2022 Ecological Integration Symposium

The Return of the "Ologists"

Texas A&M University

April 7 – 8 2022

College Station, Texas

PROGRAM BOOK

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Symposium Schedule

April 7th and 8th, 2022
Annenberg Presidential
Conference Center
Texas A&M University

Thursday, April 7th

Time	Event	Location
8:15 am – End of day	Registration (Morning Snacks + Refreshments)	Annenberg Presidential Conference Center (APCC)- Lobby
8:45 – 9:00 am	Welcoming Remarks	APCC- Frymire Auditorium
9:00 – 10:00 am	**Dr. Richard Karban**	APCC- Frymire Auditorium
10:10 – 11:10 am	**Dr. Karen Beard**	APCC- Frymire Auditorium
11:25 am – 12:25 pm	**Dr. Peter Marra**	APCC- Frymire Auditorium
12:25 – 1:30 pm	Lunch	Leach Teaching Gardens
2:00 – 3:00 pm	**Dr. Corrie Moreau**	APCC- Frymire Auditorium
3:10 – 4:10 pm	**Dr. Dan Blumstein**	APCC- Frymire Auditorium
4:30 – 5:30 pm	**Speaker Panel**	APCC- Frymire Auditorium
6:00 – 7:30 pm	Happy Hour	Carney's Pub and Grill 3410 S College Ave, Bryan TX 77801

Friday, April 8th

Time	Event	Location
8:15 am – End of Day	Registration (Morning Snacks + Refreshments)	APCC- Lobby
8:15 – 9:00 am	Poster Check-In	APCC- Lobby
9:00 – 10:00 am	**Student Oral Presentations**	APCC- 1011B, 1011C, Presidential Dining Room
10:00 – 10:15 am	Break for Snacks and Refreshments	APCC- Lobby
10:15 – 11:15 am	**Student Oral Presentations**	APCC- 1011B, 1011C, Presidential Dining Room
11:15 am – 11:30 am	Break for Snacks and Refreshments	APCC- Lobby
11:30 – 12:30 pm	**Student Oral Presentations**	APCC- 1011B, 1011C, Presidential Dining Room
12:30 – 3:00 pm	Lunch	*On your own*
2:30 – 3:00 pm	Poster Set Up for Students Presenting Posters	APCC- 1011BC
3:00 – 5:00 pm	**Student Poster Session**	APCC- 1011BC
5:00 – 5:30 pm	Awards and Closing Remarks	APCC- 1011BC
6:00 pm	Social (Food + Drinks provided)	*Lee Fitzgerald's Home*

Plenary Speaker Line-Up, Thursday, April 7th

Dr. Rick Karban 9 - 10 am

Professor, Entomology, University of California Davis

Talk TBA

Dr. Karen Beard 10:10 - 11:10 am

Professor, Wildland Resources, Utah State University

The Coqui Invasion in Hawaii: Ecological Consequences and Possible Solutions

Dr. Peter Marra 11:25 am - 12:25 pm

Laudator Si' Professor, Biology and Environment, Georgetown University

Studying Birds in the Context of the Annual Cycle: Seasonal Interactions and Carry-Over Effects

Dr. Corrie Moreau 2 - 3 pm

Martha N. & John C. Moser Professor of Arthropod Biosystematics and Biodiversity, Cornell University

Natural History Museum Collections, Insect Science, and Diversity in STEM – Three critical aspects of Ecology and Evolution

Dr. Dan Blumstein 3:10 - 4:10 pm

Professor, Ecology and Evolutionary Biology, University of California, Los Angeles

Conservation Behavior: A Fearful Perspective

Oral Presentations

Friday, April 8th, 9 - 10 am

Start Time	APCC - 1011C Landscape and Riverscape Ecology	APCC - 1011B Ecology in Conservation	APCC - Presidential Dining Room Insect Ecology
9:00 am	Tatyana Canales Spatial distribution of road-kills and factors influencing road mortality for Florida Panther	Zachary Hutchens Urbanization increases isolation of a threatened fish species in East Texas streams: a 20-year perspective	Jorge Medina Duran New species discovered in Aggieland? Morphological and molecular evidence reveals two new gregarine parasites (*Apicomplexa*) from crickets collected at Texas A&M campus
9:12 am	David Rosenbaum Occupancy and abundance of the Alligator Snapping Turtle in Texas	Liam Wolff Predictors of site occupancy of Bachman's Sparrows in Texas	Andie Miller Allochronic mating behavior in *Spodoptera fugiperda*
9:24 am	Hayden Roberts Tributary streams provide migratory fish with access to floodplain habitats in a regulated river: evidence from Alligator Gar, *Atractosteus spatula*	Jodie McVane Cover crops for conservation agriculture	Cassandra Durden Animal endectocides: a one health framework for the simultaneous control of multiple vector-borne diseases
9:36 am	Johnathan Ellard Assessing multi-scale movement of Alligator Gar in the Lower Brazos River Basin	Natalie Hamilton Predicted range shifts for bat species in Texas	Ali Lira Olguin Taxonomic revision of the genus Megistopoda Macquart, 1852 (Diptera: Streblidae) and preliminary results of their species delimitation
9:48 am	Corey Fielder Spatial ecology and habitat use of the Texas Alligator Lizard		Jennifer Rhinesmith-Carranza KGBeetles: Insect Espionage and the Manipulation of Public Information

Oral Presentations

Friday, April 8th, 10:15 - 11:15 am

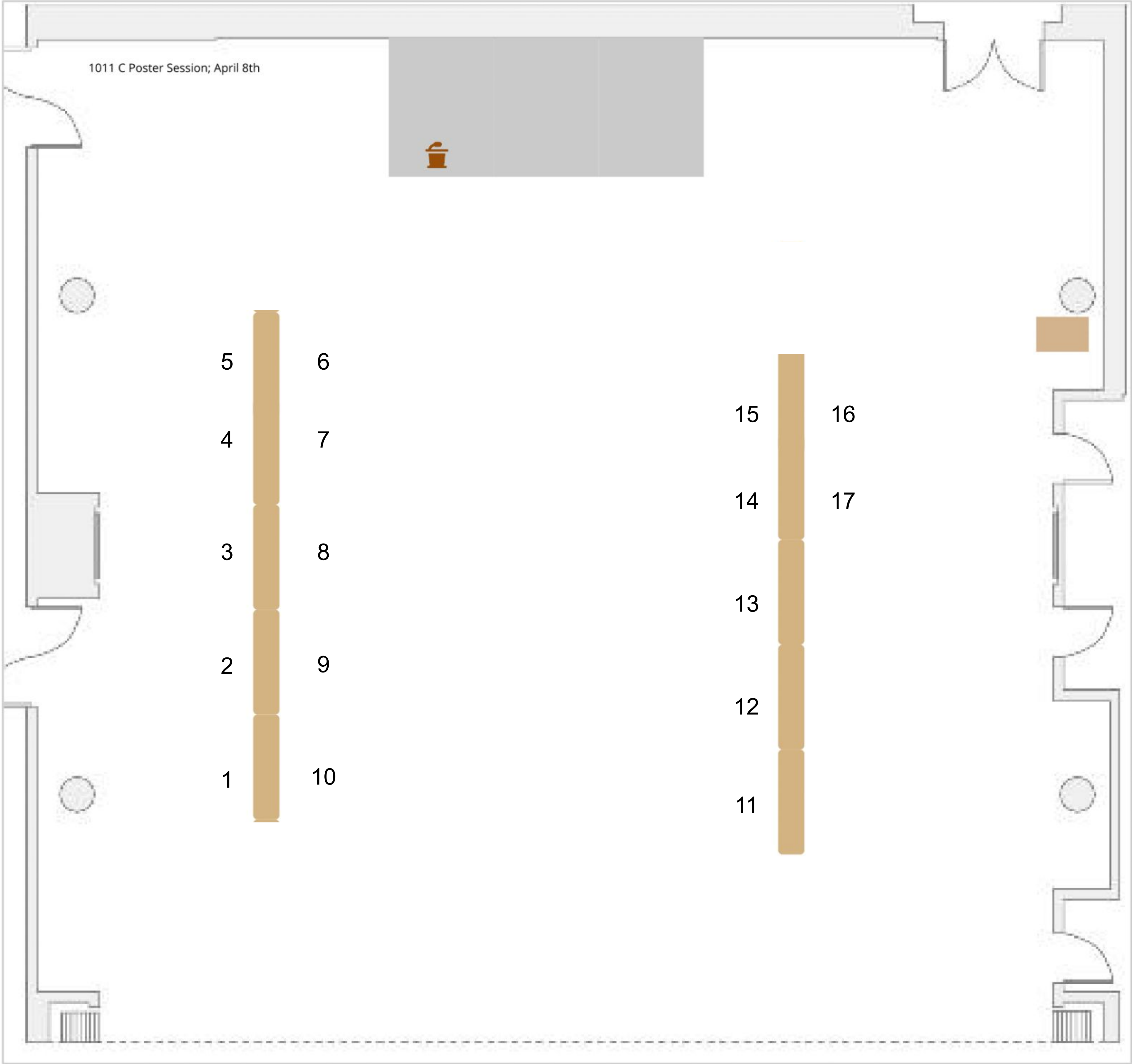
Start Time	APCC - 1011B Disease Ecology and Parasites	APCC - 1011C Community Ecology	APCC - Presidential Dining Room Behavioral Ecology
10:15 am	Scott Clark Impact of climate and land use on the spatial distribution of Rickettsiosis incidence in the United States	Rose Blanchard Changes in mosquitofish fin size in response to the presence of predators	Melanie Florkowski Gut microbiome diversity associated with exploratory behavior in a wild-caught songbird
10:27 am	Esha Kothapalli Spatial heterogeneity of climate and land use impacts on distributions of *Ehrlichia chaffeensis* Infections in the United States	Maria Alejandra Hurtado Materon Variability in ecological attributes of abundant species and phylogenetic distance increases with taxonomic diversity: insights for assembly mechanisms of Neotropical bat communities	Jacob Wolff Guadalupe Bass (*Micropterus treculii*) movement is predictable: implications for conservation
10:39 am	Katrina Keith Avian haemosporidian diversity in south Texas: new lineages and variation in prevalence between sampling sources and sites	Madeleine Thornley A quantitative dietary analysis o the white-tailed hawk at Mustang Island State Park	Colton Watts The evolution of female ornamentation in polygynous mating systems through selection for increased survival
10:51 am	Mycha A. Van Allen Comparing small mammal disease frequency between native and non-native grass rangelands in south Texas	Kylie Perez Vegetation selection and activity patterns of bats in the Texas coastal bend	
11:03 am	Jordan Salomon Host preference of Triatoma gerstaeckeri, a North American insect vector of the Chagas disease parasite	Keith Andringa No differences in body size and condition of Purple Martins (*Progone subis*) along an urban-rural gradient in Texas.	

