

11th TTABSS Presentation Abstracts

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β -lactamase genes in Enterobacteriaceae from the food animal and human surveillance programs in the United States

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KEYWORDS: Beta-lactamase genes; Enterobacteriaceae; blaCTX-M-65; food animal

The spread of beta-lactamase-producing Enterobacteriaceae is a major public health concern around the globe. The study aimed to identify and explore the distribution of beta-lactam resistance genes reported in three surveillance programs (cecal, retail meat, and human) in the United States. We retrieved and analyzed data from the United States National Antimicrobial Resistance Monitoring Systems. A total of 109 beta-lactamase genes were detected in Enterobacteriaceae; 3 genes in *E. coli* (blaCMY-2, blaTEM-1A, and blaTEM-1B), 6 genes in *Salmonella enterica* (blaCARB-2, blaCMY-2, blaCTXM-65, blaTEM-1A, blaTEM-1B, and blaHERA-3), and 2 genes in *Campylobacter* spp. (blaOXA-61 and blaOXA-449) have been detected across food animals (cattle, chicken, swine, and turkey) and humans over the study period. blaCTXM-55 has been detected in *E. coli* isolates from the four food animal sources while blaCTXM-15 and blaCTXM-27 found only in cattle and swine. In *Salmonella enterica*, blaCTXM-2, blaCTXM-9, blaCTXM-14, blaCTXM-15, blaCTXM-27, blaCTXM-55, and blaNDM-1 were uniquely detected in human isolates and blaSHV-12 in cattle, swine, and humans. blaOXAs were the only genes detected in *Campylobacter* spp. The proportions of beta-lactamase genes in *E. coli* includes: blaCTXM-1; 0.1-3.5% (2017-21), blaCTXM-15; 0.3% (2018), blaCTXM-55; 0.3-5.0% (2017-18), blaCTXM-27; 0.3-2.3% (2016-21), blaCMY-2; 0.21-12.4% (2016-21). The proportions in *Salmonella enterica* includes: blaCTXM-1; 0.01-1.9% (2013-21), blaCTXM-15; 0.05-0.91% (2015-21), blaCTXM-55; 0.03-6.3% (2013-21), blaCTXM-65; 0.4-14.7% (2013-21), blaCMY-2; 0.7-57.1% (2004-21), blaSHV-2; 0.7-5.3% (2011-18), blaSHV-12; 0.07-1.96% (2014-21), and blaNDM-1; 33.3% (2011). While the proportion of blaOXA-61 in *Campylobacter* spp. ranges from 7.2-96.3% (2013-21). This study provided information on the beta-lactamase genes detected in Enterobacteriaceae in food animals and humans in the United States. This information is necessary for a better understanding of the epidemiology of these genes in the USA and globally.

Is it something in the water: Ecomorphological variation of the Twin-striped Clubtail dragonfly (*Hylogomphus geminatus*) as a function of stream metrics

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KEYWORDS: ecology; entomology; dragonfly; freshwater; ecomorphology

Identifying environmental factors influencing ecomorphologically variable taxa (such as ectotherms like insects) is crucial in understanding effects of landscape disturbance. Moreover, identifying taxa that can serve as indicators of environmental quality (as a function of disturbance) is equally as important. One such species is *Hylogomphus geminatus* (Insecta: Odonata, dragonflies and damselflies), an amphibious predator. Odonates should be environmental indicators, sensitive to terrestrial and aquatic environmental aberrations. With relatively short generation times, their ecomorphology may signal recent changes to environmental variables and landscape conditions. Abiotic stream variables known to influence insect morphology include temperature, turbidity, and dissolved oxygen, while some biotic variables like prey availability have direct relationships with size. Although those variables have known relationships with insect morphology, odonate ecomorphology is poorly understood, limiting their potential as indicators. Case in point: the original taxonomic description of *H. geminatus* noted size differences from populations on either side of the Apalachicola River in Florida but did not suggest any mechanisms for these differences. Measurements taken from preserved specimens support this observation. This region is experiencing anthropogenic activities (urbanization, deforestation) and natural disturbances (intense weather events) that affect water chemistry and flow, but we have yet to understand their influence on ecomorphological variation in *H. geminatus*. Because size in odonates is negatively associated with water temperature and turbidity and positively associated with prey availability, I hypothesize that there will be colder, clearer streams with higher prey availability east of the Apalachicola River, resulting in larger *H. geminatus* nymphs and adults. Other detected differences will reveal landscape or anthropogenic variables for which *H. geminatus* may serve as an indicator species.

Meta-lay beliefs in undergraduate STEM milieu: How do students perceive their instructors' beliefs?

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KEYWORDS: Mindset; higher education; instruction; beliefs

Previous literature has demonstrated that the beliefs instructors espouse about their students' intelligence and ability (lay beliefs) can greatly affect their students' college experiences and equity outcomes. The aim of this qualitative exploratory study is to investigate how undergraduate STEM students form perceptions of their instructors' lay beliefs about their students' intelligence and ability. Recent work has begun to refer to these perceptions as "meta-lay beliefs". Specifically, three lay beliefs will be inspected: mindset (the malleability of intelligence), universality (What portion of individuals may succeed?), and brilliance (Is innate talent required for success?) beliefs. Investigators conducted 24 cognitive interviews with a diverse group of students from four American universities. Currently, these interview transcripts are being qualitatively analyzed to identify overarching themes, or "codes" relating to the following two research questions: 1) What are the messages that are being communicated and used by students to infer their instructors' lay theories? and 2) How are these messages being communicated? Our emerging results indicate that various messages about lay beliefs are being conveyed from instructors to their students, including what the instructor attributes students' outcomes to (e.g., students' innate capabilities, work ethic), how the instructor defines success, and what traits they believe predict success. Furthermore, these belief cues are communicated in a range of ways, such as instructional activities, instructor tone, and assessment questions. This work bears importance because it can help improve instructors' cognizance of what impressions their behaviors leave on students and provide STEM instructors with evidence-based recommendations for how they can communicate positive belief messages to their students. Furthermore, this study may eventually inform interventions about meta-lay beliefs aimed towards STEM instructors. The broader impact of such interventions may be that they can help reduce, or even eliminate, gender and racial achievement gaps stemming from students' perceptions of instructors' beliefs.

