatively correlated to conspecific egg mass survival. These tadpole factors were also more important in predicting egg mass survival than riverscape factors such as volumetric flow rate. I also present preliminary analysis on our review of conspecific oophagy by tadpoles in which we report general conditions and distribution of the behavior within Anura and are conducting multivariate analyses to determine whether commonality in species traits exists within anuran species recorded having tadpoles exhibit conspecific oophagy.

2:15 PM – Occupancy and dispersal in a recently established population of the endangered St. Croix ground lizard (*Pholidoscelis polops*) and implications for conservation

Nicole Stevens, Nicole Angeli, Kristen Ewen, Lee Fitzgerald
Ecology and Evolutionary Biology, Texas A&M University
nstevens@tamu.edu

In St. Croix, US Virgin Islands, land-use changes and introduced mammalian predators led to the extirpation of the St. Croix ground lizard (*Pholidoscelis polops*) from over 99% of its historic range. Before human intervention, there were only around 200 individuals on two tiny offshore cays. In 2008, fifty-two of these remaining *P. polops* were translocated to predator-free Buck Island Reef National Monument (BUIS) where their population began to expand. Prior research analyzed the BUIS population until 2014, modeling its distribution (41% of BUIS) and abundance (around 1100 individuals). Our analysis has expanded on this initial framework to showcase more recent population trends. N-mixture modeling and subsequent spatial interpolation suggests that there are around 9000 individuals on BUIS and *P. polops* now occupy the entire extent of the island. The model covariates that best predict site presence include temperature, vegetation cover, habitat type, and elevation. Niche modeling using MAXENT indicates that human presence has little impact on whether lizards occupy specific sites, though this may vary where there is permanent human habitation. Knowledge from this project will be used to inform future translocation efforts of *P. polops* back to mainland St. Croix, where we hope to repatriate the species using the BUIS lizards as a source population. While invasive mammal populations persist on St. Croix, new integrative research on species interactions and re-emergent landscape conditions may provide valuable insight on how naïve prey and introduced predators can coexist.

Oral Presentations

2:00 PM - 3:00 PM Session
Rudder Tower, Room 401

2:30 PM – Functional Diversity in Songbirds of Concern

Katrina Keith, Gary Voelker,
Ecology and Conservation Biology, Texas A&M University
katrinadkeith@tamu.edu

Genetic diversity is an essential component of assessing the conservation needs of species. Toll-like receptors (TLRs) are innate immune receptors which recognize pathogens, and the genes that code for these structures can be important measures of functional genetic diversity in and amongst populations of birds in decline. The Black-capped Vireo (*Vireo atricapilla*), Painted Bunting (*Passerina ciris*), and Varied Bunting (*Passerina versicolor*) are found in a variety of habitats, including high-elevation habitats known as sky islands in Mexico and Texas. The Black-capped Vireo was delisted in 2018 from the Endangered Species Act, but is still scarce. The Painted Bunting is in decline, as is the Varied Bunting, whose restricted range is additional cause for concern. These three species and their populations show varied amounts of functional diversity and evidence of selection in their TLR genes. This information can help to inform their conservation status and subsequent action by conservation groups.

2:45 PM – Nest Survival of White-tailed Hawks in South Texas During the 2021-2022 Breeding Season

Madeleine Barham

Madeleine T. Barham, Danielle K. Walkup, Clint W. Boal
Department of Rangeland, Wildlife, and Fisheries Management, Texas A&M University
madeleine.thornley@tamu.edu

The white-tailed hawk (*Geranoaetus albicaudatus*) is a neotropical bird of prey listed as state-threatened in Texas, where they breed in open areas throughout the Gulf Coast of the state. Texas' coast contains 25% of the state's human population and is undergoing rapid development and population growth. Previous research conducted in the northern-most extent of the white-tailed hawk breeding range indicates anthropogenic activities may have a negative impact on their breeding activities. Population estimates and demographics are largely unknown, which pushes the state listing of this species. Estimates of white-tailed hawk nesting success show high variability both spatially and latitudinally. More investigation of their breeding ecology and nest success throughout the Gulf Coast of Texas is necessary to expand our current understanding of productivity and inform conservation planning for the species. We monitored 40 white-tailed hawk nests along the coast in south Texas: 22 in 2021 and 18 during the 2022 breeding season. The preliminary daily nest survival estimate for all nests pooled was 0.9944 (95% CI = 0.9889 – 0.9972), which translates to an estimated nest survival of 63.8%. This is at the high end of previously reported estimates. This could be attributed to the broad spatial distribution of our sample that may conceal any localized patterns of nesting failure, or to the temporal period in which we collected data compared to studies conducted in previous years. Future analyses will further investigate potential variation in nest survival, incorporating environmental factors and latitude.

Oral Presentations

2:00 PM - 3:00 PM Session
Rudder Tower, Room 410

2:00 PM – Population genetic structure of Townsend's big-eared bats in the western United States

Katelyn Sanchez

Ecology and Conservation Biology, Texas A&M University
khopesanchez@tamu.edu

The Townsend's big-eared bat (*Corynorhinus townsendii townsendii*) is geographically widespread, occupying an extensive range throughout the western United States, often migrating between dense aggregations in summer maternity colonies and winter hibernacula. *Corynorhinus t. townsendii* is considered a species of special concern by the California Department of Fish and Wildlife; thus, assessing the genetic health of this bat throughout California can be informative for management and conservation initiatives. To examine *C. t. townsendii* genetic health, we used nuclear data (microsatellites) to assess the population genetics of bats ($n = 209$) from 13 hibernacula roosts in the Inyo and White Mountain region of California and Nevada. To assess genetic diversity, we calculated F_{st} in ARLEQUIN and found eight significant pairwise F_{st} values at both low ($F_{st} < 0.1$) and moderate ($F_{st} > 0.1$) levels. These F_{st} results suggest that colonies are not highly genetically isolated from one another and that hibernacula of *C. t. townsendii* are genetically healthy, potentially affording resistance to current and future threats. Our results suggest that current populations of Townsend's big-eared bats retain connectivity and gene flow between both maternity colonies and hibernacula and these roosts should be conserved for the future genetic health of this bat across California and Nevada. Future work should examine additional genetic, ecological, and behavioral data to assess sex-based dispersal patterns as well as relatedness within and among hibernacula.

2:15 PM – Measuring Mantled Howler Monkey (*Alouatta palliata*) Testes via Parallel Laser Photogrammetry: Expanding the use of Non-Invasive Methodologies

Austen Ehrie, Alec A. Iruri-Tucker, Yasmin B. Lord, Kevin D. Hunt, P. David Polly, Adam M. Fudickar, Michael D. Wasserman
Department of Biology, Texas A&M University
ajehrie@tamu.edu

Parallel laser photogrammetry is an up-and-coming methodology that can be used to collect morphological measurements of organisms non-invasively. This method involves attaching two parallel laser beams at a known inter-beam distance to a camera. When a photo of an organism is taken, the lasers project onto the photo and act as a scale so that image analysis programs like ImageJ can be utilized. Traditionally, this methodology has been used to measure certain body markers (limb length, crown-rump length, etc.) as proxies for overall body size. However, recent studies have attempted to measure other body parts within a variety of contexts. Here, we add to this growing body of applications by measuring the testes of wild mantled howler monkeys (*Alouatta palliata*) with the eventual goal of testing hypotheses about the evolution of sperm competition. Because testes are relatively small and more globular than other body parts traditionally measured with parallel laser photogrammetry, tests of this methodology are required to determine whether it can detect differences between individuals. We measured the testes of eighteen individuals and found an average size of 36.16cm^3 and a range of 16.35cm^3 - 54.36cm^3 . These sizes are consistent with previous studies that collected measurements by hand, suggesting that parallel laser photogrammetry may become increasingly useful for future research.

Oral Presentations

2:00 PM - 3:00 PM Session
Rudder Tower, Room 410

2:30 PM – The eco-evolutionary dynamics of sexual traits that increase mate encounter rates

Colton Watts, Courtney L. Fitzpatrick
Department of Biology, Texas A&M University
j.colton.watts@gmail.com

Sexual selection occurs when reproductive success is limited by intrasexual competition for mates or gametes, but it can also occur when reproductive success is limited by mate encounter rates. Mate encounter rates depend in part on the abundances of individuals in the environment and, consequently, sexual selection to increase mate encounters should depend on a population's ecological dynamics. However, mate encounter rates also directly affect ecological dynamics through effects on population mean reproductive success, a key determinant of population growth. Thus, sexual selection on traits that affect mate encounter rates is both a cause and consequence of ecological dynamics. To investigate the consequences of this eco-evolutionary feedback loop for sexual trait evolution, we develop a quantitative genetic model of a sexual trait that increases mate encounter rates by enhancing an individual's detectability by potential mates. By explicitly linking individual mating success to expected population dynamics, we show that the resulting eco-evolutionary dynamics generally cause the sexual trait to converge on an equilibrium value that, once established, cannot be replaced.

2:45 PM – Aggression and Parental Care of *Nicrophorus orbicollis*

Shannon Jarratt-Harris, C.B. Cunningham, E.C. McKinney, J.B. Moss, A.J. Moore
Department of Ecology and Conservation Biology, Texas A&M University
harrisshannon73.sh@tamu.edu

Parental care can be defined as any expressed trait that enhances offspring fitness while simultaneously mitigating unpredictable hazards. Aggression is notably involved in ensuring successful parenting efforts in many taxa. Prospective genes associated with parental behavior include genes that were likely co-opted from precursor aggressive behaviors during the evolution of parental care. Aggressive behavior typically renders temporal and energetic costs potentially selecting for flexible parental care in species where aggression plays a role in ensuring offspring survival. Winner/loser effects often show to be a key accessory of aggressive behaviors like competition. To understand aggression's role in parental care and possible winner/loser effects, I investigate male intra-specific competition's impact on subsequent parental behavior, expression of two key gene receptors, the octopamine α receptor and the octopamine/tyramine 1 receptor of *Nicrophorus orbicollis* and if winning/losing could be reflected in those expression patterns. Here I show socially experienced males parented more than socially inexperienced males. Despite this, female parents are consistent with the amount of care provided, ensuring the integrity of the quantity and average mass of the larvae. Additionally, I found differential expression for octopamine α receptor and no evidence for winner/loser effects in either the octopamine α receptor or the octopamine/tyramine 1 receptor. Implicating octopamine α receptor's involvement in both aggression and parental care.