Oral Presentations

Friday, April 8th, 11:30 am - 12:30 pm

Start Time	APCC - 1011B Ecology of Biological Invasions	APCC - 1011C Ecology of Plants and Ecosystems	APCC - Presidential Dining Room Genetics in Ecology
11:30 am	Erin Shepta Do native (*Cyprinodon rubrofluviatilis* and *Fundulus zebrinus*) and invasive (*C. variegatus* and *F. grandis*) cyprinodontids partition their niche? Morphological, dietary, and isotopic evidence for trophic segregation from a large river in Texas	Katie Sanbonmatsu A global analysis of mosses reveals low phylogenetic endemism and highlights the importance of long-distance dispersal	Annabel Perry CaveCrawler: how coding and cavefish can help us understand evolution and human disease
11:42 am	Emily Brockinton Importance of anthropogenic determinants of *Tubastraea coccinea* invasion in the northern Gulf of Mexico	Samuel Neely Taphonomic bias and paleoecological insights from modern mangrove peats	Minal Jamsandekar The evolution of four chromosomal inversions underlying ecological adaptation in Atlantic Herring using long-read sequencing
11:54 am	Miranda Peterson Plants on the move: the current trend and future risk of Japanese Honeysuckle invasion in the southern United States	Josh Lerner Ecosystem-level patterns in tidal wetland resistance and resilience	Mary Smith Sequence and lineage characterization of major histocompatibility complex class I genes in Atlantic Herring using a comparative genomics approach
12:06 pm		Moeka Ono Soil carbon balance under different prescribed burning frequencies	

Poster Session Layout



Poster Presentations

Friday, April 8th, Afternoon

Station	Presenter	Title
1	Emily Leeke	Characterizing flea community diversity on wildlife within Sam Houston National Forest
2	McKenna Sanchez	Elevation in relation to avian malaria in the Chihuahuan desert and Edwards Plateau
3	Katelyn Sanchez	Prevalence of Avian Malaria in Armenia Birds of the Caucasus Mountains
4	Sophia Gartenstein	Repatriation of Illegally Collected Alligator Snapping Turtles Into Native Texas Waters
5	Nicole Stevens	Multiple stable-isotope compositions of Rock Iguana (*Cyclura carinata*) scat distinguish anthropogenic impacts on diet and sedimentary biogeochemistry
6	Miriam Catalan	A novel field methodology to calibrate thermal dissipation sap flow sensors by characterizing radial sap flux profiles
7	Nyka Erickson	Generalist Pollinators and Pollinator Syndromes: A Case Study in North American Orchids
8	Hannah Mitchell, Coralie Domergue, Sarah Song, Gabrielle Davis	Evolution of sexual systems in the moss family Orthotrichaceae
9	Emily Russavage	The Correlation Between Direct and Indirect Defenses in Sorghum: Protection Against an Invasive Aphid Pest?
10	Kasuni Daundasekara	The evolutionary-genomic history of genes underlying serpentine tolerance in *Caulanthus amplexicaulis var barbarae*
11	Elyssa Garza	Using comparative genomics to understand serpentine tolerance in *Caulanthus amplexicaulis*
12	Isabella Svoboda	Microplastics in a post-hurricane peat deposit, Long Key, Florida
13	Courtney Plummer	Aquatic macroinvertebrates as sentinels of changes in local stream conditions in East Texas
14	Benton Fry	Multi-scale drivers of hypolimnetic oxygen depletion in six Minnesota lakes
15	Juan Lara	Taxonomic and morphological diversity of fish assemblages in Big Cypress Creek, Texas
16	Sandra Erue, Nelson Nwaiwu	Compound-20 (analog of curcumin) prevents acrolein-induced changes in rats
17	Yasmin Quintana	Isotopic niche overlap between the invasive armored catfish and native fish species in the Usumacinta River, Guatemala

ORAL PRESENTATION ABSTRACTS

Session 1, Friday, April 8th, 9 - 10 am

Section: Ecology in Conservation
Room: APCC 1011B

9 AM – Urbanization increases isolation of a threatened fish species in East Texas streams: A 20-year perspective

Zachary Hutchens[1], Jake Swanson, Carmen G. Montana
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The Sabine Shiner (*Notropis sabinae*) is a small-bodied cyprinid, of which populations were historically reported as stable and abundant in east Texas streams. Contemporary surveys have not yielded Sabine Shiner in the streams where it was assumed to be abundant. Despite being listed as a species of greatest conservation need in Texas, little information is available about the ecology and current status of the populations inhabiting east Texas streams. We assessed the movements and habitat associations, abundance, and ecological aspects of Sabine Shiner in streams within the La Nana Creek watershed of East Texas, where the species was assessed about 20 years ago. We hypothesized that alteration of flow regime and substrate modification due to urbanization have caused a decline in the population size in this watershed. We conducted monthly surveys of fish and in-stream habitat conditions from August 2020 to August 2021 in reaches along Banita Creek and La Nana Creek. On average, Banita Creek had shallow water with low flow, more diverse instream habitats, and lower values of salinity, conductivity, and turbidity compared to La Nana Creek. The movements of Sabine shiners were tracked monthly using Visual Implant Elastomer tags. Over a year-long survey, we collected 267 Sabine shiners from Banita Creek and 10 individuals from La Nana Creek. Out of this total, 169 individuals were tagged with a recapture of 98 individuals from a small reach on Banita Creek indicating the potential isolation of this population in this urbanized creek. Given the geographic restriction of this species in east Texas streams and its conservation status, our results have important contributions for management, restoration and conservation implications of the species.

9:12 AM –Predictors of Site Occupancy of Bachman's Sparrows in Texas

Liam Wolff[1], Daniel Saenz, Clifford E. Shackelford, I-Kuai Hung, Christopher M. Schalk
[1]Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University
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The Bachman's Sparrow (*Peucaea aestivalis*) is a woodland savanna specialist that relies on fire-maintained, open woodlands or early successional fields with a dense, herbaceous understory. Across its range, fire suppression and habitat loss have caused population declines, yet most research has focused on populations east of the Mississippi River. In Texas, this species is at the westernmost fringe of its range where vulnerability to extirpation is heightened. Our research paired detection data with habitat measurements to build statistical models that predict Bachman's Sparrow site occupancy. We placed autonomous recording units (Wildlife Acoustic SM4s and Minis) to detect sparrows at sites of potential occupancy based on a species distribution model and measured local vegetation characteristics and one regional covariate at each plot. We paired measurements with presence/absence using the R package "unmarked" to build hierarchical occupancy models ranked by Akaike Information Criterion (AIC). We detected Bachman's Sparrow at 40 of 240 sites (naïve occupancy estimate = 0.17). The top detection model had two covariates, midstory density and herbaceous ground cover, while the top occupancy model included herbaceous ground cover, midstory density, basal area, and canopy height and distance to source population. These results suggest that management for Bachman's Sparrow should focus on practices that minimize midstory and reduce basal area in mature stands to promote herbaceous ground cover growth, especially near source populations.

Section: Ecology in Conservation
Room: APCC 1011B

9:24 AM – Cover Crops for Conservation Agriculture

Jodie McVane[1], Muthukumar Bagavathiannan
[1]Department of Soil & Crop Sciences, Texas A&M University
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Cover crops have a multitude of benefits to keep our soils healthy and water clean. They were frequently used in the past and need to be fashionable once again. Cover crops are grasses, legumes, and forbs planted in mixes or singular for seasonal vegetative cover. Some of the benefits include weed control, protecting and feeding soil life, increasing water infiltration, and filter pollution from water bodies. Cover crop's ability to increase soil carbon, reduce erosion, and mitigate greenhouse gases is also positive for addressing climate change on agricultural landscapes. My research focuses on evaluating four summer cover crop mixes for post-harvest weed suppression in southeast Texas. The covers were planted on Sep 1, 2020, and Oct 4, 2021, and were terminated naturally by the first killing frost. Preliminary results show mixes containing grass species provided the best weed suppression compared to the other mixes evaluated in College Station, TX. This research offers valuable information for developing suitable cover crop mixes for the Southeast Texas region and other comparable geographies.

9:36 AM – Predicted range shifts for bat species in Texas

Natalie Hamilton[1]
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Texas is home to 33 species of bats, the highest species richness out of the 50 US states. Although there is this abundance of bat species in Texas, they face threats such as landscape fragmentation and changing climate, which can lead to loss of foraging areas or roosting habitat. However, because bats are highly mobile, it is predicted that species will be able to rapidly shift their range in response to changing climate. Understanding the changing distribution of species can aid in conservation planning by directing actions toward future predicted distributions or more vulnerable species. In this study, I mapped the distribution of bat species in Texas under present and future conditions with the goals of: 1) understanding how species richness changes across the state and 2) identifying species most vulnerable to population decline or local extinction. Using climate and landscape data, I generated distribution models for 26 species of bats in Texas in the present and the year 2070. Overall, the key findings of this study are that the species richness across the state is predicted to decrease by 2070, with areas in central and southern Texas the most vulnerable to species loss. Additionally, a large proportion of species are predicted to expand their range within Texas, but about 40% of the study species are predicted to experience range contractions. These models can be useful for pinpointing refugia, which can be starting points for detailed surveys and habitat maintenance, and also for identifying priority species for conservation actions.

Section: Landscape and Riverscape Ecology
Room: APCC 1011C

9 AM – Spatial distribution of road-kills and factors influencing road mortality for Florida Panther

Tatyana Canales[1]
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The Florida panther, *Puma concolor coryi*, has been described as an umbrella species, heavily impacting the ecological community they are in. The Florida panther historically roamed throughout the southeastern United States from Louisiana to southwestern Florida, and has now been limited to wild populations within the southern tip of Florida, specifically Big Cypress National Preserve and the Florida Panther National Wildlife Refuge, due to anthropogenic habitat degradation. Despite the conservation of the Florida panther, the population continues to experience threats from the continued development of expanding roadways through vital habitat. Hence, the objective of this study is to investigate the spatio-temporal trends of Florida panther road kills and determine the effects of roadway development and automobile traffic on the roadkills. To perform the investigation, data was collected from open access sites, including the Florida Fish and Wildlife Conservation Commission, which was used to create a document with the time and location of roadkills and presences in Florida from 1980 to 2021, and the Florida Department of Transportation, which contained road data from 2011 onward. The data was used to create a map displaying the points of occurrence of roadkills and overlaid with historical road and traffic data. I then identified potential variables influencing the likelihood of roadkills and quantified the relative importance of each factor using boosted regression trees. I found that a majority of the cases occurred along rural roads, particularly expressways and major collectors. Of these roads, it was most common for Florida panthers to die by vehicular strike along 2 laned roads that had medians between 20-24 feet, and were often paved or curbed with vegetation. While many roads did not record the average speed traveled, the most common speed seemed to be 60-65mph. These findings indicate that there may be a correlation between the narrow, rural roads surrounding vital habitat, and the continuous increase in Florida panther roadkills. This agrees with the behavioral patterns of the species, seeing that they are known to be elusive, and avoid contact with people, and frequently traversed areas.