Does sex chromosome evolution recapitulate phylogeny?

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Dwarf willows, which occur at high elevation and latitudes, are placed on subgenera *Chamaetia* based on their morphology. However, this group is polyphyletic, and the dwarf phenotype has evolved at least four times independently. The location of sex-determination genes has not been mapped in dwarf willow species. I am focusing on two sister dwarf willow species *Salix reticulata* and *S. nivalis* and a third, distantly related dwarf willow *S. phlebophylla*. I am using this system to investigate the patterns of sex chromosome evolution with regard to shared sex-associated SNPs and genes. We sampled 24 males and 24 females for each species and sequenced a reduced representation libraries of exon anchored loci throughout the genome. Paired-end reads were mapped to the *S. purpurea* reference genome (with only chr15W) for all three species. The genomic regions statistically associated with sex were identified by conducting a genome-wide association study (GWAS) and heterozygosity was calculated for each sex to identify ZW or XY systems. For *Salix nivalis*, 15 SNPs located between 3-7.5Mb on chromosome 15 showed associations with sex in a GWAS analysis. For *S. reticulata*, 441 SNPs located between 2.9-8.6Mb on chromosome 15 showed association with sex. And, for *S. phlebophylla*, 38 SNPs located between 2.9-8Mb on chromosome 15 showed association with sex. For all three species, mean heterozygosity was more in female indicating that all three species are female heterogametic. Because *S. nivalis* and *S. reticulata* are closely related, we expected these two species to share more sex-associated SNPs and genes with one another than either of them share with *S. phlebophylla*, however, we did not find that pattern. We suggest that various factors may generate these patterns including a recent and strong bottleneck in *S. nivalis*.

Nymphal habitat selection in the Calvert's Emerald, *Somatochlora calverti* (Odonata: Corduliidae), and its associated odonate assemblage

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KEYWORDS: Dragonfly nymphs; habitat analysis; nymphal ecology

Despite their relative absence in conservation management, adult odonates are well-documented in the U.S. Nymphs, however, are understudied despite being more affected by anthropogenic land-cover changes; consequently, there have been few systematic evaluations of nymph-habitat relationships, especially for sensitive taxa. My research is working to obtain data on habitat use, both abiotic/biotic components, for the nymphal stage of the odonate assemblages that includes a sensitive species, *Somatochlora calverti*, to better inform conservation decisions and the species' scarce literature. Endemic to the north Florida region, the ecology of *S. calverti* is poorly understood, hindering management efforts. *S. calverti* was considered for the Endangered Species List in 2010; listing was warranted but never granted due to data-deficiency, which hindered assignment of definitive status. All field observations have been of adults; nymph habitat is speculated to be seepage streams but is undocumented, which is problematic for conservation. Therefore, my research objective is to address these deficiencies by documenting the nymphal habitat of *S. calverti*. Streams of known past occupancy based on vetted *S. calverti* records from citizen-science databases will be sampled via kick-netting to dislodge nymphs from substrate. Nymphs will be preserved in 70% ethanol for microscopic identification. Physicochemical variables will be recorded as factors that are known to affect nymph development and survival in other species. To assess landscape-scaled habitat, occurrence points for *S. calverti* and its assemblage will be mapped and compared to random locations. Landscape characteristics will be quantified at each site, and ordination will be performed to determine multi-scale habitat associations influencing odonate occurrence. Though collection of *S. calverti* is unlikely, my study will provide the first empirical investigation into *S. calverti* nymphal ecology, which is imperative for listing efforts and adding to the species' sparse literature for future researchers.

Climate Variability in the Gulf of Mexico revealed by a 250-year *Siderastrea siderea* coral Sr/Ca-SST reconstruction

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KEYWORDS: Coral; geochemistry; paleoclimate

The Gulf of Mexico (GOM) is a climatically complex system with sensitivities varying spatially and seasonally to remote forcings such as Atlantic Multidecadal Variability (AMV) and Pacific Decadal Variability (PDV). However, the short length of instrumental records hinders our ability to investigate if these multidecadal signals are persistent through time. Thus, reconstructing past sea surface temperature (SST) in the GOM is critical to understanding past, present, and future climate variability in this region. Strontium to calcium ratios (Sr/Ca) in long-lived massive corals, provide robust SST reconstructions, yet few records exist in the Gulf, and none to date in the northern Gulf. Here, we examine an monthly-resolved *S. siderea* Sr/Ca-SST record for Flower Garden Banks (FGB; 27° 52.5'N, 93° 49'W) from 1755–2005. Coral Sr/Ca-SST during the 20th century display PDO like variability in addition to an increasing SST trend of 1.25 °C with winters exhibiting more warming than summers. Further, the interval from 1750–1800 during the Little Ice Age is cooler than 1880–2005 with the coldest temperatures occurring between 1810–1840. This cool interval is consistent with global cooling due to massive explosive volcanic eruptions cool global temperatures but also aligns with the tree ring AMV signal from Gray et al. (2004). Temperatures during this interval are cooler in the Northern Gulf compared to the southeastern Gulf (Dry Tortugas). These temperature difference might suggest the northward extent of the major current in the GOM, the Loop Current, is reduced during this time. Further, a high-resolution foraminifera Mg/Ca-SST record from the northern GOM and annual speleothem $\delta^{18}\text{O}$ record from western Florida show similar decadal variability to FGB, but it is difficult to determine whether it is AMV or PDV. To discern the drivers of variability in the GOM is necessary to extend this record further back in time.