Oral Presentations

2:00 PM - 3:00 PM Session
Rudder Tower, Room 501

2:00 PM – The production of destruction: How society invented the flammable Lost Pines "Forest" of Texas

Lee May

Department of Ecology and Conservation Biology, Texas A&M University
nleemay@tamu.edu

Property destruction during wildfire, while influenced by natural phenomena and anthropogenic climate change, is ultimately dependent on material landscape conditions. This concept of destruction, often quantified in financial amounts, is a social construction based on human values applied to material objects. Studies show a correlation between increased wildfire destruction and exurban development in fire-adapted ecosystems, commonly referred to as the Wildland-Urban Influence (WUI). Few studies, however, focus on the active social-ecological processes that produce the WUI and concomitant wildfire destruction. Addressing the root causes of wildfire destruction, rather than the symptoms, requires a conceptual shift away from the study of specific landscapes, such as the WUI, to the study of social-ecological processes. My study applies this framework to a case study of the 2011 Bastrop County Complex Fire. The Bastrop County Complex Fire was neither the largest fire by size nor the longest fire by duration in Texas' 2011 fire season alone, yet it remains the most destructive and arguably most impactful wildfire in Texas history. The root cause of this destruction lies in incentive-based economic pressures that encourage modification of the surrounding ecosystem and development of the WUI. Using environmental history, I present a discursive investigation of the foundational systems and processes that produced material conditions susceptible to wildfire destruction in 2011 and explore whether these systems and processes have changed. Preliminary assessments indicate that these conditions remain and are setting the stage for another potentially destructive fire.

2:15 PM – How does fire history affect plant communities' regeneration in tropical savannas?

Mariana Dairel, Alessandra Fidelis

Department Ecology and Conservation Biology, Texas A&M University
mariana.dairel@tamu.edu

Fire is an important ecological factor influencing structure and diversity of savanna ecosystems. Fire exclusion can change plant community structure leading to losses in biodiversity, affecting functional diversity and ecosystem services. Moreover, fire exclusion is one of the major threats to the resilience of tropical savannas. In this study we aimed to analyze the plant community regeneration in tropical savannas with different times since exclusion and were then burned. We hypothesized that the longer the time since last fire is, the slower the vegetation regeneration will be. We established 30 plots in each area with distinct fire histories: (F+): 16 burning, excluded from fire for 10 years; (F-): 6 burning events, excluded from fire for 19 years. Both areas have unburned plots (E) and burned ones (B). After fire, we found that total biomass plots increased over time ($p < 0.001$) in both areas, while not differences were found in (E). After fire, live biomass at F+ was three times higher than at F-, showing the same values as before fire one year after burning. The live biomass at F- continuously increased over time ($p < 0.01$). The biomass composition was similar between treatments in both areas. The biomass was mostly composed of graminoids which represented 85% of live biomass in both areas. At F-, fire increased graminoids ($p < 0.01$). Further, F+ areas presented higher species diversity ($H' = 2.33$) when compared with F- ($H' = 1.61$). Thus, fire history affects plant community regeneration and shows to be an important factor for community assembly, increasing the diversity and, consequently, the resilience of tropical savannas.

Oral Presentations

2:00 PM - 3:00 PM Session
Rudder Tower, Room 501

2:30 PM – Activity related to lunar brightness and diel activity patterns of Tapiridae and Felidae species across Neotropical sites

Stefanie Bergmanson

Texas State University
sbclara@icloud.com

Tapirs serve important ecological roles (e.g., as seed dispersers) as seed dispersers and have serious conservation and management needs due to anthropogenic influences of their habitats. However, details of their ecology are not well understood as tapirs are difficult to study because of the secretive nature and usually low densities over wide areas. I used circular statistics and a null model approach to analyze a set of camera trap records (N= 8,889) from 16 sites in Central and South America. I examine the diel activity patterns and amount of activity along lunar phases for the Lowland tapir (*Tapirus terrestris*), Mountain tapir (*Tapirus pinchaque*), and Baird's tapir (*Tapirus bairdii*), as well as their main potential predators Jaguar (*Panthera onca*) and Puma (*Puma concolor*). For all species I used a null model approach to evince highly chronocoincident activity patterns among sites, thus allowing the examination of activity using a wider scope, instead of a site based traditional approach. Most species showed trends for nocturnal activity patterns. Pairwise comparisons of activity patterns between Tapiridae and Felidae species indicated significant temporal partitioning. Baird's and Lowland tapirs showed a preference for activity during relatively bright nights (waxing gibbous) whereas Jaguar and Puma showed preference for the brightest nights in the lunar cycle (full moon in both cases). In conclusion, the high degree of temporal partitioning between Tapiridae and Felidae suggests an avoidance of predators regardless of lunar brightness. Results also reveal strong evidence for similar activity patterns across broad geographical scales that allow for more biologically meaningful inferences to be made in relation to wildlife monitoring and conservation in the Neotropics.

2:45 PM – Fiber Hemp Agronomy for South Central Texas

Jodie M. McVane

Texas A&M University
jodiemr@tamu.edu

Industrial fiber hemp, *Cannabis sativa* L., is an emerging new crop with enormous potential. Different applications include paper, substitute of plastics, building materials, animal bedding, and phytoremediation of contaminated soils. Given that this is a new crop, there is a need to develop locally suitable agronomic practices. In this research conducted at the Texas A&M field research farm near College Station, TX three hemp planting timings (Mar 30, Apr 20, May 18) were evaluated. Best planting dates determine the best opportunity for obtaining maximum yields in the Southeast Texas region. Results showed that the late March planting timing provided the best hemp growth, biomass, and fiber yield, compared to the later planting timings. Findings from this research provides critical agronomic production knowledge for the adoption of fiber hemp in this region.



POSTER SESSION ABSTRACTS

Friday, March 31st 12 - 2 pm

Posters

Poster #1 - Characterize urban tree attributes using terrestrial LiDAR and quantitative structure model

Elizabeth Elkins

Midwestern State University

ecelkins0815@my.msutexas.edu

Tree above ground biomass (AGB) has been identified as an essential climate variable that quantifies the amount of carbon stored in terrestrial ecosystems. Recent advancements in terrestrial Light Detection And Ranging (LiDAR) remote sensing technology makes it possible to create detailed three-dimensional (3D) models of individual trees on a centimeter scale. Therefore, we can calculate AGB in a non-destructive and possibly more accurate way compared to current forestry practices. These practices use relationships of tree species and generic allometric equations to estimate AGB, hence susceptible to errors and uncertainties. This project assesses the accuracy and potential of the LiDAR technology and tree segmentation algorithms that calculate above ground tree attributes and estimate AGB. We also aim to explore the post-processing algorithms looking for improvements or ways to streamline the workflow. We scan several trees within Midwestern State University campus using LiDAR and analyze the point clouds with tree segmentation / modeling algorithms. We then validate the estimated above ground attributes by comparing them to the actual field measurements. By analyzing 3D reconstruction models utilizing the point cloud, we observe that the algorithm creates detailed and plausible models. This is crucial because of its implication in larger scales such as for local/regional forests by using satellite-derived data. This technique provides a non-destructive approach for estimating tree AGB and has real-world impacts on local stakeholders by informing them of the potential of LiDAR technology and data-based practical recommendations of terrestrial carbon sink and sustainable forestry management strategies.

Poster #2 - Microhabitat estimation for the sedge wren in a south Texas wildlife refuge

Miranda Peterson, Mei-Kuei Lu, Karsyn White, Brian Rich, Taylor Donaldson

Ecology and Conservation Biology, Texas A&M University

mrp126@tamu.edu

North America bird populations have declined over the last half century, and grassland birds in particular have experienced more drastic, consistent, and widespread declines. Moreover, there has been a steep decline in migrating birds over North America over the last decade. The Welder Wildlife Refuge (WWR) is located in one of the largest avian migratory flyways in North America. The sedge wren is a migratory grassland bird which passes through the refuge. While grasslands are overall dominated by a nearly continuous cover of grass, they are usually not homogeneous and can include several microhabitats. Thus, our goal is to estimate the microhabitat for the sedge wren within a 40 acre patch located in the WWR. To accomplish our goal, we will use drone imagery collected at the site to 1) generate indices based on abiotic and biotic predictor variables for the sedge wren, 2) run an unsupervised, machine learning classification to estimate vegetation cover and spatial heterogeneity, 3) identify vegetation species using a spectral library, then 4) combine the products from the first three steps to estimate sedge wren microhabitat within the 40 acre site. Our site imagery was taken in October 2022 using a drone with a multi-sensor camera and a dual camera imaging system, which measures ten bands. For our next steps, we will use ENVI software to 1) generate indices 2) run an unsupervised, machine learning classification 3) identify vegetation species using a spectral library, then 4) estimate sedge wren microhabitat.

Posters

Poster #3 - Seeking to mitigate avian malaria in Texas: The Grasshopper Sparrow

Nicole Dautreppe, Gary Voelker, Heather Prestridge, Ziyu Wang, Lyndi Hall
ndautreppez@tamu.edu

This research poster presents a study of the prevalence of avian malaria in grasshopper sparrows, a species considered to be of greatest conservation need. From data collected in Texas, we have evidence suggesting a population decline in grasshopper sparrows of -2.8% from 1980-2006. The study aims to understand the level of threat avian malaria poses to the survival of grasshopper sparrows, and its potential threat to other bird populations. Avian malaria is a disease caused by *Plasmodium reticulum*, a protozoan parasite carried by mosquitoes, and has already been shown to have detrimental impacts on other bird populations. The Biodiversity Research and Teaching Collections department at Texas A&M University collected tissue samples from Grasshopper sparrow specimen to test for the presence of the malarial parasite. Polymerase chain reaction (PCR) was used to test for malarial parasites in the collected tissue samples. We seek to understand the disease's effect on the species' overall fitness and find physiological/genealogical factors that may be correlated with susceptibility or resistance.

Poster #4 - Influence of Pesticide Usage on Avian Malaria Prevalence

McKenna Sanchez and Katelyn Sanchez
Ecology and Conservation Biology, Texas A&M University
mckennasanchez@tamu.edu

Exotoxins have been impacting wildlife populations since the 1960s. Pesticide usage is becoming an increasingly controversial topic as its negative effects on the environment, wildlife, and humans become known. We investigated the relationship between the prevalence of avian malaria in areas of high pesticide usage versus areas of low pesticide usage in samples from Texas birds. We used samples from two sites, one that has been under consistent agricultural use with pesticides (cultivated) and one that is pesticide free (uncultivated). Avian malaria is a persistent threat with the global average infection probability of wild birds over 10% for three of the four haemosporidian parasite genera. Previous ornithological research has focused on the relationship between pesticide usage and avian mortality and abundance but the question of whether pesticide usage bears an indirect effect on the health of birds, such as increasing their susceptibility to disease, has yet to be studied. In this project we focused on birds that are separated by two categories: diet (insectivorous or granivorous) and foraging location (ground or tree). We used data from four orders of birds: Columbiformes, Galliformes, Piciformes, and Passeriformes. We expect that areas of high pesticide usage would correlate with high presence of avian malaria, especially for insectivorous, ground-foraging birds.