9:12 AM – Occupancy and abundance of the Alligator Snapping Turtle in Texas

David Rosenbaum[1], Christopher M. Schalk, Daniel Saenz
[1]Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University
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The Alligator Snapping Turtle (*Macrochelys temminckii*) is a Threatened species in Texas that has been proposed for federal protection. However, there is a paucity of contemporary data regarding its status at the southwestern extent of its range, which includes eastern Texas. In 2020 and 2021, we conducted hoop trap surveys at 51 locations throughout the purported range of the species in Texas to elucidate its occupancy probability and average site abundance. We analyzed survey data with hierarchical models that allowed us to quantify detection error and infer what variables influence occupancy, abundance, and detection. We confirmed the species in all watersheds between the Brazos and Red River watersheds at 61% of surveyed locations. Mean detection probability of the species was 0.77, and was influenced both methodologically by the spacing of traps, and environmentally by lunar phase and water flow velocity. Mean occupancy probability in permanent water bodies was 0.82, while mean estimated abundance across all surveyed sites was 7.57. Mean site density was 8 individuals/km. *Macrochelys temminckii* occurs in highest abundances at median latitudes within its Texas range and is more probable to occur in aquatic habitat contained within highly-forested catchments. Variation in measured in-stream habitat characteristics did not influence either its occupancy or abundance, despite the known microhabitat preferences of the species. Distributional patterns of the species are driven by land features that vary on large spatial scales. This research corroborates evidence provided from other taxa that watershed land cover can exert influence on aquatic communities.

Section: Landscape and Riverscape Ecology
Room: APCC 1011C

9:24 AM – Tributary streams provide migratory fish with access to floodplain habitats in a regulated river: evidence from Alligator Gar, *Atractosteus spatula*.

Hayden Roberts[1], Joshuah Perkin
[1]Department of Ecology and Conservation Biology, Texas A&M University
hcr@tamu.edu

Fishes that migrate in freshwater with periodic life history strategies are particularly sensitive to river regulation. However, persistence of these fishes in highly regulated rivers may be related to tributaries providing necessary spawning and early life stage habitats. To explore this, we studied the movement behavior of Alligator Gar, *Atractosteus spatula*, and hydrology in a highly regulated North American river, the Brazos River. We hypothesized that: (1) due to the degree of river regulation on the Brazos River, flood pulses would be much more limited than less regulated tributaries: and (2) fish movements into tributaries would be best predicted by higher flows and temperatures. Our analysis revealed that flood pulses were drastically reduced on the main-stem, but not a tributary, and tributary occurrence was highest above mean temperatures (i.e., 25℃) and when flows exceeded a 3 pulse per season (i.e., 300 cms) frequency. These results provide a framework for advancing the conservation of migratory fishes in regulated rivers and further emphasize that tributary use may buffer main-stem populations against the effects of river regulation.

9:36 AM – Assessing Multi-scale Movement of Alligator Gar in the Lower Brazos River Basin

Johnathan Ellard[1], Hayden C. Roberts, Daniel J. Daugherty, Paul B. Fleming and Joshuah S. Perkin
[1]Department of Ecology and Conservation Biology, Texas A&M University
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In recent decades, interest in conservation and management of Alligator Gar has promoted research efforts to better understand the species' ecology, with a heavy focus on movement dynamics. Population level fish movement is often thought to be a heterogenous mixture of stationary and mobile individuals that make up a leptokurtic distribution, but this has only been recently suggested to occur with Alligator Gar. Further, movement behavior of this species is often looked at a coarser scale rather than finer spatial and temporal scales or evaluated together. Therefore, the goal of this study was to evaluate multi-scale movement of Alligator Gar using data from mobile telemetry surveys tracked at 24hr (fine-scale) and monthly (coarse-scale) temporal extents. Movement data collected from a subset of individuals (n=13) at the coarse-scale, and five individuals at the fine-scale revealed heterogeneous distributions of fish dispersal across the population and individual levels. At the coarse-population level, leptokurtosis was present, indicating heterogeneity of mobility among individuals in the population. This was validated at the coarse-individual level where a heterogenous mixture (i.e., kurtosis ~3 or >3) of movement distributions was observed making up population level leptokurtosis. At the individual level, there was no leptokurtosis at the fine-population level, but at the fine-individual level, there was also a mixture of movement distributions. Multi-scale movement analysis of individuals may provide new information to contribute to the management practices of Alligator Gar, other species, and life history strategists not strongly represented in existing meta-analyses of fish movement.

Section: Landscape and Riverscape Ecology
Room: APCC 1011C

9:48 AM – Spatial Ecology and Habitat Use of The Texas Alligator Lizard

Corey Fielder[1], Jared Holmes, Toby Hibbitts, Wade Ryberg
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corey.fielder01@tamu.edu

Texas Alligator Lizards, *Gerrhonotus infernalis*, continue to be a secretive and relatively understudied species. Due to their cryptic nature and status as a species of least concern, little effort has been made to describe the ecology and life history traits of this species in their natural habitat. Only one study to date has attempted to describe the ecological aspects of Texas Alligator Lizards, and no field research on this species has been conducted in Texas. This study aims to better describe this species' ecology by collecting data on their behavior, spatial ecology, and habitat use on a seasonal basis at Selah, Bamberger Ranch Preserve, Blanco County, Texas. To date, we have captured and attempted to radio track 43 lizards (22 males and 21 females) resulting in 10 months of overlapping data on movement activities and habitat usage. We looked at the effect of sex and season on spatial movements; there was a significant effect of season ($p=0.013$), but we did not see an effect of sex ($p = 0.828$) or the interaction between the effects of sex and season (F2,45 = 0.061, $p = 0.940$). Summer and Fall microhabitat use were similar with a strong association with dense canopy cover, sloped terrain, rocky refuge (boulders >30 cm) and structural habitat such as woody shrub trees and fallen woody debris on the ground. Winter microhabitat use consisted again of dense canopy cover and sloped terrain but was

Section: Insect Ecology
Room: Presidential Dining Room

9 AM –New species discovered in Aggieland? Morphological and molecular evidence reveals two new gregarine parasites (*Apicomplexa*) from crickets collected at Texas A&M campus

Jorge Medina Duran[1], Jordan Moore, Hojun Song
[1]Department of Entomology, Texas A&M University
jorgemedinad@tamu.edu

Recent phylogeny-aware high-throughput metabarcoding 18S eDNA data has prompted the idea that a protist group known as gregarines is the most diverse eukaryotic lineage in terrestrial environments. Gregarines belong to the Apicomplexa, a phylum that is better known for including vertebrate parasites of medical importance responsible for diseases such as malaria. They, however, do not infect vertebrates but instead inhabit a broad arrangement of invertebrate lineages, including insects. The fact that they utilize insects as hosts has been used to explain its putative great diversity as it is thought that gregarines and insects have cospeciated. The study of the taxonomy and diversity of gregarines, however, has been neglected and most of what is known come from old descriptions based only on morphology. We have surveyed the gregarines of the field cricket *Gryllus aff. texensis* at the main campus of Texas A&M to contribute to the understanding of the diversity of this protist group. We used an integrative taxonomic approach that combines 18S molecular data, morphology, and host utilization to delineate the gregarine species and we found that there are two putatively new species inhabiting the cricket host. We found that the morphological evidence alone was not enough to separate them from previously described species, but the molecular data unequivocally delineate them as two distinct lineages. The above demonstrates that the use of integrative taxonomy is necessary to delineate gregarine species and to build on our understanding of the unprecedented diversity of this enigmatic apicomplexan group.

Section: Insect Ecology
Room: Presidential Dining Room

9:12 AM – Allochronic mating behavior in *Spodoptera frugiperda*

Andie Miller[1], Greg Sword, Ashley Tessnow
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Spodoptera frugiperda, commonly known as the fall armyworm, is a species making headlines with their rapid 5-year invasion of the Eastern Hemisphere. A species endemic to the Americas, *S. frugiperda* is now a global superpest of major crops including corn, rice, and sorghum. Although a great deal of attention is being paid to *S. frugiperda* as an invasive species, many aspects of the species' biology remain unknown in its native range. A classic characteristic of this species is the presence of two morphologically identical but genetically distinct strains, the corn (C) and rice (R) strains, originally named based on studies of host plant preference. Evidence of host plant preference in these strains, however, is inconsistent and indicates that additional factors may be responsible for keeping these strains reproductively isolated. Both lab and field studies have revealed that *S. frugiperda* strains exhibit allochronic variation in mating behavior with the two strains preferentially mating at different times of night. This allochronic mating behavior has been hypothesized to be a possible mechanism maintaining the distinct strains, however, little is known about this behavior in nature. In this presentation, I will present results from ongoing lab and field-based experiments designed to test hypotheses about allochronic variation in fall armyworm mating behavior and its consequences for reproductive isolation between the two genetically distinct strains.

9:24 AM –Animal Endectocides: A One Health Framework for the Simultaneous Control of Multiple Vector-Borne Diseases

Cassandra Durden[1], Koyle Knape[2], Macie Garza[3], John Carey[2], Sarah A. Hamer[1], Gabriel L. Hamer[3]
[1]Department of Veterinary Integrative Biosciences, Texas A&M University
[2]Department of Poultry Science, Texas A&M University
[3]Department of Entomology, Texas A&M University
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Due to factors including climate change and globalization, vector-borne diseases continue to emerge worldwide and threaten both human and animal health. Diverse control methods have been used to target arthropod vector populations, with environmental insecticides being the most common. As an alternative to widespread environmental distributions, host-targeted insecticides (endectocides) allow for application of chemicals directly to vertebrate species. Our long-term goal is to suppress populations of multiple vector species by endectocide treatment of the key host species that are responsible for feeding the vectors in nature. Here, we evaluate domestic chickens as a key host that has been shown to provide bloodmeals to triatomine vectors of the Chagas disease parasite and mosquito vectors of West Nile Virus. We hypothesize that arthropod vectors that feed on endectocide-treated chickens will have a higher rate of mortality compared to control groups. In experimental trials, chickens will be given one of three endectocides: Safe-Guard® Aquasol (Fenbendazole), Ivomec® Pour-On (Ivermectin), and Bravecto® (Fluralaner), dosed orally. We will then feed starved, adult *Culex quinquefasciatus* females and 3rd-5th instar *Triatoma gerstaeckeri* vectors on live, restrained chickens at 0 days, 3 days, 1 week, 2 weeks, 1 month, and 2 month time intervals post-treatment while monitoring the fed vectors for their survival. With trials currently underway, we expect that chicken-targeted endectocides will show promise for deployment to peridomestic natural habitats where integrated vector control approaches are needed to further combat Chagas disease, mosquito-borne arboviruses, and other vector-borne diseases.