Exploring the relationship between plant defense strategies, white-tailed deer preference, and flammability in native shrub species in Texas

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KEYWORDS: Plant Flammability; Plant defense; Palatability; Herbivores

Grazing and fire have a long history in Texas. Fire and herbivores can both increase plant flammability and alter the composition of biomes. Flammability and the extent of herbivores' ingestion are influenced by plant functional traits. A plant can defend itself from herbivores' that browse by using physical defense, chemical defense, or a combination of the two and can persist in fire-prone ecosystem through their different life history strategies. In light of the recent advancement in our understanding of the trade-off among different types of plant defense against herbivores and the relationship between plant flammability and palatability, I tested the difference in flammability between armed and unarmed species as well as two groups of shrubs based on white-tailed deer preference to answer two questions: 1) Does least preferred shrubs for white-tailed deer are more flammable than moderate to low preferred shrubs? 2) Do armed plants have lower flammability than unarmed plants? I found that the least preferred shrubs are more flammable than moderate to low preferred shrubs. However, I haven't found any significant difference in flammability between unarmed and armed species. This study might help to improve the understanding of the trade-off between the physical and chemical defense of plants against mammalian herbivores and the unified framework for fire and herbivores' effects on plant life history.

Zebra Mussel Invasion: Identifying Sites Critical to the Spread and Establishment of an Aquatic Invasive Species

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KEYWORDS: Zebra Mussels; Invasive Species; Habitat Suitability; Graph Theory

One of today's greatest conservation challenges is the proliferation of invasive species. A particularly ecologically and economically damaging invasive species is the zebra mussel (*Dreissena polymorpha*). Zebra mussels are already present within parts of Texas and if current trends persist, this invasion front may reach New Mexico. Our study aims to use network analysis and habitat suitability indices, to identify the sites most critical to the spread and establishment of zebra mussels in Texas and New Mexico's water bodies. Network analysis was used to estimate landscape connectivity and how the spatial arrangement of water bodies may facilitate the spread and introduction of zebra mussels to new habitats. We created a network consisting of water body nodes and connecting roadway edges, using a maximum edge length of 363 KM based on Texas boater movement surveys. Using graph analysis, we identified water bodies critical to the spread of zebra mussels in all three networks by acting as hubs, stepping stones, or cut points. However, due to high connectivity throughout the network, no cut points were identified. Habitat suitability indices were created to identify the water bodies most conducive to zebra mussel establishment. We then compiled a list of sites that were found at least twice among the top 10% of most suitable habitats, hubs, and stepping stones. These 21 sites represent the sites most critical to zebra mussel establishment and spread. By identifying these critical sites, we can help resource managers guide the allocation of limited time and resources for early detection and outreach campaigns.

Antibiotic Resistant 'Superbugs' in the Mississippi Gulf Coast

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KEYWORDS: AMR; antibiotic resistance; antimicrobial resistance; multidrug resistance; MDR; Mississippi Gulf Coast; *E. coli*; *Enterococcus*

Background: Microbial contamination and spread of antimicrobial resistance and multidrug resistance in various environments, particularly in water sources, is a global emerging public health concern. The Mississippi Gulf Coast serves as a very important resource for several recreational, public use, travel, and economic purposes. Therefore, it is important to monitor, understand, and mitigate the occurrence and distribution of pathogens and drug resistance, as collecting such data will help improve the state's environmental and public health control measures and serve as an important resource for keeping our coast clean and sustainable.

Methods: In this study, we collected and analyzed surface ocean water samples from ten sites across the Mississippi Gulf Coast over a period of 10 months for the following specific aims:

- 1) Enumerate pathogenic bacteria using the EPA methods 1603 (*E. coli*) and 1600 (*Enterococcus*)
- 2) Identify the patterns of drug-resistance with Kirby-Bauer disc diffusion method

Results: Data collected over ten months from February 2020-July 2021 suggest the prevalence of highly concerning levels of indicator bacteria (*E. coli* and *Enterococcus*) in Mississippi coastal waters. For *E. coli* contamination, 9 out of 10 sites fell beyond the water quality standards set by EPA for recreational waters (126 *E. coli*/ 100 mL). Similarly, we detected high amounts of *Enterococcus* contamination, with 7 out of 10 sites falling beyond the standards set by the EPA (35 cfu/100 mL). For *E. coli* strains, there was high resistance to erythromycin (94.9%), and cephalothin (82.2%). *Enterococcus* strains exhibited alarming resistance to ciprofloxacin (75.9%), and erythromycin (75%). Moreover, many of the isolates were positive for a concerningly high amount of multidrug resistance on almost all sites across all sampling events.

Future Directions:

- Quantitative PCR analysis of antibiotic resistance genes.
- Source tracking to determine sources of contamination and antibiotic resistance.

deAMPLifying the Immune Response? Antimicrobial Peptides Evolution in Chiroptera

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KEYWORDS: innate immunity; defensins; bioinformatics pipelines; gene annotation; non-model organisms

High viral tolerance coupled with an extraordinary immune response makes bats a good model to study host-pathogen evolution. Although many immune-related gene gains and losses have been previously reported in bat genomes, important gene families such as antimicrobial peptides (AMPs) that trigger innate immunity upon invasion by extraneous agents remain understudied. We analyzed the gene family evolution of some AMPs in Chiroptera to determine how they are phylogenetically distributed and evaluated the effectiveness of bioinformatics pipelines designed to annotate genome assemblies. To construct a bat-specific AMPs dataset, we manually curated amino acid sequences of the major AMPs families, including defensins and cathelicidins, from Boreoeutherian and Laurasiatherian species obtained from the ENSEMBL and NCBI databases. The curated sequences were then used in a homology search in 20 high-quality bat genome assemblies using orthofisher. The resulting dataset was subjected to a prediction analysis with ampir to ensure the accurate identification of the peptides for downstream analyses. Gene annotation was furtherly achieved with MAKER2 using multiple sources of evidence. Several AMP families were recovered, including two defensins subfamilies: α and β -defensins. While α -defensins appear to have been lost in 3 species, β -defensins were more diverse and found in multiple copies among all the species. Likewise, cathelicidins were retrieved in all but two species. Characterizing the multigene family evolution of specific AMPs is crucial since their up and downregulation has been associated with positive or negative outcomes in the host caused by differential regulation of inflammasome pathways. The results of this study highlight the importance of building species-specific libraries for genome annotation in non-model organisms. Furthermore, our results attempt to provide a robust framework for a more comprehensive understanding of pathogen tolerance in bats.