Posters

Poster #5 - Parental Budgets and Feeding Behavior of Nesting White-Tailed Hawks

Jordyn B. Walborn, Caitlin A. Clark, Madeleine T. Barham, Danielle K. Walkup, and Clint W. Boal
Plant Pathology and Microbiology; Rangeland, Wildlife and Fisheries Management, Natural Resources Institute,
Texas A&M University, U.S. Geological Survey, Texas Cooperative Fish and Wildlife Research Unit, Texas Tech
University
jordynwalborn@tamu.edu

Members of the Accipitriformes usually have sexually divided parental roles in which the female contributes more to nestling care and nest defense whereas the male provides the majority of food and defends the larger territory. The white-tailed hawk (*Geranoaetus albicaudatus*) is one of North America's least studied birds of prey, and little quantitative information is available regarding parental care and feeding behavior during the breeding season, although we hypothesize white-tailed hawks divide parental roles similar to other Accipitriformes. One goal of this study is to describe the sex-specific differences or similarities of nesting white-tailed hawks in context of behavioral budgets related to feeding of nestlings. To determine the behavioral budgets, we placed trail cameras at 12 white-tailed hawk nests containing hatchlings throughout south Texas properties in spring 2021. Cameras were set to take 60 seconds of video whenever they were triggered by movement, with a 60-second pause between triggers. Cameras were active 24 hours per day and ran from 14 April to 3 July 2021. We are assessing relationships of nestling age with adult attendance and feeding frequency, and contrasting nest attendance by male and female members of pairs. Analyses are ongoing and methods will be presented from the parental budgets and feeding behavior of white-tailed hawks during the 2021 breeding season.

Poster #6 - Lights Out Texas: A novel pipeline for detection of highly pathogenic avian influenza and ticks in wild passerines

Mycha A. Van Allen, Amanda Harvey, Amanda Harvey, Meredith Anderson, Sujata Balasubramanian, Wendy Tang, Gabriel Hamer, Heather Prestridge, Sarah Hamer
Rangeland, Wildlife, and Fisheries Management, Texas A&M University
mycha.vanallen@tamu.edu

Migratory bird death by window collision contributes to the increasing patterns of bird decline worldwide. The Lights Out initiative of the National Audubon Society urges building owners and managers to turn off extra lights during migration to protect avian migrants from lethal collisions with buildings. We pose that these window-strike birds can provide novel insight into the role of avian migrants in the ecology and epidemiology of emerging zoonotic diseases. Migrating birds may enhance the spread of important pathogens and vectors, bringing highly pathogenic avian influenza (HPAI) or tick-borne diseases into new areas. Ticks are responsible for many emerging vector-borne zoonotic diseases. Additionally, an HPAI outbreak among poultry and several species of wild birds was confirmed in 2022 by the USDA in at least 48 states. Large-scale chicken depopulations brought on by outbreaks can result in severe economic losses. Thus far, most surveillance for HPAI is in poultry, waterfowl, and raptors, with little known about the possible role of passerines. In this study, we are interested in the detection of ticks and HPAI in Lights Out birds. We collected oral and cloacal swabs from Lights Out specimens and tested them for HPAI. Additionally, we inspected birds for the presence of attached ticks. In 2022, we sampled 509 birds, 315 of which were tested for HPAI using qPCR with no positive results, and one tick was discovered. Data from building-collision casualties may help to gain a better understanding of the role avian migration plays in spreading ticks, tick-borne pathogens, and HPAI.

Posters

Poster #7 - Improving disease resistance and queen quality of managed *Apis mellifera jemenitica* Rutter colonies in Saudi Arabia

Keegan Nichols, Dr. Juliana Rangel
Entomology, Texas A&M University
Knichols@tamu.edu

The Western honey bee, *Apis mellifera*, is an economically important pollinator that is used for agricultural production throughout the world. Due to their importance for food security, honey bee colonies of various subspecies are managed in practically every country around the world to ensure that their crops are provided with sufficient pollination. In Saudi Arabia, the native subspecies, *Apis mellifera jemenitica*, is managed due to its heat tolerance which allows more efficient foraging during the intense summer heat. But, despite being well adapted to its native geography and environment, *A. m. jemenitica* still faces common viral and parasitic stressors that can impact colony health and efficiency. Due to the relatively underdeveloped beekeeping techniques practiced in Saudi Arabia, many colonies that exhibit high *Varroa* mite infestation levels go untreated. Working with collaborators at King Khalid University in Abha, Saudi Arabia, we will establish the prevalence and intensity of *V. destructor* and *Nosema* infestations in managed colonies along the north-south region of the Red Sea. Additionally, and most importantly, for the first time ever we will screen colonies for the presence and prevalence of common honey bee-associated viruses throughout Saudi Arabia's apiaries. This work will build the foundation going forward when constructing a breeding program to improve the health and productivity of managed *A. m. jemenitica* colonies.

Poster #8 - Differences in Africanized and European honey bees (*Apis mellifera*): visitation of larval cells by nurses

Ashyaa Brown, Marcela Martinez; Juliana Rangel
Prairie View A&M
abrown293@pvamu.edu

The Western honey bee (*Apis mellifera*) is arguably the most important global pollinator, being responsible for contributing approximately \$200 billion per year to the worldwide economy, primarily through the provision of pollination services of agricultural crops. While honey bees are not endemic to the Americas, the United States harbors populations of several subspecies, including the hybrid between bees of European descent and those descendent of the African subspecies *A. m. scutellata*. These bees, known as "Africanized" honey bees, are known for their aggressive demeanor, but also for their ability to swarm often and develop faster than bees of European descent. In this study, we compared the rate at which honey bee larvae are fed in colonies of European versus Africanized maternal ancestry. In particular, we used scan sampling to monitor the visitation rates of nurse bees tending to developing larvae in their several stages of development. We found that nurse bees of European descent tend to visit (and feed) developing larvae at a higher frequency than nurse bees of Africanized descent, regardless of the larval stage of development. Understanding the visitation rates between these two subspecies will allow us to further understand differences in their effectiveness in combating parasites, including the parasitic mite, *Varroa destructor*, which proliferates in colonies with high nurse visitation rates. The study will provide further insight into observable differences between the two honey bee mitotypes, and will increase our understanding of life history traits among separate lineages of this important pollinator.

Posters

Poster #9 - Pesticide residues in wax lead to premature self-removal behavior in honey bees (*Apis mellifera*)

Sydney Martinez, Jordan T. Ellis
Entomology, Texas A&M University
smartinez03@tamu.edu

Honey bees face many stressors that decrease their health and have the potential to lead to colony collapse. One of these stressors is pesticides that are commonly used by farmers. Previous research has shown that exposure to pesticides can lead to accelerated behavioral maturation which has a negative impact on a colony's health. In this study, relevant levels of pesticides commonly found in honey bee hives will be tested on Honey Bees. Exposing the bees to pesticides that are commonly used by farmers will allow us to better understand the role that pesticide plays in the behavioral maturation of honey bees. Developmental stress in honey bees can lead to premature self-removal behavior where bees walk out of the colony before they can fly and die. Our study examines if pesticides can cause this self-removal and if pesticides have further physiological effects. To test this, we tagged a control group of bees that emerged from the brood and groups that were developmentally stressed with pesticides on the same day. These bees were then observed for self-removal behavior. We also observed the hypopharyngeal glands (HPG) of these bees to see if bees are aging up prematurely. The bees that fall out of the colony will be collected and dissected to obtain and measure the size of the HPGs to determine if the pesticides are leading to the HPG to shrink in size. This research could help inform beekeepers what pesticides could lead to a colony collapse.

Poster #10 - Activity Patterns and Potential Interactions Among Cattle, White-tailed Deer and Wild Pigs

MacKenzie Hoffman, Ty Werdel, Mike D. Proctor, Stephen L. Webb
Rangeland, Wildlife, and Fisheries Management, Texas A&M University
lumackhoffman@tamu.edu

White-tailed deer (*Odocoileus virginianus*), domestic cattle (*Bos* spp.), and non-native, invasive wild pigs (*Sus scrofa*) co-occur across large portions of their distributions, particularly on native rangelands. It is unclear when and how each of these species can impact the behavior and activity of the others. Of particular importance is how wild pigs interact with native wildlife and domestic livestock because of the potential for disease spread, shared habitat, and indirect or direct competition. Our objective is to understand how each species' presence potentially affects the activity and detection of other species at camera survey sites. Camera traps were deployed on two ranches in southcentral Oklahoma during September–November 2019, 2020, and 2021 for an average of 17 days. A total of 29 cameras were deployed; 13 at Coffey Ranch, and 16 at Oswalt Ranch. White-tailed deer were detected 181, 372, and 508 times on Oswalt Ranch in 2019, 2020, and 2021, respectively. On Coffey Ranch, deer were detected 141 in 2019, 262 times in 2020, and 612 times in 2021. On Oswalt Ranch, wild pigs were detected 5, 84, and 26 times in 2019, 2020, and 2021, respectively whereas they were detected 11 times in 2019, 123 times in 2020, and 49 times in 2021 on Coffey Ranch. Domestic cattle were detected 7–189 and 33–54 times across the 3 years on Oswalt and Coffey ranches, respectively. Activity patterns and overlap will be estimated using the 'overlap' package in R. These results will shed light on general activity patterns of 3 large mammal species and how they interact, which will have implications on species management and the potential for disease spread.

Posters

Poster #11 - The complete mitochondrial genome of the gecko tapeworm, *Oochoristica javaensis*.

Chelsea Thorn, Charles Criscione
Biology, Texas A&M University
cthorn@tamu.edu

Most host-parasite immunology studies involving parasitic flatworms are restricted to fish or mammalian host systems. We aim to develop a reptile-helminth system to fill a gap in our understanding of the evolution of vertebrate immunology with respect to helminth infections. To this end, we are developing genomic resources for the gecko tapeworm *Oochoristica javaensis*, a tapeworm native to southeast Asia that uses gekkonid lizards as definitive hosts. In the U.S.A., this tapeworm is commonly found infecting the invasive Mediterranean gecko, *Hemidactylus turcicus*. Available data on tapeworm gene expression are restricted to just a few species that infect mammals or fish. The development of genomic resources in other systems can provide a basis for comparative analysis of tapeworm infections across diverse taxa. We used short- and long-read sequence data from several individuals to assemble the first complete mitochondrial genome of *O. javaensis*. We identified 2 distinct haplotypes. Haplotype 1 is 13,885 base pairs and haplotype 2 is 13,914 base pairs long. As with other tapeworms, there are 12 protein coding genes, 22 transfer RNA genes, and 2 rRNA genes. The A + T content of haplotype 1 is 71.62% and haplotype 2 is 71.78%. Phylogenetic analysis of protein coding genes supports the placement of *O. javaensis* in Cyclophyllidea. Future work in this system will address the evolutionary host-defense and parasite counter-defense interactions between the gecko host and its parasite. We also plan to characterize parasite gene expression across its developmental stages in its intermediate host (beetles) and final host (geckos).