Section: Insect Ecology
Room: Presidential Dining Room

9:36 AM –Taxonomic revision of the genus *Megistopoda* Macquart, 1852 (Diptera: Streblidae) and preliminary results of their species delimitation

Ali Lira Olguin[1], Carl W. Dick, Roxana Acosta-Gutierrez
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Bat flies (Diptera: Streblidae and Nycteribiidae) are obligate, blood-feeding ectoparasites of bats, parasitizing only bats. Bat fly species belonging to the genus *Megistopoda* are characterized by presenting the femur III longer, thorax shieldlike, and stenopterous wings. *Megistopoda* species are therefore unable to fly and their ability to move among host individuals is restricted and this lack of flight can lead to strong host associations. The genus *Megistopoda* is composed of three described species *M. aranea*, *M. proxima* and *M. theodori*, each of which has been found to be associated with host species belonging to the New World leaf-nosed bats (Chiroptera: Phyllostomidae) genera Artibeus or Sturnira. With only three widely distributed species, *Megistopoda* is an understudied genus and species delimitation has not been rigorously assessed. Most of the characters used to identify *Megistopoda* species are ambiguous and intraspecific variation is usually not considered. In this talk, I will present the results obtained during my master's studies, where we analyzed morphological characters and a total of 12 body measures of 852 *Megistopoda* individuals (obtained from museum collections and recent fieldwork) from across their geographic range. We identified nine putative species, six new to science, but describing diagnostic characters. Two analyses (ANOVA and PCA) were performed to recognize significant differences among the quantitative characters. Thorax chaetotaxy, the femur III length, and the wing measures were the most informative to recognize morphospecies. Future research will include phylogenetic analyses using morphological and molecular data to determine relationships, host associations, and geographic distributions among *Megistopoda* species.

9:48 AM – KGBeetles: Insect Espionage and the Manipulation of Public Information

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Volatile organic compounds make up one part of a suite of public information that many insects use to guide resource location, evaluation, and acceptance. Many of these volatile compounds are of microbial origin, and can serve to attract, deter, and even misinform potential patrons of this public information. The ubiquity of microbes in the environment and the existence of their associated volatile compounds as potential inter-kingdom cues or signals might lend itself to the evolution of manipulative behaviors by those who are able to change the microbial, and concomitantly the volatile, profiles of resources. This talk explores results from an assay evidencing this clandestine manipulation of public information by the carrion burying beetle, *Nicrophorous vespilloides* (Herbst) (Coleoptera: Silphidae), and the potential consequences this campaign of misinformation may have on competitors in the carrion system.

ORAL PRESENTATION ABSTRACTS

Session 2, Friday, April 8th, 10:15 - 11:15 am

Section: Disease Ecology and Parasites
Room: APCC 1011B

10:15 AM – Impact of climate and land use on the spatial distribution of Rickettsiosis incidence in the United States

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Rickettsiosis is a tick-borne illness that is prevalent in the United States. It is primarily caused by transmission through its vector, *Rickettsia*, most commonly by arthropod bites. Rickettsiosis can be treated using the antibiotic doxycycline, but diagnosis of rickettsiosis is extremely challenging, and symptoms do not appear until approximately 1-2 weeks after transmission. Recent studies have found that climate change has a positive effect on rickettsiosis. However, land use effects have not been fully studied. In this study, the impact of climate and land use was further investigated to see how it impacts the spatial distribution of rickettsiosis in the United States from 2012 to 2015. Climatic and land use data were collected from years 2010 to 2015 and 2012 to 2015, respectively, and incidence data were collected from 2012-2015. The climatic data was collected from PRISM climate group, the land use data was collected from the Multi-Resolution Land Characteristics Consortium, and the incidence data was collected from the National Notifiable Disease Surveillance System. I then merged and analysed all geo-referenced variables describing climatic conditions and land use features to identify potential factors influencing Rickettsiosis incidence using a multinomial logit model. The preliminary results indicate that the highest incidence of rickettsiosis occurs in the southeast of the United States, with most counties having 1-14 cases per year, and some having greater than or equal to 15 cases per year. More specifically, Arkansas' counties have the most populated incidence rates.

10:27 AM – Spatial Heterogeneity of Climate and Land Use Impacts on Distributions of *Ehrlichia chaffeensis* Infections in the United States

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Recent studies have shown that geographic ranges of ticks and tick-borne diseases are increasing. Changes in climate and land use have been shown to increase the incidence of tick-borne diseases. *Ehrlichia chaffeensis* infection is an emerging tick-borne disease caused by *Ehrlichia chaffeensis* in the United States. *Ehrlichia chaffeensis* infection causes nonspecific flu-like symptoms and can be potentially fatal in humans. The trend of *E. chaffeensis* infection has been increasing since 2000. Hence, I aim to identify spatial patterns and detect hot spots of *E. chaffeensis* infections from 2012 to 2015 and examine the impacts of climate variables and land use factors on *E. chaffeensis* incidence. First, I collected the incidence data of *E. chaffeensis* infections, climate variables, and land cover land use data from the National Notifiable Disease Surveillance System, PRISM climate group, and the National Land Cover Database. I mapped and overlaid all data using ArcGIS. I analyzed the geo-referenced variables describing climatic conditions and landscape features to identify potential factors influencing the likelihood of incidence of *E. chaffeensis* infections using a multinomial logit model. Preliminary results indicate that the incidence of *E. chaffeensis* infections is more prevalent in the southeastern region of the United States.

Section: Disease Ecology and Parasites
Room: APCC 1011B

10:39 AM – Avian Haemosporidian Diversity in south Texas: new lineages and variation in prevalence between sampling sources and sites

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Avian haemosporidian parasites (Haemoproteus, Leucocytozoon, Plasmodium) in Texas are relatively understudied for such a large geographic area with diverse ecoregions. Our study sites in south Texas, located in two adjacent ecoregions, present the opportunity for investigating patterns and possible causes of infections between habitats, and characterizing the baseline makeup of the avian malaria community. We assessed the avian malaria community using their mtDNA cytb gene in 576 birds, 25.69% of which were infected. The overall detection rate was much higher from blood samples than tissue samples, and the more arid ecoregion had a significantly lower overall prevalence. Findings also revealed significantly lower Plasmodium infections in the more arid ecoregion. We identified 25 novel lineages, which included 16 Haemoproteus, 2 Leucocytozoon, and 7 Plasmodium lineages. This information establishes a baseline of prevalence for these ecoregions and provides insight into the disease ecology of resident and migrant birds of this area. We assert that baseline knowledge of this type is necessary for meaningful comparisons to areas of high anthropogenic change, and essential to aiding conservation efforts of birds in the future.

10:51 AM – Comparing small mammal disease frequency between native and non-native grass rangelands in south Texas.

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Wildlife disease, especially zoonotic disease, is an increasing concern for wildlife managers, veterinarians, and public health officials. Small mammals can be reservoirs for zoonotic diseases of concern, such as typhus, hantavirus and Lyme disease that cause human illness every year. Many small mammal species occur in grassland regions. Across the state of Texas, 99% of the grasslands that formerly dominated the landscape have been lost. Human activity has significantly altered these grasslands by conversion to monocultural pastures, agriculture, invasive species introduction, and development. Conversion and degradation of native grasslands increase the fragmentation of suitable habitats for these small mammals. Here I propose a study design comparing the disease frequency in small mammals between a native and non-native grass rangeland in south Texas. This study aims to assess whether there is a biological significance in restoring or preserving grassland ecosystems to manage wildlife disease.

Section: Disease Ecology and Parasites
Room: APCC 1011B

11:03 AM – Host preference of *Triatoma gerstaeckeri*, a North American insect vector of the Chagas disease parasite

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Chagas disease is a zoonotic, neglected tropical disease impacting >7 million people across the Americas. The disease is caused by a vector-borne protozoan parasite – *Trypanosoma cruzi*- for which triatomines are the vector. Triatomines blood feed on diverse host taxa, including mammals, birds, and herpetofauna; however, only mammals can serve as reservoirs of *T. cruzi*. Therefore, host choice can sculpt the level of infection in the vector, and ultimately, human risk. We hypothesize that triatomines will show host preferences when options are available. We created a large dual-choice olfactometer to allow pairwise combinations of: no host (empty chamber); dog; human; and chicken. In each trial, a single *T. cruzi*-negative *Triatoma gerstaeckeri* 5th instar nymph was placed in the central entry portal and allowed 55-minutes while we monitored behavior. Host choice was defined as insect movement toward a host chamber, resulting in their collection. Pilot studies indicate an association with level of triatomine activity and engorgement; therefore, all were starved at least 2-weeks prior to trials. Trials with one or two hosts, 40% (10/25) of triatomines did not leave the entry portal. Host choice was made on average in 16 minutes (range 3-54). Early data indicate chicken is the most common host choice, with 6/15 insects making the choice of chicken, compared to only 2/10 for dogs, 2/10 for humans, and 2/10 selecting the empty chamber over a dog. Future work will include *T. cruzi*-infected insects to explore parasite manipulation of vector-host choice.

Section: Community Ecology
Room: APCC 1011C

10:15 AM – Changes in mosquitofish fin size in response to the presence of predators

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The Western mosquitofish is a small freshwater fish that has internal fertilization and gives birth to live young. These fish tolerate a wide range of environmental conditions and commonly feed on mosquito larvae. The ability for the fish to survive in many habitats and its utilization for mosquito control has led to the mosquitofish being the most widely distributed freshwater fish in the world, and has been studied in detail for years. The changes the body shape of the mosquitofish undergoes in response to different predators has been studied in detail, however, the differences in size of the fins in the presence and absence of sunfish predators have not been studied. The differences in body shape include a larger caudal region in predator-present environments but has not specifically focused on the caudal fin. This project focused on the dorsal, caudal, and gonopodium of the western mosquitofish in environments with predators present and absent, to see if there is a significant difference in the size of these fins between the two predator regimes. This study noted that there is a significant difference between the gonopodium sizes, with fish from predator free environments having significantly larger gonopodia. In addition, this study found that there were not significant size differences between the caudal fin, and dorsal fin from mosquitofish from predator present and predator absent environments.

Section: Community Ecology
Room: Presidential Dining Room

10:27 AM –Variability in ecological attributes of abundant species and phylogenetic distance increases with taxonomic diversity: insights for assembly mechanisms of Neotropical bat communities

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Understanding the mechanisms shaping species composition of assemblages is critical for incorporating ecological and evolutionary perspectives into biodiversity conservation. To increase our understanding of processes that shape species identity within ecological communities, we quantified the relative support of community assembly mechanisms by assessing how species richness relates to functional and phylogenetic biodiversity of Neotropical bat assemblages. We assessed the association of functional diversity (divergence, dispersion, uniqueness, and evenness) with functional categories (body size, jaw, diet, foraging, and overall) and phylogenetic diversity with species richness for 20 assemblages. Furthermore, we contrasted functional and phylogenetic diversity against null models to remove any confounding effect of species richness on the diversity of each site. Functional divergence of the jaw, skull, and body size and overall increased with species richness, indicating that the variability in ecological attributes among abundant bats increases as the assemblages contain more species. Taxa were more distantly related as richness increases, but distances among closely related species remain constant. Despite variability spanning from trait segregation to aggregation, we found a consistent tendency to a cluster of functional traits, particularly in abundant species. The positive correlation between functional diversity with species richness results from a progressive ecological differentiation between the most abundant species. It suggests that decreasing overlapping in feeding preferences between abundant species could reduce competition inside assemblages and promote coexistence with rare species in assemblages.