Atropine alters prey-capture and predator avoidance behaviors in African clawed frogs (*Xenopus laevis*)

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KEYWORDS: prey-capture, trade-offs, *Xenopus*, muscarine

Animals must make life-or-death decisions to maintain energy balance while avoiding predation. Choosing to either escape from a detected threat or to stay and forage is one such decision. To investigate the role of baseline cholinergic signaling through muscarinic receptors in modulating these trade-off decisions, we quantified juvenile *Xenopus laevis* quantified behavior and food intake in a foraging-predator tradeoff task (modified after Duggan et al., 2016) after an injection of the muscarinic receptor blocker atropine (50 mg/kg). We hypothesized that atropine would modulate signaling through muscarinic receptors involved in the behavioral decision making made when presented with opposing appetitive and avoidance provoking stimuli. Contrary to our prediction, we found that prey-capture behaviors were significantly reduced in atropine-injected frogs compared to saline-injected frogs. Atropine-injected frogs performed fewer forearm sweeps, spent less time exploring edges, and spent less time in contact with prey. However, other behaviors like locomotion and latency to contact prey did not significantly differ in atropine-injected frogs. Our findings suggest atropine does not reduce predator-avoidance behaviors during this trade-off task, but instead could suppress prey-capture behavior.

Tempo and mode of diversification of the spiny/bristly mice, genus *Neacomys* (Cricetidae: Sigmodontinae)

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KEYWORDS: South America; biogeography; ancestral area; dispersion; Sigmodontinae.

Genus *Neacomys* (Cricetidae: Sigmodontinae) represents a diverse radiation that successfully colonized most of the biomes in South America. The accelerated rate of species description in the last decade, with the concomitant generation of genetic information and postulation of phylogenetic hypotheses have resulted in an increased knowledge on the taxonomy and systematics of the group. However, other aspects, such as its evolutionary history, remain unclear. Here, I used different analyses on the most inclusive Cytochrome-b dataset for the genus (20 out of 23 species) as a proxy to assess its tempo and mode of diversification. My results place the origin of *Neacomys* in the late Miocene (9.34 Mya) and suggest its most recent common ancestor (MRCA) occupied the lowlands of the Boreal Brazilian Dominion. Apparently, climate change and landscape dynamics in that epoch promoted deep divergence between five major clades. Subsequent dispersion and vicariance events allowed the colonization and diversification in emerging habitats, thus resulting in the current widely distributed species assembly. This new hypothesis contrasts with previous works in which the origin of the genus was dated in the Pliocene, and by the first time gives an idea of the biogeographical context during the evolution of almost all the recognized species.

Anatomical evidence supporting an interaction between GABAergic and CRF-producing neurons in the subcortical visual system.

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KEYWORDS: GABA; CRF; subcortical visual system; *Xenopus laevis*

Fear and anxiety result in the expression of a range of defensive behaviors, which are aimed at escaping from the source of danger or motivational conflict. An important brain area for coordinating the behavioral response to visual threats is the superior colliculus of the brain, an area involved in subconscious visual detection and response. Previous work in our lab showed that optic tectum (OT), the homolog of superior colliculus in non-mammalian vertebrates, contributes to decision making on predator avoidance/prey capture tradeoffs. The neuropeptide CRF modulates discrete aspects of prey capture and predator avoidance, but the mechanisms underlying this modulation are unknown. We used dual-labeling immunofluorescence and laser confocal microscopy to study the relationship between CRF and GABA producing neurons in the optic tectum of the South African clawed frog, *Xenopus laevis*. We found that (1) GABAergic interneurons sent projections CRF+ neuron, (2) some CRF+/GABA+ neurons showing a pattern that CRF was partially colocalized with and sometimes surrounded by GABA, (3) GABAergic neurons all expressed calbindin and parvalbumin. This research provides neuroanatomical evidence for a potential GABA regulation on CRF signaling pathway.

Resource-use strategies and stress tolerance in invasive and native species in semi-arid conditions

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AFFILIATION(S): (1) Texas Tech University

KEYWORDS: Competition; gas exchange; invaders; VPD; water acquisition

Evidence from many sources shows that the number of invasive species in arid and semi-arid conditions is rising. This rise is correlated with management practices that favor the spread of invaders. However, the physiological basis for this dynamic, especially under stress, is not clear. To understand which traits allow invasive species to survive in arid lands, several physiological mechanisms will be accessed, trying to comprehend the degree of similarity and dissonance of these responses in comparison with the native species and which of these traits have an adaptive value under stress. For such, native and exotic species will be grown in a greenhouse in different soil and atmospheric water conditions in a full factorial design. We seek to evaluate whether the classical stress-coping mechanisms are present in invaders, as also other competitive and acquisitive resource responses. We will measure gas exchange responses to changes in vapor pressure deficit (VPD), hydraulic properties, expression of osmoprotective and regulatory compounds, as well as changes in plant growth and allocation patterns. These will be used to help explain how the sum of these responses translates into a competitive advantage in face of a stressor factor. We believe that the invaders pursue different strategies of acquisition and use of resources in comparison with the native species. Specifically, we hypothesize that invasive species display a high capacity of adjustments of their gas exchanges in face of severe water restriction, a higher sensitivity to VPD changes, and accumulation of osmoprotective and regulatory compounds that allow extraction and water savings under stress (i.e., they are drought avoiders). We expect this to come at a benefit under low and moderate stress, but come at a significant carbon uptake cost under a combination of high soil and atmospheric water stress. In the end, we hope to gather a set of responses that will be able to explain the underlying mechanisms and stress-coping strategies used by the invaders.