Poster #12 - Carnassial relative blade length (RBL) as an indicator of carnivoran dietary ecology

Isaac Brown, Triniti Clarke, Duncan Vick, A. Michelle Lawing, Leila Siciliano-Martina
Geology and Geophysics, Texas A&M University
irbrown@tamu.edu

Carnivorans exhibit a wide variety of diets, ranging from the herbivorous diet of the giant panda (*Ailuropoda melanoleuca*) to the obligate carnivory observed in felids. The length of the trigonid blade relative to the total carnassial tooth length (known as the relative blade length, or RBL) is functionally related to shearing and grinding ability in terrestrial carnivorans, where a greater RBL value correlates to a greater degree of carnivory. To explore the nature of this relationship, we extracted RBL values from 6 studies representing a sample of 213 carnivoran species. These data allowed us to evaluate the variation in RBL values across carnivora and provided new areas of inquiry. There is a clear distinction in RBL values between caniforms and felids. The caniforms (e.g., bears, skunks, martens) possessed a wide range of RBL values under 0.8, suggesting that members of the group typically have a less carnivorous and more generalist diet than felids. Felids had high, uniform RBL values of 1.0, leading to further questions about the ecological and evolutionary limits to the morphospace associated with this functional trait. Overall, the reliability of relative blade length as a dietary indicator and its presence in many taxa provides a useful pathway for research into this diverse and ecologically vital taxonomic order.

Posters

Poster #13 - Evidence for temporal niche partitioning between two wild Suidae species in the Neotropics

Anthony Gomez, Valeria Reyna, Dr. Ivan Castro-Arellano
ajg148@txstate.edu

The mechanisms that facilitate species coexistence is one of the central questions in ecology. Spatial and trophic partitioning has been heavily studied but segregation of the temporal niche has received less attention. The collared (Pecari tajacu) and white-lipped (Tayassu pecari) peccaries are similarly sized species with sympatric distributions throughout the neotropics. We assessed overlap of activities between these two species using 6,900 records of activity generated by camera trap data from six sites located throughout Central and South America. Using a null model simulation, we determined that for both species activities among sites overlap more than against a random expectation ($P < 0.001$), indicating a consistency of their activity patterns independent of the sites they occurred. Then, using pooled data of all sites for each species, we determined both species had a heterogeneous use of the diel cycle (Rayleigh test, $P < 0.001$ for both species) with a clear preference for diurnal activity. Finally, we found differences in activity patterns between these species (Mardia-Watson-Wheeler test, $W = 57.18$, $P < 0.001$) with the collared peccary using more heavily earlier times of the day (0600 to 1200 hrs), while the white-lipped peccary preferred the afternoon times (1200 to 18000 hrs). Currently the delta time in-between species activity detection is set to 15 minutes. However, further investigation into altering the delta time to 1 minute for comparison is ongoing. Ecological information on the mechanisms of coexistence of these species can be helpful for their management and conservation in the tropics.

Poster #14 - Survey of Vulnerable Amazonian Manatees Using Environmental DNA (eDNA): Methods for Surveys in Remote Field Settings

Kaitlyn Romoser, Izeni Farias, Tomás Hrbek, Miriam Marmontel, Leonardo Sena, Kirk Winemiller
Ecology and Conservation Biology, Texas A&M University
kaitlyn.romoser@tamu.edu

Trichechus inunguis (Amazonian manatee) is the only exclusively freshwater manatee. The IUCN lists them as a vulnerable species, with population decline projected to continue during the coming decades. Threats to the *T. inunguis* population, such as illegal hunting, water pollution, and alteration and destruction of habitat, make reliable survey methods necessary for assessing distribution and abundance. In this study, we used environmental DNA (eDNA) methods to test for *T. inunguis* presence in three locations along the Amazon River (Tefé, Manaus, Belém). At each location, water samples were collected at sites spanning a disturbance gradient from urban to protected reserves. We developed a field methodology to preserve DNA for up to 13 days or more without requiring freezing or cooling of samples. This method performed similarly to traditional cooling methods used for eDNA research. In the lab, samples were processed by DNA extraction, PCR amplification, and Illumina sequencing. Detection of Amazonian manatee DNA was more than three times greater in the Tefé region of the western Amazon where human impacts were lowest, but manatee DNA also was detected at one or two sites in the Manaus (central Amazon) and Belém (eastern Amazon) regions. Our methodology appears to be highly effective for detecting aquatic species in support of biodiversity conservation in tropical rivers.

Posters

Poster #15 - SARS- Cov-2 in Mammal Species

Jennifer Berry, Dr. Ivan Castro-Arellano

Texas State University

jlb502@txstate.edu

Spillback of SARS-Cov-2 from humans to animals has shown to be a very real possibility that might occur in domestic, laboratory, and nature settings. These spillbacks could become a concern to public health, as spillback could create potential endemic transmissions cycles beyond just human intra-population transmission. Also, the emergence of new, and more virulent, strains due to these inter-species transmission events is a potential risk that needs to be evaluated. An initial step to assess the magnitude of this threat is to closely generate and maintain taxonomic lists of which animals have acquired this virus, as well as their physiological response to it, including any documentation of spillback to humans. This research narrows this topic down to mammalian species, with the goal to create a comprehensive list of every mammal species that has tested positive for SARS Cov 2 to date, as such a list is not available or severely outdated. The full list shows 45 different mammal species that have tested positive so far. Our search showed that with available data most animals did show symptoms, and disease had lower severity than in humans and with a much lower fatality rate. The animals tested positive in a variety of environments. In many cases it has to be ascertained whether spillback to humans is possible, so that remains a relevant research need. The type of monitoring and testing done also often makes it difficult to tell whether intraspecific transmission occurred

Poster #16 - Direct fire is a potential agent of selection on animals

Peter Dorn, A. Michelle Lawing, Joseph W. Veldman

Ecology and Evolutionary Biology, Texas A&M University

rdorn@tamu.edu

Animals possess traits that enable them to survive wildfires, but the evolutionary relationship between direct fire and animals is poorly understood. While recognition is growing that immediate fire could select for adaptive traits in animals, little work has been done to support this hypothesis. In this poster, we propose that direct fire is a possible agent of selection on animals. We will use an agent-based model (ABM) of fire spread and animal escape to compute animal survival probabilities for different animal traits, survival strategies, and fire behaviors. We expect that trait variation confers differential fire survival probability, that different fire evasion strategies occupy different locations in trait space, and that shifts in fire behavior affect fire evasion strategies in different ways. We further expect that overall survival probability is high, regardless of trait or strategy. As fire regimes shift beyond their historical variability, species may not have the suitable traits to survive and persist. It is important to know how flexible species are to changes in fire behavior, and if these changes can influence the effect of selection on animals.

Posters

Poster #17 - Impacts of Roads in Biodiversity, A Study of Roadkill of The Florida Panther (*Puma concolor coryi*)

Javier Garcia Saldana, Miranda Peterson, Hsiao-Hsuan Wang, and William E. Grant
Ecology and Conservation Biology, Texas A&M University
javiergrc01@tamu.edu

In the case of the endangered Florida panther (*Puma concolor coryi*), the complex road network system in Florida restricts its movement, reduces its habitat, and is directly linked to its mortality as a result of vehicular trauma. Our goal was to study the dynamics of roadkill of Florida panthers and to understand how road characteristics affect Florida panther mortality. To address the goal of our study, we produced yearly maps of male and female Florida panther mortalities as a result of vehicular trauma throughout the state of Florida between 1972 until 2021 using ArcMap 10.7.1. We analyzed the data and compared vehicular trauma mortality to other causes of mortality. We then compared demographic factors such as age range, life stage, and sex of panthers that died as a result of vehicular trauma. Our preliminary results show that 386 out of 598 (64.55%) Florida panther mortalities occurred as a result of vehicular trauma between 1972-2021. We also found that of the vehicular trauma panther mortalities, 157 (40.67%) were female, 227 (58.81%) were male, and 2 (0.52%) were of unknown sex. Young male adult panthers between 2-3 years old appear to be the most susceptible group to suffer from vehicular trauma. Our preliminary results support past research on the negative impacts of roads on biodiversity. We plan to quantify the road characteristics effects on vehicular trauma and hope this results will aid in selection of areas for conservation.

Poster #18 - Behavior, constraints, and morphological response of a rapidly evolving invader, *Podarcis siculus*

Breann Richey, Marco Zuffi, Stefano Scali, Marco Mangiacotti, Roberto Sacchi, Loris DiVozzo, Mirko Guasconi, A. Michelle Lawing
Ecology and Evolutionary Biology, Texas A&M University
brichey@tamu.edu

Invasive species represent an incredible challenge for the conservation of species, ecosystems, and economies. Despite this, the mechanisms underlying successful invasion of new habitats remain challenging to clearly define. Amphibians and reptiles together make up just 2% of all studies in invasion literature, despite 18% of reptiles and 25% of amphibians being threatened by invasion. Here, we investigate factors facilitating invasion success on local, regional, and global scales across both native invasive and foreign invasive populations. This research will investigate the roles of behavior, habitat, and congener presence on invasion success in the Italian wall lizard, *Podarcis siculus*. This system is particularly compelling to ask these questions in because of a repeated history of rapid adaptation and documented risk of invasion to multiple threatened and endangered congeners. Deeper understanding of the ecological and evolutionary factors facilitating invasion success, especially at the native to invasive interface, will better allow us to understand how to mitigate invasions and their consequences.

Posters

Poster #19 - The Role of Behavior in Invasion Success: Using Behavioral Syndromes to Identify Behaviors that Aid in Species Invasions

Anni Wu, Anissa Berrouayel, Marina Salel, Rebecca Kumar, Michelle Lawing, Breann Richey
Ecology and Conservation Biology, Texas A&M University
anniwu620@tamu.edu

Biological invasions can have a significant impact on the ecosystems that they affect. In order to reduce these impacts, it is important to understand the mechanisms that allow invasion to be successful. In this study, we examine an invasion syndrome, a suite of correlated behaviors, in the globally invasive Italian Wall Lizard, *Podarcis siculus*. Here we identify and score three behaviors: aggression, boldness, and neophilia. These behaviors were chosen because they represent the most common behaviors in invasion behavioral syndromes, and therefore are expected to contribute to invasion success. We test these behaviors across recently introduced (10-20 years) and anciently introduced populations (1-2 millennia), as well as native populations. By testing these specific behaviors across multiple populations, we determine whether invasion history influences the presence of these traits.