10:39 AM –A Quantitative Dietary Analysis of the White-Tailed Hawk at Mustang Island State Park

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The White-Tailed Hawk (*Geranoaetus albicaudatus*) is a common raptor in Latin America and the southern tip of the USA. Only one of the three subspecies, *G. a. hypospodius*, resides in the northernmost extent of its range in coastal TX. The White-Tailed Hawk is one of North America's least-known birds of prey, and their life history and population demographics have received little empirical attention. The northern distribution of White-Tailed Hawks in America historically was described as including the American Southwest. Lack of fire on the landscape at the end of the 19th century is thought to have resulted in a range contraction due to woody encroachment. While there is insufficient data and a lack of reliable estimates for the White-Tailed Hawk, current beliefs are that population numbers are stable or increasing in south Texas. More research is needed as breeding and nesting habits remain obscure. Previous studies indicate that the White-Tailed Hawk is sensitive to nesting disturbance and will quickly flee when approached. This discussion will cover an introduction to an ongoing study researching the nesting ecology of the White-Tailed Hawk during the breeding season in south Texas using nest cameras, and the results of a quantitative dietary analysis at Mustang Island State Park during the 2021 breeding season will also be presented.

Section: Community Ecology
Room: APCC 1011C

10:51 AM – Vegetation Selection and Activity Patterns of Bats in the Texas Coastal Bend

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Bats have a greater diversity of behavior and diet than any other mammalian order. Therefore, understanding activity patterns and vegetation selection of these bats is imperative in the success of maintaining bat populations in south Texas. The emergence of *Pseudogymnoascus destructans*, a cold-adapted fungus and the causative agent of white-nose syndrome (WNS), has also led to steep declines in some North American bat populations. In more recent studies, conducted on the San Antonio Viejo Ranch belonging to the East Foundation, activity patterns for four summer resident bats was conducted - Eastern Red Bat (*Lasirius borealis*), Cave Myotis (*Myotis velifer*), Evening Bat (*Nycticeius humeralis*), and Brazilian Free-tailed Bat (*Tadarida brasiliensis*). These results showed peak nightly activity hours for these bats. For all species included in the study, total bat activity peaked at 02:00, with a secondary peak occurring between 05:00 and 06:00. It is crucial to determine how bats respond to changes in vegetation type and species composition given different land uses. From this, we can understand and provide a baseline for activity patterns and vegetation selection for these south Texas bats to prepare for future disturbances. This lack of information has led me to research effective management strategies needed to protect these vital species in a more comprehensive and cohesive manner than previously understood.

11:03 AM – No Differences in Body Size and Condition of Purple Martins (*Progne subis*) Along an Urban-Rural Gradient in Texas

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Purple Martins (*Progne subis*) are a New World insectivorous passerine species that are in decline across their entire range. The eastern subspecies is almost entirely dependent on human provided nest structures, which are increasingly being provided by “landlords” in urban settings. In response, Purple Martins have expanded their ranges into cities, yet little is known about the physiology of urban populations. Previous studies on avian body condition across urban-rural gradients have been conflicting, and almost always focus on granivorous species. In this study, I captured Purple Martins (n = 83) at 12 nesting sites across central Texas. For each bird, I measured mass, muscle and fat score, skull length, wing chord, and tail length. I used these measures to calculate a Scaled Mass Index for each individual, as well as calculating an Urban Land Use Index for each nesting site. I used generalized linear modeling to test the relationship between Urban Land Use Index and Scaled Mass Index, mass, muscle score, fat score, and skull length within sex. I found no significant difference in any measure of body size and condition across an urban-rural gradient, suggesting that urban and rural habitats may provide equal resource opportunities for breeding Purple Martins. These data provide evidence that conservation opportunities for Purple Martins exist within urban habitats, with little physiological impact on individuals.

Section: Behavioral Ecology
Room: APCC 1011BC

10:15 AM – Gut microbiome diversity associated with exploratory behavior in a wild-caught songbird

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The gut microbiome plays an important role in host physiology with effects ranging from immune system development to nutrient utilization. However, our understanding of gut microbiome assembly in wild species is still poor. Many of the microorganisms that colonize the gut originate in the environment and the host organism's behavior dictates which microbes they will encounter. We hypothesized that wild birds that are more exploratory will have more diverse gut microbiomes due to their exposure to diverse environments. To test this prediction, we captured wild house sparrows (Passer domesticus) and collected fecal samples to measure the diversity and composition of the gut microbiome. We then introduced each individual to a novel environment and measured their activity levels and the number of objects in the environment they interacted with. We found that alpha diversity of the gut microbiome positively correlated with the number of objects the birds interacted with independent of activity levels. These results suggest that more exploratory birds encounter more types of environmental microbes that contribute to their gut flora. Alternatively, increased diversity of the gut microbiome may contribute to increased exploratory behavior. Experimental testing will be required to determine the directionality of this relationship.

10:27 AM –Guadalupe Bass (*Micropterus treculii*) Movement is Predictable: Implications for Conservation

Jacob Wolff[1], Lindsey C. Elkins, Joshuah S. Perkin, Jessica E. Pease, Timothy B. Grabowski, Preston T. Bean, Nathan G. Smith
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Fish movement and dispersal are critical for individual survival, metapopulation regulation, and community dynamics. Movement of stream fishes was initially regarded as fundamentally restricted, with most individuals remaining within 50 m of the stream during their lifetime. Later movement studies revealed two components to populations: a more abundant stationary component (stationary fish) and a less abundant mobile component (mobile fish) with little indication of individuals changing their behavioral strategy. This 'restricted movement paradigm' (RMP) has experienced considerable refinement since its initial inception, but its basic principles have not been tested in Guadalupe Bass (*Micropterus treculii*). We assembled Guadalupe Bass radio telemetry data from the Pedernales, South Llano, and Colorado rivers in Texas to test the RMP. We developed models for movement expected under the RMP using fish size, caudal fin aspect ratio, stream size, and time since tagging within the R Statistical Package 'fishmove', and then compared these expectations with observed field data. Results revealed a consistent pattern of leptokurtosis, i.e., a distribution of movement distances characterized by a high peak representing stationary fish and long tails representing mobile fish. We also found RMP-modelled predictions frequently matched field observations for the mobile component in the South Llano River (67% of observations), Pedernales River (83%), and Colorado River (100%); as well as the stationary component in the South Llano River (56%), Pedernales River (78%), and Colorado River (78%). We plan to use the information from this model to inform habitat connectivity prioritization schemes to benefit conservation and management of Guadalupe bass.

Section: Behavioral Ecology
Room: APCC Presidential Dining Room

10:39 AM –The evolution of female ornamentation in polygynous mating systems through selection for increased survival

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Conspicuous traits used in intersexual interactions ("ornaments") are widely hypothesized to evolve through competition for mates (sexual selection). However, ornaments are often exhibited by females living in polygynous mating systems where male mates are plentiful. Recent theory also suggests that competition for high-quality males that increase female reproduction alone has weak effects on female ornament evolution. We hypothesize that, rather than evolving through competition for high-quality mates that increase reproduction directly, female ornaments may evolve through competition for socially mediated resources that enhance female survival. Using a population genetic "proof-of-concept" model, we consider two scenarios: (i) female ornaments produce non-random associations with males that provide resources to all their female associates (the "constitutive benefit" model) and (ii) female ornaments modify interactions with males to obtain resources that otherwise would not be provided (the "facultative benefit" model). We show that either mechanism can—in principle—lead to the evolution of female ornaments, but they differ in the necessary conditions. In particular, costs of ornamentation much more strongly limit ornament evolution in the constitutive benefit model because unornamented females also obtain resources from males, albeit less frequently. In both models, the ornament can precipitate its own extinction following an initial spread due to effects on the coevolution of male resource provisioning, though the underlying mechanisms differ. We propose that female ornamentation is most likely to evolve through competition for survival-increasing resources if costs of ornamentation are small and there is substantial non-heritable variation among males in the resources they provide.

ORAL PRESENTATION ABSTRACTS

Session 3, Friday, April 8th, 11:30 - 12:18 pm

Section: Ecology of Biological Invasions
Room: APCC 1011B

11:30 AM – Do native (*Cyprinodon rubrofluviatilis* and *Fundulus zebrinus*) and invasive (*C. variegatus* and *F. grandis*) cyprinodontids partition their niche? Morphological, dietary, and isotopic evidence for trophic segregation from a large river in Texas

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Biological invasions have occurred worldwide with significant ecological, evolutionary, and economic impacts on recipient ecosystems. We used an integrative approach based on morphological traits, stomach contents, and stable isotope ratios (δ13C and δ15N) to examine multiple dimensions of the niche of native Texas Cyprinodontids (*Cyprinodon rubrofluviatilis* and *Fundulus zebrinus*) and their invasive congeners (*C. variegates* and *F. grandis*). We analyzed specimens collected during multiple surveys in the Brazos River and Red River basins. Because of their phylogenetic relatedness, we predicted high overlap in the feeding habits and habitat use between native and invasive congeners. A principal component analysis performed on 24 morphological traits associated with habitat use and feeding ecology suggested some overlap in morphological space occupied by the two *Cyprinodon* species, but no overlap between the two Fundulus species. High overlap on dietary and isotopic niche space was observed between the two *Cyprinodon* and two *Fundulus* species. Values of δ13C and δ15N ratios revealed that the native and invasive *Cyprinodon* species occupied virtually identical isotopic niches, while *Fundulus* showed only slight differences. While species differed in their morphological niche space, similarities in the feeding ecology between Cyprinodontid congeners could lead to negative ecological interactions such as competition for food resources. Understanding how invasive species compete with native species could be a useful method to help predict and potentially mitigate their impacts in the future.

11:42 AM – Importance of anthropogenic determinants of *Tubastraea coccinea* invasion in the northern Gulf of Mexico

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Tubastraea coccinea is an invasive coral that has had ecological, economic, and social impacts in the Atlantic Ocean, the Caribbean, and the Gulf of Mexico (GoM). *Tubastraea coccinea* is considered a major threat to marine biodiversity whose occurrence in its non-native range is mainly associated with artificial structures such as oil/gas platforms and shipwrecks. A recent species distribution model identified important determinants of *T. coccinea* invasion in the northern GoM and projected its potential range expansion. However, the potential effects of anthropogenic factors were not considered. We used boosted regression trees to investigate the importance of oil/gas platforms and shipping fairways as determinants of *T. coccinea* invasion in the northern GoM. Our results indicated that maximum salinity, distance to platform, minimum nitrate, and mean pH were the first to fourth most influential variables, contributing 31.9%, 23.5%, 22.8%, and 21.8%, respectively. These findings highlight the importance of considering the effects of anthropogenic factors, such as oil/gas platforms, as potential determinants of range expansion by invasive corals. Our results provide new insights into how oil/gas platforms and artificial reefs, such as Rigs-to-Reefs, program might be managed to mitigate colonization by invasive corals.