Recombination rate and gene density are correlated with clines of diversity and patterns of differentiation in the Grace's Warbler (*Setophaga graciae*)

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KEYWORDS: clines; genetic diversity; differentiation; natural selection

Understanding the drivers of spatial patterns of genetic diversity and population differentiation is crucial to understanding how biodiversity originates and is maintained. Spatial patterns of genetic diversity and population differentiation are the result of extrinsic and intrinsic factors to which organisms are subject. Extrinsic factors include population genetic factors like gene flow, natural selection, and genetic drift. Intrinsic factors are inherent to genomes and include properties like recombination rate, mutation rate, chromosome size, and the density of gene content. To evaluate how these intrinsic and extrinsic factors interact to produce empirical patterns of genetic diversity and differentiation we leverage a whole-genome population re-sequencing dataset of 53 individuals of the Grace's Warbler (*Setophaga graciae*). The Grace's Warbler has a latitudinally broad distribution, extending from southern Nevada to northern Nicaragua. Specifically, we explored how latitudinal clines of diversity manifest in this species – across genomic, chromosomal, and sub-chromosomal scales. In addition, we explored heterogeneity in patterns of differentiation across the genome. Lastly, we evaluated how the strength and direction of these clines and patterns of differentiation are influenced by gene content and recombination rate. Leveraging the fact that recombination rate and gene density can both serve as proxies for the diversity-reducing effects of natural selection, we show that clines of genetic diversity that match the genome-wide pattern are more likely to be found in regions of the genome that are subject to high recombination and/or have lower gene content. This suggests that clines matching the genome-wide pattern are more likely to reflect 'neutral' processes, such as differences in population demography across individuals and populations. We find a negative correlation between recombination rate and F_{ST} and a positive correlation between recombination rate and d_{XY} , suggesting that differentiation between populations in this species is in part mediated by selective forces.

Can Illicit Drugs be Detected in Apex Predators? *Alligator mississippiensis* as a Case Study for Methamphetamine Contamination in Various Tissue Types.

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KEYWORDS: alligators; contaminants; narcotics

The Gulf of Mexico is a vast area that includes many different habitats such as mangroves, estuaries, and swamp lands. This area includes both highly urbanized areas and more remote areas. Many studies of environmental contaminants cover substances such as pesticides, pharmaceuticals, and personal care products. However, in more recent years a new class of contaminant is starting to surface: illicit drugs. This study focuses on the detection of such contaminants, specifically amphetamine, MDA, MDEA, MDMA, and methamphetamine, in the keystone species *Alligator mississippiensis* collected from the Houston, TX area and the Rockefeller Wildlife Refuge in Grand Chenier, LA. *A. mississippiensis* are of particular interest as they are not only apex predators, but they are considered environmental indicators as well as trophic regulators. Given that this species is a highly opportunistic predator, it is suggested that there may be a potential of this chemical transferred to this apex predators through environmental exposure and/or trophic transfer through contaminated prey items. This study utilizes tissues adipose, liver, and scutes collected from alligators in the Houston, TX area and the Rockefeller Wildlife Refuge in Grand Chenier, LA. Tissues were homogenized and processed using QuEChERS salt extraction methods. Chemical analysis using liquid chromatography mass spectrometry (LC MS) indicate that amphetamine was found in alligator adipose, liver and scute tissue at both locations in the range of 0.17 ppb. This study will highlight the use of various tissue samples to determine the narcotic concentrations in an apex species along with the deposition and endpoint for such substances within an organism.

Reconstructing the phylogeny of an understudied wood-warbler genus (*Leiothlypis*)

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KEYWORDS: birds; whole-genome resequencing; warblers; genomics; speciation; DNA; phylogenetics

For organisms that rarely appear in the fossil record, sequencing DNA from living species serves as one of the most powerful tools for peering into the past and understanding their evolutionary relationships. Wood-warblers (Aves: Parulidae) represent an exceptionally diverse, colorful, and relatively young clade of birds that evolved in Central America and comprise many familiar migratory species that pass through Texas. However, for six warbler species in the genus *Leiothlypis*, these evolutionary relationships remain poorly understood due to a lack of comprehensive genetic information. Here, I am using whole-genome resequencing to reveal evolutionary processes among these six species and piece together their histories in the contexts of phylogenetic relationships, demographic changes over time, and patterns of genome-wide differentiation. Thus far, I have selected 4-5 samples for each species, sequenced their DNA on an Illumina NovaSeq 6000, and assembled their genomes. In the coming weeks, I will build phylogenies for all six species, determine how and where their genomes differ from each other, and test whether their relationships are obscured by deep coalescence and past gene flow. Based on trends observed in other wood-warblers, I expect to find strong evidence of these species hybridizing in the past and find the greatest differentiation between species on sex chromosomes and other regions of low recombination. By assessing these patterns, I will then set the stage for determining A) when speciation occurred among *Leiothlypis*, B) whether each species responded differently to past climate change, and C) whether the presence of structural variants in warbler genomes are tied to demographic parameters or other aspects of their evolutionary histories.

Symbiosis in the Time of Drought: Can Arbuscular Mycorrhizae increase Industrial Hemp (*Cannabis indica*) in the southern High Plains?