Poster #20 - Determining the Role of Neophilic Behavior in the Invasion Success of the Italian Wall Lizard

Audra Hicks, Breann Richey, Dr. Michelle Lawing
Ecology and Conservation Biology, Texas A&M University
audrahicks@tamu.edu

Invasive species are one of the most serious threats to global biodiversity. The Italian Wall Lizard, *Podarcis siculus*, is a globally successful invader, but the mechanisms allowing them to invade successfully are poorly understood. Behavior likely plays an important role in the success of species invasions. This research analyzes a common behavior in an invasion-related behavioral syndrome: neophilia. Neophilia is the attraction to novel items and is expected to be advantageous to invasion success, due to the importance of adaptation to novel environments, ecosystems, and prey in the process of invasion. Understanding the distribution of neophilic behavior across invasion histories will increase understanding of the role of behavioral traits in the success of invasive species.

Posters

Poster #21 - Boldness in the Italian Wall Lizard (*Podarcis Siculus*) and its Invasive Success

Sim Khemani, Breann Richey
sk241159@tamu.edu

Invasive species can wreak havoc on environments where they successfully establish, and in order to mitigate detrimental impacts, it's crucial to understand the factors that lead to invasive species' success. Historically, certain species have a proclivity for success as invaders, indicating invasive species should possess some sort of attribute that allows them to live successfully in their new environment. In multiple invasion-related behavioral syndromes, a tendency toward boldness bolsters the success of an invasive species. By testing the globally invasive Italian wall lizard, *P. siculus*, from populations of different invasion histories, this study aims to explore the relationship between boldness and species success post-introduction.

Poster #22 - Diet of the Invasive American Bullfrog (*Lithobates catesbeianus*) in Western New Mexico

Ryan Frazier, Bryce Clements, Griffin Nicholson, Lee Fitzgerald
Ecology and Conservation Biology, Texas A&M University
Aggieryan22@tamu.edu

The American Bullfrog (*Lithobates catesbeianus*) is a widely successful invasive species impacting biological communities now at a global scale. In the Western United States, the *L. catesbeianus* can be observed in a large variety of habitats. Another aspect to consider is the diet of the species. Its wide fundamental niche has been hypothesized as a main cause of successful introductions. However, despite the knowledge regarding diet and trophic niche breadth, there is still a lack of broader analysis in many introduced locations and at a global scale. To take a more detailed look at their diet in their introduced range in New Mexico, I collected *L. catesbeianus* specimens along the Gila River and conducted a stomach content analysis. After removing stomach contents from specimens, I taxonomically identified, weighed, and calculated the volume of each stomach item. I present here my preliminary results. Within these preliminary results, I report the dietary importance to non-native American Bullfrogs of each taxonomic group found in their stomachs. Additionally, I report differences in the trophic niche between *L. catesbeianus* sexes and size classes. Finally, I discuss future directions of my research to incorporate my stomach analysis from New Mexico in a global meta-analysis of American Bullfrog diet studies. This meta-analysis will investigate changes in the trophic niche of bullfrogs dependent on habitat type, geographic location, and other variables.

Posters

Poster #23 - Anuran Acapella: Variation of mating calls for *Leptodactylus fuscus* in Toco, Trinidad

Madison Clark, Ryan Mohammed, Adrienne Brundage, Kevin W. Conway
Ecology and Conservation Biology, Texas A&M University
madison-clark@tamu.edu

Frog calls are an innate skill utilized by male frogs for defense and for attracting a mate. These calls have high phenotypic flexibility, with environmental factors such as temperature altering the propagation of the sound from the vocal cords, leading to a greater influence from their habitat. In this study, the calls produced by males of the leptodactylid frog *Leptodactylus fuscus* were recorded in rural and urbanized areas in Toco, Trinidad (n=21) to assess variation in mating calls within the species in both a narrow and broad context. The calls of male *L. fuscus* follow a distinct pattern, rising in frequency and reaching a plateau at the end of a distinctive “wheep” call. The maximum frequency (Hz) of calls recorded from males located in urban areas (n=10, average max frequency= 2618.4375 Hz) were significantly higher ($P=.028$, $P< .05$) than those recorded from males located in rural areas (n=11, average max frequency= 2458.7 Hz). Higher temperatures and noise pollution in urban areas may lead to physiological changes in the characteristics of anuran calls.

Poster #24 - Assessing the Impact of Environmental Drivers on Fish Community Dynamics in a Headwater Stream

Erica Hagemeyer, Jeffrey Wozniak
Sam Houston State University
eah066@shsu.edu

Drivers of fish diversity are based on nutrient availability, habitat heterogeneity, and environmental parameters. In pristine headwater systems the influence of these parameters can change through time and space, having a direct impact on fish diversity. Fish are vital to the stream because they help cycle nutrients and mitigate algal growth. This work will be conducted in Harmon Creek, Huntsville, Texas, a second order stream within the Trinity River Basin. This project seeks to explore how fish community dynamics vary amongst the stream’s diverse habitats (e.g., pools, riffles, and runs). Historical assessments of fish community dynamics indicate that the Blacktail Shiner (*Cyprinella venusta*) and Western Mosquitofish (*Gambusia affinis*) are the most dominant species. In this project we will resurvey the Harmon Creek ecosystem to determine shifts in species composition and propose to conduct controlled mesocosm experiments on how the current dominant species may respond to changes in key environmental drivers.

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Poster #25 - Biotic and abiotic factors influencing population dynamics of two endangered fish species (Smalleye Shiner *Notropis buccula* and Sharpnose Shiner *N. oxyrhynchus*) in a Great Plains River in Texas

Chase Nimee, Mike Curtis, Kaley Cave, David Hoeinghaus, Zacchaeus G. Compson, Carmen G. Montaña
Stephen F. Austin State University
nimeecr@jacks.sfasu.edu

Fish population dynamics are driven by intrinsic (i.e., biotic) and extrinsic (i.e., abiotic) factors that contribute greatly across space and time. The degree at which populations are influenced by one or both factors is still a matter of debate. We examined biotic and abiotic variables that may influence the distribution of two endangered fish species (Smalleye Shiner *Notropis buccula* and Sharpnose Shiner *N. oxyrhynchus*) in three segments of the upper Brazos River basin in Texas: the Brazos River mainstem (BR), Salt Fork (SF), and Double Mountain Fork (DMF). Physico-chemical instream descriptors were measured in-situ and the abundance and composition of the two endangered shiners and co-occurring species were quantified. Our findings suggest that the two populations of endangered shiners were widely distributed among the BR mainstem and DMF, but were absent from the SF. Native shiners dominated the assemblages within the BR mainstem and the DMF, while salt-tolerant species, such as *Cyprinodon rubrofluviatilis* and *Cyprinella lutrensis*, were abundant within the SF. Local environmental conditions (e.g., conductivity and stream flow) varied across the three segments, yet other parameters, such as dissolved oxygen, pH, and water depth, remained relatively constant throughout the study. Saline conditions present in the SF may be an important driver influencing the distribution of the two endangered shiners in this segment. Heterogeneity within the BR mainstem and DMF may be responsible for the diversity of fish species seen in these segments. Our results can be used by stakeholders to make decisions about the most effective conservation strategies of imperiled Great Plains fish species.

Poster #26 - Anatomical Survey of the Olfactory Apparatus in the Walking Catfishes (Siluriformes: Clariidae)

Cameron Olsen, Kevin W. Conway
Ecology and Conservation Biology
Texas A&M University
cameron.olsen@tamu.edu

The Family Clariidae is a diverse group of facultative airbreathing catfishes (Siluriformes) distributed throughout Africa and Asia, and introduced into the southeastern US. Members of this group are referred to as walking catfishes due to the ability of some species to travel short distances across land. Clariid catfishes exhibit remarkable variation in body shape and length, and exhibit a range of ecological strategies, ranging from stout-bodied “generalist” species to highly elongate, eel-like “specialist” species that inhabit shallow water and make nocturnal excursions onto land to hunt terrestrial prey. Despite this ecological diversity, information on the sensory organs of clariids is limited, available only for a small number of generalist species. To provide new information on clariid sensory organ anatomy, we surveyed the olfactory apparatus of thirty-nine clariid catfishes representing eight genera (including both generalists and specialists). Using a combination of light and scanning microscopy techniques, we document the gross anatomy of the olfactory apparatus, including the olfactory rosette and the accessory chamber, and for the first time document micro-surface structure and cellular composition of the olfactory lamellae. Preliminary results suggest the number of lamellae may differ between species of clariids, though we note a strong positive correlation between body size (standard length) and number of olfactory lamellae. *Gymnallabes typus* and *Platyallabes tihoni* possess a potentially novel organization of the lamellae of the olfactory rosette with posterolateral extensions of lamellae. The olfactory rosette of *Gymnallabes typus* displays greater vascularization than the olfactory rosette of *Clarias agboyiensis*, as observed via histology.

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Poster #27 - Population Structure of Red River Pupfish (*Cyprinodon rubrofluviatilis*) in Three River Segments of the Upper Brazos River, Texas

Caroline Crisp, Chase Nimee, Mike Curtis, Kaley Cave, David Hoeinghaus, Zacchaeus Compson & Carmen G. Montaña
Stephen F. Austin State University
crispc1@jacks.sfasu.edu

The Red River pupfish (*Cyprinodon Rubrofluviatilis*) is a native cyprinodontid found in saline streams of the upper Red and Brazos river systems of western Oklahoma and Texas. The species is listed as a threatened species in Texas, and given the ongoing anthropogenic threats related to habitat alteration in the upper Brazos River, we aimed to investigate the occurrence and populations size structure of the Red River pupfish in three sites in the Salt Fork of the upper Brazos River that appear to vary in local environmental conditions and anthropogenic influences. We expected that high occurrence of this fish would correlate with suitable sites containing water with high conductivity and salinity. We measured water quality and physical habitat variables to examine how they correlate with species occurrence and individual size classes. Overall, we observed differences in environmental conditions among the three sites. Water conductivity and flow was high at one of the sites and correlated with the high occurrence of Red River pupfish, but also larger individuals were found at this same site, which differed from the other two sites on substrate composition, dominated by mud and sand, and potential traces of oil on sediments. Despite altered conditions observed in this specific site, our preliminary findings suggest the Red River pupfish is a very euryplastic fish, and current physical or chemical stream characteristics may not be a major limiting factor of its abundance/occurrence. The population-level differences in body size were observed among sites suggesting that habit alteration may influence attributes of life history and fitness in these threatened populations, however, further research will continue to better inform conservation status of this species in these harsh segments of the upper Brazos River, Texas.