Section: Ecology of Biological Invasions
Room: APCC 1011B

11:54 AM – Plants on the move: The current trend and future risk of Japanese honeysuckle invasion in southern United States

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The invasion of non-native species contributes to the modification of biogeochemical cycles, inhibition of natural regeneration of native species, and the loss of ecosystem biodiversity and productivity. The Japanese honeysuckle (*Lonicera japonica*) is a vigorous invader of the southern United States. Hence, our objective is to understand how JH invasion status has changed, identify what variables are determinants of invasion, and how climate will affect its future distribution. To accomplish this, we analyzed the two most recent sets of U.S. Forest Service field measurements of Japanese honeysuckle in the south U.S. and compared our results with existing models, which were based on less-recent data. Our results indicate Japanese honeysuckle increased by approximately 53% in the number of plots invaded. Distance to the nearest known propagule source ranged from 12 km to 125 km with a mean (+SE) of 8.08 km (+ 6.11 km). From cycle one to cycle two, Japanese honeysuckle appears to increase in coverage in Kentucky, Tennessee, South Carolina, Arkansas, and Louisiana. In Oklahoma, Japanese honeysuckle does not seem to increase in coverage, but does increase in westward spread. Our model provided important insights into the management of Japanese honeysuckle, which threatens southern U.S. forests. Armed with knowledge of current and potential future high-risk areas, forest managers can develop long-term monitoring and control strategies for effectively slowing range expansion and mitigating its effects.

Section: Ecology of Plants and Ecosystems
Room: APCC 1011C

11:30 AM – A global analysis of mosses reveals low phylogenetic endemism and highlights the importance of long-distance dispersal

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Digitization of herbarium specimens and DNA sequencing efforts in the past decade have enabled integrative analyses of patterns of diversity and endemism in a phylogenetic context. Here, we compare the best available floristic databases to a comprehensive specimen database to examine spatial patterns of moss phylogenetic assembly. We developed a phylogeny of 3654 moss species using 25 markers and compiled a global specimen database from online repositories. We calculated floristic and phylogenetic measures of diversity and endemism and performed randomizations to test for significant deviations from expectations. We use rarefaction and extrapolation to alleviate substantial differences in sampling effort across the globe. We used both phylogenetic and floristic methods to test for spatial regionalization. We compare our specimen-based results to those obtained using a floristic dataset. We found that phylogenetic diversity is more robust to missing data than species richness. Additionally, mean phylogenetic distance was significantly higher than expected in areas with high species richness, indicating that reported richness in these areas is likely a product of repeated colonization. We also found that phylogenetic endemism is low globally. Finally, phylogenetic regionalizations cluster into a Holarctic/Holantarctic temperate region, a pantropical region, and a region composed of Australia, New Zealand and South Africa. These results provide further evidence to support several important theories developed in moss biogeography, including the role of long-distance dispersal in shaping floristic patterns, the dominance of anagenesis in driving patterns of island diversity, and the role of climatic instability in driving patterns of assembly in the Holarctic.

Section: Ecology of Plants and Ecosystems
Room: APCC 1011C

11:42 AM – Taphonomic Bias and Palaeoecological Insights from Modern Mangrove Peats

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The presence of mangrove peat in the geologic record can be used to track and assess mangrove community dynamics, including detritivory, changing mangrove sub-environments, and the occurrence of catastrophic events, such as hurricanes. Characterization of modern mangrove peat provides insight into peat taphonomy, with implications for understanding ancient wetland paleoecology and nutrient cycling in coastal wetlands. Many researchers have analyzed particle size of modern mangrove peats to understand the peat to coal transition; we aim to understand the plant debris to peat transition because detritivory and other taphonomic processes are not new phenomena in coastal swamps. We collected mangrove peat cores (15 cm depth) from two sites at Barnes Sound, Key Largo, Florida: a basin site, which is generally flooded, has a thick leaf and a tidally influenced fringe site that has a sparse leaf mat. In this study, we use peat particle size as a proxy for rates of decomposition in wetlands, enabling comparisons between ancient and modern wetlands. The accumulation of thick leaf mats in basin mangrove sites where nearly continuous flooding excludes burrowing crabs and limits access of pulmonate snails to the leaf litter, could be the modern mangrove depositional environment most comparable to that of ancient peat.

11:54 AM – Ecosystem-level patterns in tidal wetland resistance and resilience

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Climate change and extreme disturbance events are increasingly altering the structure and carbon dynamics of ecosystems, including tidal wetlands. These ecosystems play disproportionately large roles in biogeochemical cycling relative to their small areas, yet we know little about how these processes are perturbed by disturbances at regional to continental scales, as potential macroecological patterns are difficult to detect by studying site-specific datasets or processes. Consequently, no firm rules have been found that govern ecosystem resistance and resilience to disturbances. Gross primary production (GPP) is a particularly well-suited metric for summarizing the heterogeneous dynamics that underlie ecosystem-level disturbance responses, and recently, a remote sensing-derived GPP dataset for all tidal wetlands in the conterminous United States was made available for the years 2000-2020, with data available at 16-day return intervals. To identify ecosystem-level patterns in tidal wetland resistance and resilience, we first established proxy metrics for resistance and resilience, effect size (E) and the return time (R) of GPP perturbation events, then cataloged the E and R of each GPP perturbation in the time series dataset. We found that the metrics E and R are correlated, and that there are consistent scaling relations between these events, i.e., smaller magnitude GPP perturbations occur more frequently than larger magnitude perturbations. We contend that our metric approach can be used in a wide range of applications across disciplines to quantify the resistance and resilience of perturbations in any time series dataset, which may yield new and important discoveries about universal tradeoffs between these two strategies.

Section: Ecology of Plants and Ecosystems
Room: APCC 1011C

12:06 PM – Soil carbon balance under different prescribed burning frequencies

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Prescribed burn is one of the prevailing forest management tools in the southern USA. Fires have the potential of both decreasing and increasing the amount of soil carbon (C), for example, through biomass and detritus combustion and stimulated productivity through increased nutrient and light availability, respectively. Although it is crucial to monitor belowground C dynamics to take advantage of burns, it remains challenging to quantify the changes in a large soil C pool primarily for its high spatial variability. This study investigated the effect on soil C balance under different prescribed burning frequencies in *Pinus taeda* dominated forests in central Texas, USA. The study site has three prescribed fire treatments that have been managed with prescribed burning annually, every 2-3 years, or left unburned for more than 20 years. Soil C balance was estimated with monthly measurements of heterotrophic soil CO2 efflux (Rh) output, and detritus inputs through litterfall and fine root mortality from October 2020 to September 2021. Results showed that litterfall detritus input and Rh output were the main components in the annual soil C balance. Stands managed with annual prescribed fire had higher annual Rh output than the other two stands with less frequent and no fires. Annual detritus inputs were not significantly different from prescribed fire treatments. Annual soil C balance is still uncertain, but there was a constant trend that greater burn frequency resulted in lower soil C gain per year.

Section: Genetics in Ecology
Room: Presidential Dining Room

11:30 AM – CaveCrawler: How Coding and Cavefish Can Help Us Understand Evolution and Human Disease

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Some diseases and evolutionary phenomena can only be studied in species which are not traditionally used for scientific research. Non-traditional model species, however, are often difficult to study due to the difficulty of accessing existing genetics data. Furthermore, even if a researcher has access to existing data, many researchers lack the computational expertise needed to draw meaningful conclusions from this data. Under the co-mentorship of Alex Keene and Heath Blackmon of Texas A&M University, I addressed the lack of analysis tools in non-traditional model organisms by creating CaveCrawler, a web-based genetics analysis tool and database which enables researchers across the world to investigate questions using the Mexican tetra, an increasingly popular model organism for studies of evolution and human disease. My mentors and I demonstrated CaveCrawler's ability to answer genetics questions by using this online software program to identify a gene which could potentially help us understand the evolution of sleep. Though the Mexican tetra is increasingly being used to tackle genetics questions, CaveCrawler's impact is not limited to this species; researchers studying other emerging model species can adapt CaveCrawler's freely available code to create their own web-based genetics analysis software.

Section: Genetics in Ecology
Room: Presidential Dining Room

11:42 AM – The evolution of four chromosomal inversions underlying ecological adaptation in Atlantic herring using long-read sequencing

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Chromosomal inversions suppress recombination and can be maintained for millions of years as balanced polymorphisms. But they are difficult to study due to complex genomic structure. We report a detailed characterization of four large inversions in the Atlantic herring genome, present on chromosomes 6, 12, 17, and 23, with corresponding sizes of 2.7, 7.8, 2.2, and 1.2 Mb, respectively, which show strong clinal gradients in their frequencies from the south to the north part of the Atlantic Ocean correlated with water temperature at spawning. We therefore named inversion haplotypes as 'S' (Southern) and 'N' (Northern). Atlantic herring is a pelagic fish and one of the most abundant vertebrates in the world, with an effective population size (Ne) over a billion. We used a pangenome and multi-genome alignment approach using PacBio HiFi and optical BioNano data from 12 individuals carrying S and N types and one outgroup species (European sprat) to accurately determine ancestral state, inversion breakpoints, and to study the structural variations surrounding breakpoints. We found extreme sequence variation and structural polymorphism near the breakpoints, mainly dominated by inverted duplications and complex repeats. To further study evolution of these inversions, we estimated dN/dS and diversity statistics (pi and dxy) using short-read data for 35 individuals, homozygotes for each S and N types. Established theories on inversions suggest that as inversion accumulates deleterious mutations over time, leading to high mutation load. Unexpectedly, none of the S or N homozygotes supported this theory, suggesting that purifying selection might be effective in removing deleterious mutations inside inversions. Moreover, nucleotide diversity values for S and N types were similar to each other and to the rest of the genome. This shows that these inversion polymorphisms have been maintained over a considerable time, hundreds of thousands of years, and that the large Ne of Atlantic herring allows efficient purifying selection of both alleles at each locus. Overall, studying large inversions in Atlantic herring has led us to gain novel insights into the evolution of inversions.

11:54 AM – Sequence and lineage characterization of major histocompatibility complex class I genes in Atlantic herring using a comparative genomics approach

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Major histocompatibility complex (MHC) genes are the most polymorphic genes in the vertebrate genome and are an integral part of the adaptive immune system. They are responsible for presenting antigenic peptides to T cells. MHC genes are classified into two major types, class I and class II. Class I genes present endogenous antigens to cytotoxic T cells that are present on the surface of all nucleated cells, while MHC class II genes present exogenous antigens to helper T cells that are present on antigen presenting cells. Class I genes in teleost fish are categorized into five lineages, U, Z, S, L, and P. In this study, we determined MHC class I genes, haplotypes, and lineages in Atlantic herring. Atlantic herring is one of the most abundant vertebrates in the world with an effective population size over one million and a census size of about a trillion individuals. Studying MHC genes in such a species will broaden our knowledge as regards nucleotide diversity of MHC genes in a large population where the effects of genetic drift are minimal. We obtained MHC class I gene sequences in Atlantic herring using ENSEMBL annotation of the reference genome and found 12 genes, distributed across chromosomes 4, 5, 7, 9, and 19. Sequence alignment showed that class I genes are highly polymorphic with respect to SNPs, indels, and CNVs. To categorize sequences into their respective lineages, we constructed a phylogenetic tree comprising class I sequences from Atlantic herring and from other fish species for which the lineages are already known. Once we obtain a better understanding of MHC class I in the Atlantic herring reference genome, we aim to expand our analysis to 24 more genomes constructed using PacBio HiFi data.