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KEYWORDS: Hemp; Arbuscular Mycorrhizae; Sustainable Agriculture; Drought; Southern High Plains

The Southern High Plains (SHP) of Texas suffered a devastating drought in 2022 that wiped out nearly 60% of irrigated cotton production, with over 70% of dryland cotton farms left fallow. To address the persistent drought conditions and soil quality issues in the region, researchers are exploring alternative crops and sustainable farming methods. Industrial hemp (*Cannabis indica*) is a promising candidate with some varieties known for innate drought and parasite resistance. This study examines four industrial hemp varieties (Puma, American Victory 1, Lucky7, and Joker) grown in 20 soil samples from two distinct hemp-producing fields managed using different soil management systems (traditional tillage and no-till) in the SHP. The study aims to determine which hemp varieties are most promising for cultivation in the SHP and how arbuscular mycorrhizal (AM) fungi, which colonize plant roots and exchange carbon for nitrogen and other nutrients, interact with the hemp plants. The study's hypothesis is that plants with high AM colonization will show significantly more biomass compared with plants with little to no colonization. One hundred and forty-three *C. indica* plants were grown for three months in the greenhouse prior to harvesting and determination of arbuscular mycorrhizal colonization levels. Preliminary results show significant differences in mycorrhizal colonization levels among varieties tested and between soil management practices. In addition, germination rates among varieties in response to soil management also differed. Further analysis will shed more light on the impact of soil quality, varietal differences, and AM interactions, with the goal of identifying strategies for improving soil health and crop yields in the SHP for hemp production.

Discovery of a novel *Wolbachia* strain associated with sugarbeet nematode suggestive of ancestral symbiosis

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Bioinformatic sequence data mining can yield unexpected, hidden microbial symbionts that might normally be filtered and removed as contaminants. This study focuses on the recovery of a complete symbiont genome from a published animal genome assembly. Specifically, this discovery was made during a broad investigation of *Wolbachia*, which is a widespread bacterial endosymbiont of insects capable of causing host reproductive manipulations by inducing parthenogenesis, male-killing, feminization, or, most commonly, cytoplasmic incompatibility. We investigated *Wolbachia* in plant-parasitic nematodes (PPNs), where their distribution remains underexplored. To date, *Wolbachia* has only been reported in *Radopholus similis*, *Radopholus arabocoffeae*, *Pratylenchus penetrans*, and a fourth nematode. The goal of this study was to more broadly sample PPN *Wolbachia* strains to enable further comparative genomic analyses that may reveal *Wolbachia*'s role and identify targets for biocontrol. Nematode-infecting *Wolbachia* may have been widespread early in the evolutionary history of the phylum, based on evidence of horizontal gene transfers. We assessed field-sampled nematode communities to search for this endosymbiont across tylenchid nematodes using genome sequencing, assembly, and phylogenetic analysis and showed some sequences were similar to gene regions in a published *Heterodera schachtii* (sugarbeet nematode) draft genome. Detailed analyses, comparing read coverage, GC content, pseudogenes, and phylogenomic patterns, clearly demonstrated that the *H. schachtii* sequence was not only a novel *Wolbachia*-like sequence, but in fact, a complete, circular genome. Among two published whole genome shotgun assemblies for *H. schachtii*, one from the Netherlands and one from Germany, only the Netherlands assembly included the novel *Wolbachia*. We speculate that the German *H. schachtii* assembly may have removed bacteria during bioinformatic steps that removed bacterial contamination. Other available *Heterodera* species were also analyzed for presence of *Wolbachia*. Future analyses will focus comparative pathways analysis between PPN *Wolbachia* strains and further sampling and microscopic localization of new *Wolbachia* in sugarbeet nematode populations.

The Effects of White Adipocytes in Breast Cancer Metastasis

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KEYWORDS: Obesity; Adipocytokines; Fatty Acids; Metastasis; Focal Adhesion Kinase; Breast Cancer

White adipocyte tissue (WAT), present in the breast tissue microenvironment, is an active endocrine organ, secreting adipocytokines. Obesity-associated perturbations in the normal secretion of adipocytokines from white adipocytes can drive cancer progression and metastasis, especially since WAT is also present in the breast tumor microenvironment. However, the underlying mechanism of activating the cell signaling pathways toward metastasis in response to those dysregulated adipocytokines remains unknown. Focal adhesion kinase (FAK) is a non-receptor cytoplasmic protein, that acts as a signal transducer between the receptor activation by adipocytokines and the downstream effector proteins that control the biological phenomenon of metastasis. However, the association between obesity-induced changes in secretory factors of white adipocytes and subsequent transactivation of the downstream effector protein impacting metastasis via FAK phosphorylation is unknown. To illuminate this potential relationship, MCF7 (Er+) and (MDA-MB-231(triple negative) breast cancer cells with low and high metastatic potential, respectively, were exposed to in vitro murine adipocyte-derived, conditioned medium. For the in vitro adipocyte model, 3T3-L1 MBX cells were used. Cells were differentiated to obesity, with fatty acid supplementation. The study shows that 3T3-L1 MBX cells, differentiated in the presence of fatty acid supplementation, were found to have significant changes in their adipokine secretions in comparison to controls. Furthermore, the conditioned medium derived from these obese 3T3-L1 MBX cells has been found to enhance the metastatic potential of breast cancer cells by increasing their migration and invasion. To further elucidate the possible activation of cell signaling pathway, the study has found that breast cancer cells increased FAK autophosphorylation followed by increased molecular expression of beta-catenin and MMP9 when exposed to either in vitro obese adipocyte conditioned medium in comparison to the untreated breast cancer cells.