Poster #28 - Morphological adaptations of the Western Mosquitofish, *Gambusia affinis*, in relation to naiad predation

Emilee Holderness, Rose Blanchard, Josh Perkin
Wildlife and Fisheries Sciences, Texas A&M University
eholderness96@tamu.edu

Predation is a strong influencer of morphological adaptations. Divergent body shapes across a single species due to predation pressures is often observed and studied in freshwater fishes. However, the role of invertebrate predators, specifically dragonfly naiads, are under-examined in that regard. This study uses the highly abundant Western Mosquitofish (*Gambusia affinis*) to explore morphological adaptations that benefit survivability in the presence of dragonfly naiads. Based on other dragonfly naiad-prey interactions, we anticipate the most successful fishes will have an elongated caudal region that acts as a 'lure' in driving predator strikes away from critical body parts. We studied 4 populations of *Gambusia affinis* and measured body shape by taking lateral images of each specimen. 10 homologous landmarks were placed on the specimens, and a Procrustes superimposition was run on the dataset to translate, rotate, and scale images into the same shape space. Following the Procrustes superimposition, aligned coordinates were imported into R for statistical analysis. Survival and capture were noted in 24-hour predation trials for each specimen.

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Poster #29 - Quantifying Movement of Seven Imperiled Pelagic-Broadcast Spawning Fishes in Three Great Plains Rivers

Lucas Stevens, Dr. Joshua Perkin, Dr. Zachary Steffensmeier, Kevin Mayes
Ecology and Conservation Biology, Texas A&M University
lucaswstevens@tamu.edu

Dam-building, barrier construction, water diversion, groundwater pumping, and drought events cause habitat loss and fragmentation in large rivers, particularly in the Southern Great Plains ecoregion. These river alterations negatively affect cyprinids belonging to the Pelagic-Broadcast Spawning (PBS) reproductive guild characterized by production of nearly neutrally buoyant ova that are swept downstream potentially long distances during development. In this study, we used mark-recapture to quantify movement behaviors of seven imperiled Great Plains PBS fishes distributed among the Canadian, Brazos, and Red river basins including Plains Minnow (*Hypognathus placitus*; 3,580 tagged, 76 recaptured), Prairie Chub (*Macrhybopsis australis*; 5,771, 213), Shoal Chub (*Macrhybopsis hyostoma*; 1,535, 47), Peppered Chub (*Macrhybopsis tetranema*; 2,944, 378), Smalleye Shiner (*Notropis buccula*; 3,306, 63), Sharpnose Shiner (*Notropis oxyrhynchus*; 3,778, 306), and Arkansas River Shiner (*Notropis girardi*; 2,231, 95). Fishes were captured by seine, tagged using visual implant elastomer to code the location and date of capture, and then movement was tracked over 5-7 months during spring and summer (between 2019-2022). Results revealed movement patterns were leptokurtic for all species except Shoal Chub, suggesting populations represented heterogeneous mixes of stationary and mobile individuals. Biased upstream movement was evident for Sharpnose Shiner, Peppered Chub, and Arkansas River Shiner, but not the remaining four species. Estimated movement distances by the mobile component of all seven species was predictive of the minimum estimated stream fragment length species require for persistence (derived from literature), revealing a link between dispersal and habitat fragmentation. Our results provide insight into the appropriate spatial scales for management actions aimed at conserving multiple species of highly imperiled PBS fishes.

Poster #30 - Mesohabitat and macroecological correlations for blue sucker (*Cycleptus elongatus*) occurrence in regulated rivers

Meghan Booknis, Hannah Evans, Hayden Roberts, Noah Santee, Rebecca Mangold, Jacob Wolff, Dr. Joshua Perkin
Ecology and Conservation Biology, Texas A&M University
megabelleb14@tamu.edu

Blue Sucker (*Cycleptus elongatus*) occurs in large rivers in North America and is negatively affected by habitat fragmentation by dams and the resulting alterations to natural flow regimes. During fish assemblage surveys in August of 2022, we found five specimens of juvenile Blue Sucker (312-428 mm total length) in the Angelina River upstream of Sam Rayburn Reservoir. Our goal for this project was to analyze Blue Sucker distribution in Texas and the mesohabitat and macroecological settings that correlated with the collections. The first objective was to research occurrence records for Blue Sucker in databases at global, national, state, and basin scales to confirm specimens were from a previously undocumented location. The second objective was to quantify mesohabitat variables and compare them to conditions reported in the literature. The third and final objective was to compare the macroecological correlates (habitat fragmentation and degree of river regulation) for the collection location with the broader distribution of the species during historical (1950-1980) and contemporary (1981-2022) time periods. Results revealed the Blue Sucker population in the Angelina River upstream of Sam Rayburn Reservoir was previously unknown, though it was within the presumed native range of the species. Mesohabitats (i.e., fast velocity, shallow depth, coarse substrates) were consistent with habitats used by the species in other rivers. The low degree of river regulation (19% of natural runoff is stored by upstream reservoirs) and high degree of habitat connectivity (280 km of mainstem habitat) for the Angelina River upstream of Sam Rayburn Reservoir were consistent with Blue Sucker occurrence on a national scale. Our results suggest the occurrence of Blue Sucker upstream of Sam Rayburn Reservoir was predictable based on mesohabitat and macroecological attributes of the species. Our findings ultimately provide additional insight into how river regulation and fragmentation might be managed to benefit the species.

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Poster #31 - Coexistence of three stream dwelling cyprinid fishes: Implications for conservation of urban streams in east Texas

Eli Torrez, Carmen G. Montaña
Stephen F. Austin State University
torrezew@jacks.sfasu.edu

Understanding how fish assemblages are structured in stream ecosystems can provide useful information in developing effective conservation measures. We examined the population structure of three sympatric shiners: Blacktail shiner *Cyprinella venusta*, Blackspot shiner *Notropis atrocaudalis*, and Sabine shiner *N. sabiniae* in La Nana-Banita stream complex system within La Nana Bayou in East Texas across three seasons (spring, summer, and fall) in 2022. The Blackspot shiner and Sabine shiner are currently listed as species of greatest conservation need in Texas. These cyprinid species are stream-dwelling, generalist invertivores, known for co-occurring in similar stream types. Given the broader habitat tolerance, Blacktail shiner is expected to be most abundant. To investigate species-habitat association and spatial-temporal distribution, we examined population structure across three seasons and three habitats: pools, riffles, and runs. Species individual body size was measured across the three habitats. The Blacktail shiner was most abundant across all seasons, with greater abundance in pool habitats during the fall season. The Sabine and Blackspot shiners were present across all seasons but were overall less abundant compared to the Blacktail. In the spring season, abundance of the Blacktail shiner were correlated with deeper pools, while Sabine and Blackspot shiners were correlated with flow and substrate type. In the summer and fall, when flow was reduced due to the drought, the three species were collected in deeper pool habitats. Among the three shiner species, the Blacktail shiner showed a large range of body size (~30-80mm) variation across each habitat and seasons. Overall, the three species occurred together in similar habitats during the spring season when habitats were connected. However, the Sabine shiner appeared associated to riffle habitats. Perhaps, the absence of riffles in summer could have influenced its absence in the summer season, when this habitat type was dried. Despite the severe 2022 summer-fall drought, populations of Blacktail shiner dominated in pool habitats.

Poster #32 - Do Living Shorelines Enhance Fish Habitats?

Claire Legaspi, Matheus de Barros, Alexandra Rodriguez, Ronald Baker
Ecology and Conservation Biology, Texas A&M University
Clairelgsp@gmail.com

Shallow coastal ecosystems are vital habitats for a diversity of species, especially juvenile fish. To combat shoreline erosion, hard armoring methods have been widely implemented. However, armored shorelines tend to degrade the natural ecosystem. Living shorelines are becoming a popular alternative to hard armoring as they are designed to counteract erosion while maintaining the natural ecosystem. Understanding if and how restoration projects enhance shoreline habitat is critical for guiding future restoration projects. The aim of this project was to evaluate multiple metrics for quantifying the values of restored shorelines as fish habitat. To achieve this aim, we compared (1) nekton community composition, (2) diets, and (3) caloric content of common fish species between living shorelines, adjacent controls, and a nearby rip—rap hardened shoreline in Mississippi Sound, AL. Community composition results revealed similar nekton communities of living shorelines and adjacent controls, while lower abundance and species richness at the rip-rap site, suggesting poorer habitat quality at the hard armored site. Preliminary diet analysis suggests Silver Perch (*Bairdiella chrysoura*) and Pinfish (*Lagodon rhomboides*) from PaP sites have more diverse stomach contents than those from CI sites. Preliminary condition results suggests Pinfish from PaP living shoreline have higher caloric content than pinfish from PaP control, suggesting access to better quality food and habitats.

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Poster #33 - Multiscale stream fish species-discharge relationships: The relative roles of evenness, density, and spatial aggregation

Rebecca Mangold, Lindsey C. Elkins, Christina Saltus, Richard Johansen, and Joshua S. Perkin
Ecology and Conservation Biology, Texas A&M University
rebecca.mangold@tamu.edu

Riverine flow alterations represent an increasing threat to global freshwater fish diversity. Species-discharge relationships (SDR), characterized by a positive correlation between river discharge and fish richness, are used to forecast fish diversity responses to changes in discharge. However, SDR are scale-dependent and subject to effects caused by differences in evenness of fish abundances among sampling locations (“evenness effects”), the number of individuals collected during sampling (“density effects”), and spatial autocorrelation caused by collections nearer to each other having more similar richness (“aggregation effects”). We used a hierarchical nesting structure to collect stream fish assemblage data so that seine hauls ($n = 1,000$) were nested within sampling reaches ($n = 100$), nested within segments ($n = 20$), nested within tributaries ($n = 5$), nested within the central Colorado river subbasin. We then used the Measurement of Biodiversity (MoB) framework (McGlenn et al 2021) to assess the relative roles of spatial scale and evenness, density, and aggregation effects on stream fish SDR. To address spatial scale, we analyzed assemblage data compiled by reach (10 seine hauls in 100 reaches), segment (50 seine hauls in 20 segments), and tributary (200 seine hauls in 5 tributaries) scales and repeated the same MoB framework for each scale. Total observed species richness correlated with discharge magnitude at the tributary and segment scales, but not the reach scale. At the reach scale, small positive N effects were offset by equally small negative SAD effects. At the segment scale, positive evenness effects were the only significant mechanism, while at the tributary scale, the SDR was driven by strong positive evenness effects that outpaced small negative agg effects among sites with high discharge.