POSTER SESSION ABSTRACTS

Friday, April 8th, 3 - 5 pm

Posters

Poster #1
Characterizing flea community diversity on wildlife within Sam Houston National Forest

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Flea-borne diseases of humans in the US include plague, murine typhus, and cat-scratch disease, with transmission cycles involving fleas feeding on wild or domestic animals and occasionally humans. The vast majority of murine typhus cases in the US are reported from Texas, and the incidence is steadily increasing. Yet, flea community distributions are not widely described. Our objective was to determine the flea community in the piney woods of Sam Houston National Forest, which receives heavy human recreational activity. We hypothesize that surveillance of fleas from wildlife will detect human pathogens. During 10 monthly visits from summer-fall 2021, 67 successful trap events (38 mesomammals and 29 rodents) represented 51 unique animals. In total, 36 adult fleas were collected across trap events representing 13 individual opossums. The infestation prevalence of fleas per opossum trap event was 61.9%. The fleas on an individual opossum upon capture varied with a mean intensity of 1.7 fleas per opossum and ranged from 1 flea to 11 fleas. Fleas were identified into four genera: *Xenopsylla* sp.(63.89%), *Nosopsyllus* sp. (5.56%), *Ctenocephalides* sp. (13.89%) and *Polygenis* sp. (16.67%). Given at least two of these flea genera include competent vector species of the agents of murine typhus and plague, future testing of these fleas will allow us to determine infection status with zoonotic agents. This work addresses the risk of human exposure to zoonotic and vector-borne agents in a recreational area near the 3rd most populated county in the US

Poster #2
Elevation in relation to avian malaria in the Chihuahuan desert and Edwards Plateau

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Avian malaria is a disease caused by haemosporidian parasites in birds across the world. These parasites are transmitted via insect vectors, and can have significant long-term and short-term health impacts on infected birds. Although there are multiple factors influencing avian malarial prevalence, those associated with changes in temperature and its impact on insect vector abundance play a significant role in the frequency of infection. Elevation is one such factor that can influence avian malaria infection rates. High elevation and cool temperatures often prevent vector survival or completion of the parasite life cycle within the vector itself. Such high-elevation areas can serve as refugia, preventing infection in birds that nest there. Here we present preliminary results investigating the correlation between elevation and avian malaria infection prevalence in birds from the Chihuahuan Desert ecoregion of Texas and Mexico, and the Edwards Plateau ecoregion of Texas.

Poster #3
Prevalence of Avian Malaria in Armenia Birds of the Caucasus Mountains

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Haemosporidians are cosmopolitan parasites that transmit avian malaria to many species of birds. While Haemosporidian prevalence and diversity have been well documented across many regions, factors that influence said prevalence and diversity are not fully understood. Three genera, *Plasmodium*, *Haemoproteus*, and *Leucocytozoon*, are being investigated to determine the prevalence and diversity of each in avian species of the understudied Caucasus Mountains region of Armenia, and I am interested in how elevation impacts parasite distribution. Relationships between hosts and their parasites will also be noted to gain a more comprehensive understanding of haemosporidian diversity and host-parasite relationships in this region.

Poster #4
Repatriation of Illegally Collected Alligator Snapping Turtles Into Native Texas Waters

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The alligator snapping turtle (*Macrochelys temminckii*) is the largest freshwater turtle in North America. As such, *M. temminckii* are sought after for human consumption and may be vulnerable to overharvest or incidental bycatch. Despite having protection from harvest in Texas since the 1970s, *M. temminckii* are still harvested illegally for food and novelty products. In 2016, USFWS agents confiscated 30 alligator snapping turtles from Louisiana poachers who transported wild caught turtles from Texas. Then, in 2020, collaborative efforts between federal and state agencies led to the decision to repatriate these individuals back into native Texas waters. To determine the feasibility of repatriation efforts, we attached VHF radios to 23 *M. temminckii*, and performed weekly post-release telemetry checks to record data on movement and microhabitat selection. Movements recorded immediately post-release were high, averaging 751.84 meters per week. By late summer and fall, average movements decreased with the lowest average movements recorded during the fall (117.69 m). Consistent with similar studies of wild *M. temminckii*, repatriated individuals were regularly found utilizing large structures in low-flowing shallow water. Past studies of wild *M. temmickii* have suggested temperature as a strong driver of movement and microhabitat selection. We found support for this, as smaller movements of repatriated turtles corresponded with lower air temperatures. Additionally, we found that *M. temminckii* regularly chose microhabitats with warmer temperatures than random microhabitats. These findings have implications for the future conservation of the species by providing further insight into habitat preservation and *M. temminckii* behavior.

Poster #5
Multiple stable-isotope compositions of Rock Iguana (*Cyclura carinata*) scat distinguish anthropogenic impacts on diet and sedimentary biogeochemistry

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The range and abundance of the Turks and Caicos Rock Iguana (*Cyclura carinata*) have been greatly reduced by invasive species and land use changes. Other anthropogenic impacts, such as those on diet, have had little attention despite the species' role in local seed dispersion. To assess and distinguish between the effects of human impact and the environment on *C. carinata* diet, we measured the stable isotope distributions of nitrogen, carbon, and sulfur (d15N, d13C, and d34S values, respectively) in scat and leaf samples from two islands with varying human footprints. Our sites were Little Ambergris Cay, which has essentially no human impact, and Big Ambergris Cay, which has permanent settlements and frequent tourism. Despite morphological discrepancies between samples from each island, our results showed little evidence of direct human impact on diet. Differences between iguana scat d13C values were not significant between islands or between scat and nearby leaf samples for any of the isotopes on Big Ambergris. However, scat d15N and d34S values were both higher on Big Ambergris than on Little Ambergris because of environmental variability. Specifically, Little Ambergris groundwater is affected by expansive microbial mats with active microbial sulfate reduction which results in d15N values similar to those of atmospheric nitrogen and drives down d34S values in red mangrove (*Rhizophora mangle*) plant tissue and corresponding iguana scat. Our results highlight how different factors affect isotopic values of both food sources and resulting animal scat and showcase the utility of using stable isotopes for dietary analysis.

Poster #6
A novel field methodology to calibrate thermal dissipation sap flow sensors by characterizing radial sap flux profiles

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Thermal dissipation (TD) sap flow sensors are considered sensitive to systematic errors, leading to potential underestimation of transpiration. Common calibration approaches used to improve sensor accuracy are losing credibility, as recent studies discovered they may misrepresent actual conductive sapwood areas when using excised stems. In this study, we tested novel methods to improve measurement accuracy of TD sensors by characterizing the radial variation along different depths of the sapwood using *L. styraciflua* diffuse porous trees growing naturally in east Texas, USA. We hypothesized that radial profile shapes are systematically linked to deviations from the original empirical relationship. High-resolution radial increments of sap flux were captured using a modified "mobile" 10-mm TD sensor inserted at various 1-mm depth increments from the outermost 5-mm to as deep as 30-mm depths. A 10-mm "fixed" sensor was then installed in the same insertion site and centered at the maximum flow, as determined by the "mobile" sensor, to collect data continuously for a few days to use for measurement processing. A second "fixed" 20-mm heater and reference probe was also installed adjacently on the same tree at a depth of 0-20 mm to record continuous data throughout the experiment (n = 7 trees). Based on observed radial variation in sap flux, characteristic curves were constructed and applied to improve in situ estimates. This novel approach shows the potential for more accurate flow estimates using precision placement of TD sensors in a tree and accounting for radial profiles.

Poster #7
Generalist Pollinators and Pollinator Syndromes: A Case Study in North American Orchids

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Coevolution between orchids and specialist pollinators is well documented and thoroughly studied. Pollinator specificity has driven the evolution of an astonishing variety of floral structures, scents, and strategies. However, many orchids have generalist pollinator strategies, and the selective pressures imposed by their multifarious pollinator associations are not heavily studied. Recent work has shown that pollinator syndromes—sets of floral traits associated with a specific type of pollinator—don't always reliably predict plant-pollinator associations. Our study attempts to illuminate how pollinator trait compositions, rather than a single pollinator or pollinator type, drive floral trait variation across the North American orchid flora. We hypothesize that there is a strong relationship between pollinator trait compositions and floral trait variation, even among broad generalist species. With a nearly comprehensive list of all known native North American orchid pollinators, we classified trait space for both pollinators and orchids. Using PCA, we will generate trait values in ordinated space for pollinator characteristics. Then, for each orchid species, we will calculate the average value and construct a distance matrix that represents pollinator-trait association similarity among orchids. Then, we will construct a second distance matrix to describe differences in floral characteristics. Finally, using mantel tests, we will assess whether there is a significant correlation between floral trait similarity and pollinator trait similarity. In essence, this study provides a novel way to understand pollinator syndromes among generalist plant species.

Poster #8
Evolution of sexual systems in the moss family Orthotrichaceae

Hannah Mitchell[1], **Coralie Domergue**[1], **Sarah Song**[1], **Gabrielle Davis**[1], Daniel Spalink, Katie Sanbonmatsu
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Mosses are the second most diverse group of land plants, approaching 13,000 species. Despite their unique life histories and evolutionary trajectories, members of this group have received little scientific attention compared to their vascular counterparts. One such feature that merits further study is the diversity of sexual systems across mosses. A peculiar sexual state that is unique to mosses across land plants, called phyllodioicy, is characterized by dwarf males that grow epiphytically on larger female individuals. Here, we explore the dynamics of sexual state in mosses using the family Orthotrichaceae as a model system. Orthotrichaceae is a diverse, cosmopolitan family that is represented by nearly all sexual states found across mosses, but phylogenetic work in the group has been sparse. We aim to investigate the evolutionary relationships within Orthotrichaceae, determine the frequency of transitions between sexual states within the family, and reveal possible trends regarding the dynamics of sexual systems within bryophytes. Using sequence data from GenBank for nine markers across all three genomes, we developed the most up-to-date phylogeny for Orthotrichaceae using RAxML. Using stochastic character mapping, we inferred the average number of transitions across the phylogeny between three different sexual states: monoicous, dioicous, and phyllodioicous. We also inferred these states at each node in the phylogeny. We found rampant paraphyly in Macromitrium, with four distinct clades of *Macromitrium* spp. We also found that Macrocoma papillosa does not group with the rest of Macrocoma. Finally, we found that a dwarf male syndrome (phyllodioicy) always evolves from a dioicous sexual state. No transitions of monoicy to phyllodioicy were found. However, we did find at least two instances of a phyllodioicous state transitioning to a monoicous one. These results provide further evidence that sex in bryophytes is extremely labile and provide a framework for understanding the evolution of dwarf males in mosses.

Poster #9

The Correlation Between Direct and Indirect Defenses in Sorghum: Protection Against an Invasive Aphid Pest?