Wolbachia-infected pharaoh ant colonies have higher egg production, metabolic rate, and worker survival

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KEYWORDS: Life history; trade-offs; endosymbiont; eusocial insects

Wolbachia is a widespread endosymbiotic bacteria with diverse phenotypic effects on its insect hosts, ranging from parasitic to mutualistic. *Wolbachia* also commonly infects social insects, where it faces unique challenges associated with its hosts' caste-based reproductive division of labor and colony living. Here we dissect the benefits and costs of *Wolbachia* infection on life-history traits of the invasive pharaoh ant, *Monomorium pharaonis*. Pharaoh ants are relatively short-lived and show natural variation in *Wolbachia* infection between colonies, thereby making them an ideal model system for this study. We quantified effects on the lifespan of queen and worker castes, the egg-laying rate of queens across queen lifespan, and the metabolic rates of whole colonies and colony members. Newly-infected queens laid more eggs than uninfected queens but had similar metabolic rates and lifespans. Surprisingly, infected workers outlived uninfected workers. At the colony level, infected colonies were more productive due to increased queen egg-laying rates and worker longevity, and infected colonies had higher metabolic rates during peak colony productivity. While some effects of infection, such as elevated colony-level metabolic rates may be detrimental in more stressful natural conditions, we did not find any costs of infection under relatively benign laboratory conditions. Overall, our study emphasizes the beneficial effects of *Wolbachia* on colony-level growth and metabolism in this species.

Meta-analysis of warming effects on soil microbial community composition and activity.

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KEYWORDS: soil warming; soil microorganisms; microbial community composition; microbial activity; soil respiration; enzyme activity; meta-analysis

Soil temperature affects the abundance and activity of microbes in the soil. Several soil warming experiments conducted over the past decade have reported change in soil microbial abundance and their functional role in the soil. However, the observed changes were not consistent across studies. We performed a meta-analysis with a dataset compiled from 62 published warming studies to examine how soil physicochemical characteristics, climate, ecosystem type, and experimental techniques influence the warming effects on soil microbial community composition and activity. We found that warming effects on total soil microbial biomass are mainly influenced by magnitude and duration of warming. The total duration of warming, warming technique used, and ecosystem type were the major predictors of bacterial abundance, while fungal abundance only affected by warming magnitude. Moreover, gram-positive bacteria were found to be more tolerant to temperature change than gram-negative bacteria; warming effects on gram-positive bacteria were only influenced by ecosystem type, but warming duration, magnitude, warming technique, and ecosystem all influenced warming effects on gram-negative bacteria. Similarly, warming effects on soil respiration varied with warming magnitude and technique. Major hydrolase enzymes seemed to be sensitive to soil pH, aridity, and ecosystem types, whereas the activity of oxidase enzymes changed with warming magnitude and technique. In conclusion, the meta-analysis showed that warming effects on microbial abundance and activity greatly vary depending on the experimental factors, ecosystem, and soil characteristics.

Optimizing Insect Metabarcoding for Studies of Insectivorous Mammal Diets

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KEYWORDS: Metabarcoding, sequence database, COI, insect diversity, sample coverage

Metabarcoding is widely used for molecular identification of organisms. For example, due to its efficiency and specificity characterizing bulk samples, the technique has been applied to bulk insect biodiversity surveys and dietary analysis. The mitochondrial Cytochrome oxidase I (COI) gene is the most widely gene used for metabarcoding in insect-related research, and although it has been used for nearly two decades, the reference databases that are used for taxonomic assignment and methods for survey still need improvement. The goal of this study was to establish best practice for molecular characterization of insect light trap collections that will be used to study ecosystem health and forest interior insectivorous bat niche. We sampled insect diversity using light traps in Tengku Hasanal Wildlife Reserve in Pahang, Malaysia. Each light trap sample was homogenized and repeatedly subsampled to identify the optimum number of subsamples required to detect total sample diversity. COI insect diversity from 72 subsamples (12 subsamples from each of six light trap collections) was characterized using an Illumina MiSeq. The minimum number of subsamples required to be sequenced to achieve at least 90 percent insect diversity coverage for each light trap was determined. Also, Malaysian and an expanded Southeast Asian regional insect databases were built from the Barcode-of-Life sequence repository and compared for performance at different taxonomic ranks. The results of these efforts will provide measures of insect prey spatiotemporal diversity upon which our subsequent research on bat dietary niche space will be framed.

Microbiome-Transcriptome-Wide Association Study (mbTWAS) of Chronic Wounds

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KEYWORDS: chronic wound, transcriptomics, mbTWAS, host-microbe interaction

Our understanding about the reasons for inter-patient variation in the species infecting chronic wounds remains poorly understood. Results from the only chronic wound microbiome genome wide association study (mbGWAS; Tipton et al. 2020) to date suggest that human genetic variation may partially explain differences in infection and may have to do with how our genetic variation encodes variation in wound bed cellular phenotypes. Because the wound bed is comprised of multiple cell and tissue types, an improved understanding of the relationship between people's DNA and microbial infection may be gained by measuring how patient genetic variation determines tissue-specific expression which in turn influences infection. Microbiome transcriptome wide association studies (mbTWAS) can leverage patient genomic variation to predict tissue-specific gene expression which is then linearly associated with microbial infection characteristics. Significant and repeatable associations indicate genes whose expression in specific tissues may be consequential to infection and may inform mechanistic hypotheses. Moreover, a better understanding of the link between patient genetics and infection could lead to preventative approaches. In this study, which is in collaboration with the Southwest Regional Wound Care Center (Lubbock, TX), consenting patients provide buccal swabs and wound debridement samples. Using the buccal swabs individuals are genotyped at around six hundred thousand loci, and microbial infection profiles are assessed using 16S sequencing. Gene expression imputation is accomplished using PrediXcan in conjunction with GTex v8-based prediction models. Estimated transcriptomes for skin, blood, subcutaneous adipose, and nerve tissue are being tested for effects on infecting species relative abundances. The outcomes of this study aim to advance our understanding of the effects of tissue-specific expression on microbial infection, provide insight into the mechanisms of the host-microbe interaction in human chronic wounds, and aid in the development and implementation of prophylactic treatments using polygenic risk scores.