Poster #34 - Erosion-control structures enhance fauna but decrease microphytobenthic productivity in restored salt marshes in Galveston Bay

Brooke Torjman, Anna R. Armitage, Laura J. Jurgens
Ecology and Evolutionary Biology
Texas A&M University at Galveston
btorjman@tamu.edu

Salt marsh restoration protects shorelines from storm surges and erosion, improves water quality, and provides critical nursery habitat and trophic support for commercially and recreationally important fishery species. Despite these important values, more than 8,000 acres of salt marshes have been lost across Galveston Bay (Texas, USA). Efforts to restore coastal wetlands in Galveston Bay have used various restoration techniques, including the installation of erosion-control structures such as geotubes or breakwaters to help reduce wave action and sediment erosion. We investigated how these structures affect restored marsh community composition and productivity. We surveyed emergent marsh vegetation, epifauna, soil characteristics, and benthic microalgae in restored marshes with and without erosion control structures in May 2022. There were no differences in above- and belowground plant biomass, total plant cover, or vegetative species composition between sites with and without erosion control structures. Likewise, soil organic content and moisture were similar across all sites. We found almost eight times more periwinkle snails and three times more fiddler crab burrows in sites with erosion-control structures. In contrast, sites without erosion-control structures had consistently higher benthic microalgal biomass, though all sites had similar assemblages dominated by diatoms and cyanobacteria. These findings indicate that erosion-control structures have stronger effects on benthic fauna and microalgae than on emergent vegetation. In addition, this provides further evidence that assessments of restored salt marshes that focus just on emergent plant cover may yield an incomplete picture of restoration success.

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Poster #35 - Microbial Activity and Response to Temporal and Chemical Gradients in the Gulf of Mexico.

Norely Faz, Ellen M. Laaker, Jason B. Sylvan, Rebecca S. Robinson, Emily R. Estes
Oceanography, Texas A&M University
norely_faz@tamu.edu

Seasonal hypoxia in the Gulf of Mexico can create dead zones that have significant economic and ecological impacts. Hypoxia is exacerbated by anthropogenic activities in the Mississippi River watershed which lead to elevated nutrient concentrations in Mississippi River discharge. Previous research has established that hypoxic conditions alter microbial activity and microbial community structure. Here, we study microbial abundance and enzyme activity under different conditions to achieve a holistic view on the metabolic response of heterotrophic microorganisms to varying geochemical parameters. Two cruises were completed during March 2021 and August 2022 on the R/V Pelican in the northern Gulf of Mexico and Mississippi River. We captured gradients in salinity, temperature, nutrient concentrations, dissolved oxygen, chlorophyll, and color dissolved organic matter (CDOM). On each of these cruises, ~100 samples were collected for cell counts and enzyme activity assays. The spring dataset showed that enzyme activity rate varied by substrate and site, with esterase having the highest activity. These values were comparable with previous studies. Enzyme activity rates exhibited a generally positive correlation with dissolved oxygen concentration in both riverine and marine sites, though esterase showed no overall trend with this parameter. CDOM rates also directly correlate to enzyme activity at each site sampled. Salinity negatively correlated with enzyme activity rates at all sites except Site 2. The driver of these relationships is unclear due to the complex biogeochemical processes taking place simultaneously. Analysis of the late summer dataset will show if these trends persist under heavily stratified, hypoxic conditions.

Poster #36 - Bacteria And Archaeal Composition On The Texas Coast Following Hurricane Harvey

Joelle A. Roman, Shawn M. Doyle, Macy Fidler, Jessica N Fitzsimmons, Lisa Campbell, Steven Dimarco & Jason B Sylvan
Molecular and Cell Biology., Texas A&M University
romanj1@tamu.edu

Hurricane Harvey was a category four storm that lasted from 17 August - 02 September 2017 and brought unprecedented rainfall to Texas and Louisiana, resulting in 124 trillion liters of freshwater entering the Gulf of Mexico (GoM). With climate change predicted to increase storm severity, Hurricane Harvey may represent an increasingly common form of future storms that moves more slowly and results in higher rainfall. Therefore, it is important to understand the impacts of Hurricane Harvey on the ecology of the Gulf of Mexico to predict how future storms will impact coastal ecosystems. To understand how the microbial ecology of the GoM was affected by Hurricane Harvey, 112 seawater samples were collected from water column profiles along the Texas coast from Galveston to Baffin Bay as well as from Flower Garden Banks National Marine Sanctuary over two cruises during September 22 - October 1st, 2017. DNA was extracted from each sample before amplification of the V4 region of the 16S rRNA gene using Polymerase Chain Reactions. Patterns of community composition reveal stronger depth-associated differences between samples than temporal differences at the same depths. We will present results of compositional analysis as well as comparisons to post-Harvey microbial communities analyzed previously from Galveston Bay to determine if those community members were enriched downstream on the TX shelf following the storm, correlations to seawater chemistry, and correlations to previously published phytoplankton group profiles from the same samples.

Posters

Poster #37 - Microplastic abundance and diversity in East Texas stream food webs

Siena Stassi, Dr. Carmen G. Montana-Schalk and Dr. Sheryll B. Jerez
Stephen F. Austin State University
stassisr@jacks.sfasu.edu

Plastic litter is observed in nearly every freshwater system. Plastic degradation within these aquatic systems pose a risk to the freshwater biota through the microplastic contamination. This study aims to help fill the gaps in knowledge of the abundance and diversity of microplastics found in East Texas stream food webs. We analyzed water, sediments, and fish stomach content analysis from streams in urban and rural areas in East Texas. We expected to find higher prevalence of microplastics in samples collected from urban streams due to closer proximity to anthropogenic activity, higher rates of plastic pollution, and contaminated run off and wastewater. We collected samples from two urban streams within the La Nana Bayou watershed, and three rural streams and two rural lakes within the Big Cypress Bayou. Water and sediment samples were collected in polypropylene tubes, while fishes from targeted trophic guilds (detritivores, insectivores, piscivores/carnivores) were collected using different fishing gears. In the lab, samples were examined using standard protocols and any microplastics found were identified, sorted by shape and color, and counted. Overall, samples collected at urban streams contained a higher abundance of microplastics as compared to rural streams. Although the diversity of microplastics did not appear to vary greatly between urban and rural sites. Carnivorous fish appeared to ingest a diverse range microplastics compared to other trophic guilds. Findings from this project provide new insights into microplastic contamination in our local streams of East Texas. Streams in this Texas region contains the highest freshwater biodiversity, yet microplastic contamination and their transfer in the aquatic food webs and potential ecological impact on wildlife and ecosystem health are still not well known.

Poster #38 - Squash defense response to striped cucumber beetles aggregation pheromone

Sofia Pimenta de Oliveira , Morgan N. Thompson , Natalie M. Aguirre, Maria Fernanda G.V. Penaflor, Anjel M. Helms
Entomology, Texas A&M University
sofiapimenta3@gmail.com

Plants can acquire information from their environment to help defend themselves against herbivore attacks. It has been documented that plants rely on airborne chemical cues derived either from insects or neighboring plants to detect the presence of a potential attacker and prepare their defenses accordingly. After recognizing a reliable chemical cue, plants may induce and/or “prime” their defenses by increasing their direct and indirect defenses. A recent study demonstrated that cotton plants can detect the aggregation pheromone of boll weevils and respond by inducing their anti-herbivore defenses. Plants in the family Cucurbitaceae face attack by the striped cucumber beetle (*Acalymma vittatum*). Male *A. vittatum* emit an aggregation pheromone while feeding that attracts females and other males. The goal of this study is to evaluate whether squash plants respond to the *A. vittatum* aggregation pheromone. Our preliminary results indicate that squash plants exposed to *A. vittatum* aggregation pheromone have enhanced defenses upon herbivory attack which may have been the reason of lower feeding damage compared to unexposed plants. As little is known about insect-derived volatile priming in plants, this project will provide valuable information to help unravel important questions related to plant defense priming and may further improve the pest management of cucumber beetles.

Posters

Poster #39 - Niche Divergence in bryophytes with extreme sex-based segregation

Luis Hurtado, Gabrielle Davis, Coralie Domergue, Hannah Mitchell, Katie Sanbonmatsu, Daniel Spalink
Ecology and Conservation Biology, Texas A&M University
luisalejohurtado@tamu.edu

Abstract: Some non-vascular plants (known collectively as bryophytes) exhibit extreme sex-based geographic segregation. Whether or not male and female populations of these species are occupying different fundamental niches remains unknown. We chose four species across all three bryophyte lineages to investigate niche divergence between geographically isolated single-sex populations. To do so, we used occurrence data from GBIF and iDigBio and the R-package 'humboldt' to quantify Niche Divergence, Niche Overlap, and niche truncation. We found that single-sex populations of the same species show significant niche divergence. However, our analyses suggest that male and female plants across all four species are not occupying the entirety of their fundamental niches, making it impossible to determine if male and female populations have undergone niche evolution, or if they are simply occupying different parts of the same fundamental niche. Our analysis demonstrates the importance of assessing the degree to which occupied niche space approximates fundamental niche when attempting to quantify niche evolution and divergence.

Poster #40 - Photostimulating the ER-chloroplast junction, but not only the ER, results in immediate cytosolic calcium release in Arabidopsis hypocotyl cells

Nicholas Chow
Biology, Texas A&M University
zivhh@tamu.edu

"The *Arabidopsis thaliana* endoplasmic reticulum (ER) forms contact sites around the chloroplast via a membrane structure which results in an ER-chloroplast junction or nexus. By photostimulating the nexus with blue/violet beam an immediate calcium wave is released to the cytosol from the Ca²⁺ stores in the ER. Similarly, photostimulating the ER with blue/violet beam results in a cytosolic calcium wave. However, FRET (fluorescence resonance energy transfer) analysis of the ER calcium wave demonstrated a delayed and significantly lower Ca²⁺ release from the ER lumen when compared to the nexus cytosolic calcium wave. Multiple ER photostimulations concentrated around the nexus and multiple ER photostimulations distributed throughout the cell results in a delayed cytosolic calcium wave. Multiple ER photostimulations, despite being photostimulated in different areas, results in similar calcium waves to a single ER photostimulation. Thus, multiple ER photostimulations couldn't simulate a nexus cytosolic calcium wave indicating that a special structure within the nexus detects blue/violet beam, coupled to the Ca²⁺ stores in the ER. Using varying levels of blue/violet beam (100/75/50/25% laser power) to photostimulate, the nexus shows a trend of decreasing cytosolic calcium as light intensity lowers. Multiple ER photostimulations demonstrates similar, but increasing, cytosolic calcium waves that are relatively invariate with light intensity. Comparison of ER and nexus photostimulation creates a model that certain levels of photostimulation produces additive responses similar to an action potential in a nerve cell.