Emily Russavage, Jeremy A. Hewlett, Adrianna Szczepaniec, Anjel M. Helms, William L. Rooney, and Micky D. Eubanks
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Plants respond to herbivory using a variety of traits. Direct defenses are plant traits that directly affect pest behavior or physiology, whereas indirect defenses are plant traits that attract natural enemies to reduce herbivory. To exploit the full suite of plant defenses for pest management, we must understand the relationship between them, as direct and indirect defenses could be negatively correlated, positively correlated, or not correlated. The sorghum aphid (*Melanaphis sorghi* Theobald), formerly known as the sugarcane aphid (*Melanaphis sacchari* Zehntner), is a pest that causes substantial damage to sorghum. We collected HIPVs from 6 sorghum varieties, studied natural enemy attraction to aphid-infested plants in an olfactometer, and measured aphid population growth to test the hypothesis that direct and indirect defenses are positively correlated or independent of one another. We found that direct and indirect defenses are positively correlated or independent of one another. For example, ATx3409/RTx436 produced high levels of volatiles (i.e., high indirect defenses) and had low aphid population growth (i.e., high direct defenses). This work indicates that indirect defenses should be incorporated into sugarcane aphid IPM programs to increase the effectiveness of crop resistance and pest management.

Poster #10

The evolutionary-genomic history of genes underlying serpentine tolerance in *Caulanthus amplexicaulis var barbarae*

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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 building highly resolved gene phylogenies from both organellar and nuclear genomes. 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.

Poster #11
Using comparative genomics to understand serpentine tolerance in *Caulanthus amplexicaulis*

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Plants growing in serpentine soils are exposed to numerous stresses: low calcium-to-magnesium ratios, increased heavy metal presence, minimal nutrients, and low water retention. Exploring mechanisms influencing serpentine tolerance will advance resources for the development of efficient nutrient uptake in agriculture and phytoremediation. Serpentine endemic (*Caulanthus amplexicaulis var. barbarae*) and its granite-living sister (*Caulanthus amplexicaulis var. amplexicaulis*) were compared to reveal loci adapted to serpentine-stressed environments. Annotated genomes and a genetic map with dense marker profiles have been generated. Integration of multiple evidences: QTL, GO annotations and descriptions, dN/dS values, and cis-acting information have refined the search for serpentine tolerance loci.

Poster #12
Microplastics in a Post-Hurricane Peat Deposit, Long Key, Florida

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We investigated the occurrence and distribution of microplastics (63 - 500 μm) in a sediment core (30 cm depth) from a mangrove beach at Long Key, Florida. A thin bark layer occurred at 27.5 cm depth bounded by sand deposits (~5 cm thick), suggesting a hurricane deposit. Overlaying the hurricane deposit is a 25 cm thick peat deposit. We hypothesize that microplastics will be more abundant in the post-hurricane than the pre-hurricane sand deposit, and there will be no difference in microplastic abundance throughout the overlaying accumulated peat. Peat subsamples were targeted at six levels within the core. Subsamples from each level were wet sieved, dried at 50°C for 24 hours, and weighed. Subsamples were treated with 30% H_2O_2 and dried at 60°C for 12 hours to dissolve organic matter. Using a density separation technique, we suspended collected inorganic matter in 40 ppt NaCl solution for 10 minutes to isolate microplastics. After vacuum filtration, separated microplastics and sediments were dried at 60°C for three hours and weighed. We report the dry weight percentages of microplastics in the core. We found that the abundance of microplastics increased (1.6 to 12.5%) from pre- to post-hurricane deposit and remained abundant throughout the overlaying accumulated peat (~12.8%); however, there was a significant decrease of microplastic abundance in the surficial peat layer. These results support that extreme weather events deposit high amounts of microplastics into coastal environments. Of concern, microplastic contamination in accumulated peat could disrupt organism-peat interactions.

Poster #13

Aquatic macroinvertebrates as sentinels of changes in local stream conditions in East Texas

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Aquatic macroinvertebrates are excellent indicators for evaluating stream health because they respond rapidly to environmental changes and provide a short time history of their response to in-stream changes and pollution. We assessed in-stream conditions and macroinvertebrate communities at two sites in La Nana Creek, Nacogdoches County, Texas that vary in landscape use. Site 1, located upstream, was surrounded by agricultural fields and Site 2 was located in a more urbanized area, near downtown Nacogdoches. Aquatic macroinvertebrates were assessed using a variety of sampling techniques across three seasons (Spring, Summer, and Fall) to evaluate the conditions of the stream. Aquatic macroinvertebrates were classified to lowest taxonomic level possible but were grouped into families for assessment of pollution tolerance. Despite high degree of anthropogenic disturbance, Site 2 had a higher richness and a higher abundance of macroinvertebrates across all three seasons. On average, Site 1 had a higher diversity. Differences in macroinvertebrate communities between the two sites may reflect impacts from local land-use. Conditions at Site 2 may have provided a better habitat for the community of macroinvertebrates, regardless of seasonal changes. Perhaps Site 1, which is affected by agriculture, may promote diversity during certain seasons, while the more urbanized site may favor diversity during others. This may be due to different habitat requirements and species tolerance at different life history stages. Continuously assessing this system will provide a better understanding of changes in stream biota across seasons and sites, which can allow for formal management and conservation plans.

Poster #14

Multi-scale drivers of hypolimnetic oxygen depletion in six Minnesota lakes

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Understanding the relationship between eutrophication-driven oxygen depletion and long periods of hypoxia is important to fisheries managers. However, few studies focus on the potential impact of invasive species, like zebra mussels that can drastically alter productivity, on oxygen depletion rates in lakes. We examined the effects of zebra mussels on volumetric hypolimnetic oxygen depletion (VHOD, g O2 m-3 d-1), the rate of oxygen decline throughout the summer, using data from the Minnesota Sentinel Lakes long-term monitoring program. We examined VHOD trends in six lakes over an eleven-year period, 2008-2019. The lakes range in size, mean and maximum depth, and trophic status. Additionally, two lakes have populations of zebra mussels (*Dreissena polymorpha*), with invasions occurring eight years apart. Dissolved oxygen and temperature profiles were collected monthly during the open water season in all six lakes. VHOD was estimated using volume-weighted linear regressions of oxygen concentrations during the summer stratified period and corrected for temperature. In Lake Carlos, the lake with earlier zebra mussel invasion, VHOD decreased sharply (0.0847 to 0.0517 g m-3 d-1) four years after zebra mussels established Our data support the hypothesis that the invasion of dreissenid mussels may lead to a decrease in VHOD in deep stratified lakes. These results suggest that zebra mussels create an additional challenge for lake managers, balancing the mismatch between an increase in cold-water fish habitat at the cost of lost productivity.

Poster #15

Taxonomic and morphological diversity of fish assemblages in Big Cypress Creek, Texas

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We investigated the spatial variation of fish assemblages in lentic and lotic freshwater systems that were directly or indirectly connected to the Big Cypress Creek (BCC), which was considered the main river source. The BCC is located within the Cypress River Basin of Northeastern Texas. Surveyed sites were located within an area 'virtually' unimpacted by anthropogenic activities. Taxonomic diversity of fish assemblages was examined at six sites including streams, ponds and lakes, and morphological traits of fishes were measured to make inferences in the functional diversity of these assemblages. Fish were collected using different fishing gears. Overall, 36 species contained in 10 families were collected. The Prairie Creek (PC), the closest stream to the main BCC contained the greatest taxonomic richness (S = 28 species) and diversity (H' = 2.9), and species appeared more evenly distributed (E = 0.89) compared to other sites. The PC had ~ 80% of the total number of species collected across all sites. Morphological diversity was also greater at PC. Among the lentic systems, Brushy Lake had the highest richness (S =19 species). Streams directly connected to the BCC shared a high redundancy of species compared to ponds and lakes, which had indirect connectivity to the BBC. We reported 31 species already listed for the Big Cypress basin. In addition, we reported four species not previously listed, including *Lepomis humilis*, *Ictalurus furcatus*, *Esox niger* and *Etheostoma spectabile*. Our findings will be useful for management and conservation purposes of fish biodiversity in the Cypress River basin.

Poster #16

Compound-20 (Analago of Curcumin) Prevents Acrolein-Induced Changes in Rats

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Research has shown that acrolein, a known environmental pollutant, contributes to the generation of free radicals, leading to oxidative stress and physiological damage. Curcumin has been known to improve damages from oxidative stress due to its antioxidative and anti- inflammatory properties. It has been reported that to exert such an effect, a large dose of curcumin needs to be consumed on a daily basis due to its high excretion through the kidney. Here, in collaboration with Dr. Chelliah from the department of pharmaceuticals, an analog form of curcumin (compound-20) was synthesized with promising more potent activity and absorption. The objective of this study was to investigate if compound-20 could prevent acrolein induced oxidative stress in rats.This study was hypothesized that one of the curcumin analogs, which is referred as compound-20 here on, is effective in prevention/reversal of toxic damage caused by acrolein by improving antioxidant system, removing free radicals and ultimately, reducing the inflammation. Therefore, Male Sprague-Dawley rats weighing 250-350kg were divided into three groups: Control group (same amount of vehicle), acrolein group (2mg/kg/day, i.p 7days), and Group 3 includes rats treated with compound-20 (10mg/kg/day, 3days, gavage) before acrolein treatment of (2mg/kg/day, 4days i.p). At the end of the treatment, rats were sacrificed, and tissues and blood were harvested for further analysis. Results showed a decreased level of GST activity, Glutathione, and SOD activity, but increased lipid peroxidation, in the group treated with acrolein. Addition of compound-20 (C20) increased glutathione, GST, AND SOD activities, while lipid peroxidation was decreased.

Poster #17

Isotopic niche overlap between the invasive armored catfish and native fish species in the Usumacinta River, Guatemala

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Ecosystems engineers are among the most impactful invasive species because of their potential to cause ecosystem regime shifts and food web modifications. Armored catfishes have become highly invasive in tropical ecosystems around the world, including the Usumacinta River, where the invasion has expanded from southern Mexico to northern Guatemala. Here, we investigated the influence of the invasive armored catfish (*Pterygoplichthys* spp.) on the isotopic space of native fishes with similar trophic ecology (*Astyanax aeneus*, *Dorosoma petenense*, *Thorichthys passionis*, *Oscura heterospila*, and *Poecilia mexicana*) and subsequent isotopic space overlap. The study was conducted during the dry season within La Pasion River (invader is abundant) and San Pedro Rivers (invader is uncommon), two major tributaries of the Usumacinta. We surveyed 18 locations per river and analyzed the δ13C and δ15N composition of primary basal sources and fish muscle tissue. The isotopic space of armored catfish was significantly larger in La Pasion River, where it is more abundant. The opposite was observed for native fishes, with isotopic spaces larger in the San Pedro River, with the only exception being *P. mexicana*. Isotopic overlap between armored catfish and native fishes (except for *P. mexicana*) was high in the San Pedro River, where the invader is uncommon. Low isotopic overlap between the armored catfish and native fishes in La Pasion River, together with apparent shifts in isotopic spaces occupied by native fishes, suggests trophic niche compression in response to interspecific competition. Findings indicate that control measures may be required for the invasive armored catfish to maintain native fish stocks.