Posters

Poster #41 - The seasonally dry forests of Peru: a re-analysis of their diversity patterns and floristic relationships

Leonardo Collazos, Reynaldo Linares-Palomino, Isau Huamantupa-Chuquimaco, Eva Padrón, María de los Ángeles La Torre-Cuadros, Manuel Roncal-Rabanal, Nikki Choquecota, Leonardo Collazos, Renzo Elejalde, Nicole Vergara, José Luis Marcelo-Peña
Ecology and Conservation Biology, Texas A&M University
jcollazos@tamu.edu

Seasonally dry forests in Peru have three floristic groups: coastal, inter-Andean, and eastern forests. With seasonally dry forests of the northern coast of the country as an exception, until recently it was difficult to further define floristically each group due to a lack of data. However, in the last 20 years various floristic studies focused on woody plants have filled knowledge gaps in critical areas. The DRYFLOR Peru database was generated with these studies, which includes 526 quantitative inventories that allow us to determine the floristic distinctions of the three groups. Additionally, we were able to clearly recognize two subgroups of seasonally dry coastal forests, two inter-Andean subgroups, and three eastern subgroups. All subgroups have an assemblage of woody plant species that distinguishes and characterizes them in terms of abundance, frequency, species richness, and levels of endemism. Although we can now better describe the floristic heterogeneity of seasonally dry forests in Peru, we have identified important knowledge gaps that require urgent attention: i) we require additional inventory efforts in the eastern forests, ii) we need to resolve the floristic affinities of the forests of the Apurimac valley (a subgroup of the inter-Andean dry forests), iii) our data agree in little more than 75% with the definitions and distribution of dry forests of the recent National Ecosystem Map of Peru, and it will be necessary to review the concept of seasonally dry forests to adequately capture its distribution in this management tool.

Poster #42 - Spatial and temporal variation in orchid-insect communities: Insights from Motion capture field cameras

Analisa Flores

Analisa Flores, Lydia Morley, Josh Grewal, Steven Turk, Kate T. Morton, Julianne S. Allred, Kai Miller
analisaflores@tamu.edu

Platanthera is the most speciose orchid genus found in North America, contributing over 10% to North America's total orchid diversity. However, information about their pollinator relationships is scarce. Just like all plants, Platanthera's pollinators play a significant role in the establishment and maintenance of healthy populations over time. Thus, discovering pollinators, and understanding how they vary over a species' range, is critical if we aim to understand the factors that drive native North American orchid evolution and diversification. In our project, we analyzed motion-capture video footage of insect interactions over 3 sites of Platanthera leucophaea within Illinois. We compared and contrasted insect activity across these sites to understand 1) how activity varies temporally, and 2) how activity varies spatially. This project involves the curation and analysis of massive amounts of data, and this presentation provides a snapshot of our work in progress. Thus, we present our findings so far, and we discuss potential confounding factors as well as future directions.

Posters

Poster #43 - Machine learning and motion capture field cameras: Can computers help us organize our raw observational data?

Lydia Morley, Claire Ntaimo

Texas A&M University

lydia.morley@tamu.edu

Direct observational data is some of the most important information for ecological and evolutionary studies. Historically, observational studies were primarily human in nature: People would go into the field and record information directly, sometimes spending hundreds of hours at a single site. In the 21st century, however, we're able to deploy video cameras to multiple sites that serve as alternatives for human observers. Field monitoring with video cameras is becoming increasingly affordable and yielding much larger amounts of data at a fraction of the human-time cost. But the increasingly large datasets come with their own problem: A large portion of the data generated is ultimately useless to researchers. For field studies that use motion capture techniques, this often comes in the form of false positives. That is, motion events that trigger videos are not always the ones that researchers are interested in. Problematically, researchers ultimately have to sift through massive amounts of field data, sometimes resulting in thousands of hours of video footage resulting in only a fraction of those hours constituting appropriate data. In this study, we use motion-capture videos taken from the Native North American Orchid Pollinator Observation Project to develop a machine learning protocol for false positive detection. We implement a fine-tuning technique to train image recognition software on our data, which we then expand to video classification. For this presentation, we test the effect of sample size and variation on the accuracy and generalizability of our protocol and present the results, along with future directions.

Poster #44 - The complete mitochondrial genome of the invasive Mediterranean house gecko (*Hemidactylus turcicus*).

Ryne Maness, Charles D. Criscione

Biology, Texas A&M University

rwaness@tamu.edu

The development of genomic resources for the invasive Mediterranean house gecko (*Hemidactylus turcicus*) presents several opportunities in studying vertebrate immune evolution. 1) Geckos, being a basal squamate clade, can provide clues into the early evolution of tetrapod immunological mechanisms. 2) The Mediterranean gecko is infected with several helminth parasites and thus, could be developed as a field-based model to study the evolution of host-parasite, immune defense and counter-defense. And, 3) the gecko could provide insight into the genetic traits that drive invasion success, especially in relation as to whether immune related genes may play an adaptive role in its establishment. To this end, we used short and long-read sequencing technologies to sequence the complete mitochondrial genome of the Mediterranean gecko. The total mitogenome size was determined to be 16,901 base pairs. It consisted of the 13 standard, vertebrate protein-coding genes, 2 ribosomal RNA genes (12S and 16S RNA), 22 transfer RNAs, and 2 non-coding regions (a light strand origin of replication (OL), and a control region (D-loop)). The A + T content of the genome was 54.6% (A, 33.2%; C, 31.1%; T, 21.4%; G, 14.3%). A Bayesian phylogenetic analysis of the mitogenome showed that *H. turcicus* has close evolutionary relationships with both *H. frenatus* and *H. bowringii*. Future research will focus on assembling and annotating the complete genome of *H. turcicus*. 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 immune evolution."

Posters

Poster #45 - The first recombination map for the blue whale, *Balaenoptera musculus*

Richie Rasulis, Nicole M. Foley and William J. Murphy
Veterinary Integrative Biosciences, Texas A&M University
rgras3@tamu.edu

Recombination generates variation through the exchange of genetic material between chromosomes. Recombination maps provide a useful way to relate the locations of loci in space. Understanding the degree of linkage between sites enhances inference of selection, introgression and can aid in identifying causal variants in genome wide associations studies (GWAs). Recently, studies have shown that resolved recombination maps can predict the distribution of the species tree among hybridizing species. Blue whales (*Balaenoptera musculus*) are the largest animals on Earth, and it was historically believed that they could not hybridize despite sharing a common diploid chromosome count of 44 with all other rorquals. However, contemporary observations and genomic analyses have revealed ongoing hybridization between blue whales and fin whales. Trees that include blue whales are of high importance because of various adaptations that are of interest to the scientific community. Including, the possibility of sympatric speciation and their low incidence of cancer despite large body size – Peto's Paradox - are areas of ongoing research. There are no publicly available recombination maps for blue whales. A recombination map would facilitate resolution of phylogenetic relationships among these charismatic megafaunas. To address this, we gathered data for 2 blue whale individuals, mapped short reads to a chromosome level reference assembly and called genome wide SNPs. Our recombination map was generated using a novel population genetic machine learning approach. reLERN is a powerful deep learning network that uses polymorphism data to calculate per-base recombination rates accurately by modelling rates across an alignment. Furthermore, it allows for small sample sizes. By generating a resolved recombination map for blue whales, we provide an essential tool to understand not only phylogenomic relationships between endangered species of rorquals but also provide a means to fully understand the role of selection and introgression in their evolutionary history.

Poster #46 - Genetic Diversity of Viruses associated with Texas wheat fields

Ashrafou Ouro-Djobo, Ken Obasa, John O. Oladokun , and Olufemi J. Alabi
Department of Plant Pathology and Microbiology, Texas A&M University
aourodjobo@tamu.edu

Texas generates approximately \$481 million in revenue annually from wheat production, making it a significant crop in the state. Various viruses that infect wheat have been detected in Texas using ELISA and qRT-PCR techniques. In the spring of 2021, the virome of wheat fields in various locations within Texas was examined using high-throughput sequencing (HTS). The HTS was performed on 33 wheat leaves from 11 Texas counties pooled into four composite samples. The HTS data analysis allowed to generated partial or complete genomes belonging to barley yellow dwarf virus (BYDV), cereal yellow dwarf virus (CYDV), High Plains wheat mosaic virus (HPWMOV), Triticum mosaic virus (TriMV), brome mosaic virus (BMV), wheat streak mosaic virus (WSMV), and wheat eglid mosaic virus (WeqMV). The analysis of these sequences showed that Texas isolates of WSMV shared high sequence identity (98–100%) with isolates from Kansas and Nebraska but low sequence identity with isolates from Ohio and Colorado. The phylogenetic analysis showed that the isolates clustered in the clade B of the virus. The results also show the presence of a new variant of the HPWMOV in Texas. The isolates of BYDV and CYDV from Texas shared 96–98% identity with other isolates from GenBank but formed distinct subclades. The results indicate a greater variability of wheat-infecting viruses in Texas than previously realized.

Posters

Poster #47 - Loci underlying plant tolerance to harsh serpentine soils

Elyssa Garza, Kasuni Daundasekara, Dr. Alan Pepper
Department of Biology, Texas A&M University
ergarzaz@tamu.edu

Plants living in harsh soils have been of special interest in understanding the adaptive mechanisms needed to tolerate selective environmental pressures and develop resources for efficient nutrient uptake in agriculture, phytoremediation, and phytomining. Of particular interest are flora endemic to serpentine soils, which are exposed to and have adapted to stresses such as living with minimal nutrients, low water retention soils, high levels of toxic heavy metals, elevated soil temperatures, and high light conditions. A comparative analysis of the serpentine endemic *Caulanthus amplexicaulis* var. *barbarae* against its granite living sister *Caulanthus amplexicaulis* var. *amplexicaulis* has been done to identify loci needed for serpentine tolerance. *Caulanthus amplexicaulis* physical and genetic maps and resequencing from a set of Recombinant Inbred Lines were created and used in a QTL analysis along with data from serpentine and granite soils to identify potential genes underlying serpentine tolerance.

Poster #48 - Genome assembly of an expanding forest pest: *Dendroctonus frontalis* (southern pine beetle)

Megan Copeland, Adekola Owoyemi, Zachary Hoover, Heath Blackmon, Claudio Casola
Department of Biology, Texas A&M University
mcc146@tamu.edu

The southern pine beetle (*Dendroctonus frontalis*) is a type of wood-boring pest found in the United States. Since *D. frontalis* depends on host trees throughout its life cycle, this species is responsible for extensive ecological damage and economic loss in the timber industry. Although it has considerable damage potential, limited information is available regarding the genomics and genetics of this beetle. We produced a high-quality, chromosome-level genome assembly using long-read and Hi-C sequencing data. Our final assembly has a size of 174MB, 707 contigs, and a scaffold N50 of 24.829 MB. Our assembly confirms the conservation of the core stevens elements that have been identified in other polyphagan beetles. By delving deeper into the genetic makeup of *D. frontalis*, this assembly provides more resources for research in functional and comparative biology.



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