Uncovering Diverse Functions of Endophytic Microbiomes in Wild and Cultivated Bananas Using Metatranscriptomics

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KEYWORDS: endophytic microbiome; gene expression; plant genotypes

Despite endophytic microorganisms playing a crucial part in promoting plant health, our knowledge of the mechanisms of protection across various plant species and genotypes is inadequate for developing microbiome-based disease control approaches. We hypothesized that wild (diploid) banana plants harbor more diverse disease-preventive microbial functions than cultivated (triploid) plants. We tested this using RNAseq on endophytic microbiomes extracted from four diploids (*Musa balbisiana*, Thai Black, *M. textilis* and *M. sikkimensis*) and three triploids (Dwarf Cavendish, Williams Hybrid, and FHIA-25) using a culture-free enrichment protocol for leaf and root tissues. Endophytic microbiome metatranscriptome diversity and function were analyzed with SAMSA2. Results showed major differences amongst plants and tissues in transcriptionally active bacteria and fungi, but little support for our hypothesis of host genotype role. Roots had different microbiome communities and functions compared to leaves. *Hymenobacter*, *Bacillus* and *Aspergillus* were most abundant in all samples while *Novosphingobium* and *Xanthomonas* were more abundant in roots and *Pseudarthrobacter* was more common in leaves. Functional comparisons showed high coproporphyrinogen III oxidase and MFS transporter expression across samples, whereas anti-sigma-E factor RseA and murein lipoprotein expression was highest in roots and hydrogenase accessory protein HypB and cation transporter expression was highest in leaves. Through hierarchical analysis, we have identified specific endophytes that facilitate nitrogen fixation, iron acquisition, sulfur metabolism, and methanol consumption, which may form key benefits for the hosts. Results also revealed that banana plants have an unexpectedly complex and diverse endophytic microbiome that shares certain components across various genotypes. Ongoing work involves comparing functional differences of specific microbes across and specific target disease-preventive functions across different banana genotypes.

Indian Flying Foxes' Role in Environmental Antimicrobial Resistance Propagation

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KEYWORDS: Antimicrobial Stewardship, Horizontal Gene Transfer, Megabats, One Health

Long-distance movement of Indian flying foxes to get food and shelter because of extreme temperatures may lead to the spread of antimicrobial resistant (AMR) bacteria. The dissemination of AMR bacteria and their associated antimicrobial resistant genes (ARGs) in the environment can cause serious public health implications. We hypothesized that spatiotemporal variation in Indian flying foxes' population density, their contact points and their immigration can cause AMR bacteria spillover to the environment. In this study, noninvasive fecal samples (n = 1150) of Indian flying foxes over a period of one year from seven different roosting sites were collected in Pakistan. The samples were analyzed for *E. coli* and its antimicrobial susceptibility using MacConkey agar and disc diffusion test. The samples were further analyzed to test the extended-spectrum β -lactamases (ESBL) producing potential of *E. coli* isolates using double disc diffusion and double disc synergism. Some highly consequential AMR in the summer samples were found against Aztreonam (5.7%) and Cefepime (3.5%), while in the winter samples, the resistance was observed against Aztreonam (16.9%), Azithromycin (22%), and Ampicillin (36.5%). Overall prevalence of Multi Drug Resistant *E. coli* was 46%. In total, 38% *E. coli* isolates were ESBL producers for both seasons. All of the ESBL *E. coli* isolates recovered from winter samples were harboring blaTEM while 16 % of them were harboring blaCTX-M gene. In contrast, none of ESBL *E. coli* isolate recovered from summer samples had blaCTX-M and 91% isolates were carrying blaTEM gene. This study also showed that Indian flying foxes are carriers of multidrug resistant *E. coli* (46%), therefore, may act as source of transmission to the environment and humans. Knowledge about the internal and external drivers of AMR propagation from fruit bats will provide foundation for environmental antimicrobial stewardship, as a One Health priority.

Targeting evolved antibiotic vulnerability in *Pseudomonas aeruginosa* through exploiting antibiotic trade-off

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KEYWORDS: antibiotic trade-off, *Pseudomonas aeruginosa*, combinatorial therapy

A random mutation in the bacterial genome can provide them a particular advantage at the cost of other disadvantages, and this potential trade-off can be seen between different traits or characteristics in bacteria. This type of cost and benefit can be seen with antibiotic sensitivity, where resistance to a particular antibiotic can make bacteria sensitive to other antibiotics, resulting from an evolutionary trade-off, also known as collateral sensitivity. To identify potential vulnerabilities in drug-resistant cystic fibrosis (CF) clinical isolate, we studied antibiotic susceptibility by disc diffusion method. Potential antibiotic resistance trade-offs were validated using experimentally evolved selective antibiotic-resistant cells. Our research identified an interesting antibiotic trade-off in CF isolate of *Pseudomonas aeruginosa* compared to lab strain counterpart. We found that, acquired resistance to gentamicin in the CF isolate makes them more susceptible to another antibiotic novobiocin compared to lab strain PA14. Other CF clinical isolates and experimentally evolved gentamicin-resistant strain of *P. aeruginosa* showed similar trade-off characteristic. In addition, our data showed that the emergence of gentamicin resistance can be restricted by treating the gentamicin-exposed cells with novobiocin. Considering these data, we aim to propose a combinational therapy to restrict the emergence of antibiotic resistance and infection re-emergence.

Using movement models to understand habitat selection and movement of Sonoran desert tortoises (*Gopherus morafkai*) in a rapidly changing landscape

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KEYWORDS: landscape ecology; movement ecology; landscape connectivity

Anthropogenic activities are degrading and fragmenting habitat in the Sonoran Desert, thereby reducing movement potential for the Sonoran desert tortoise (*Gopherus morafkai*) throughout its range. Barriers to movement among populations disrupt important natural processes like gene flow and demographic rescue, making barriers one of the greatest threats to long-term persistence of the species. In response to intensifying landcover alteration, preserving and restoring landscape connectivity has become a focus of conservation efforts for desert tortoises. However, identifying important areas for landscape connectivity for tortoises is dependent on our knowledge of the species' resource needs and movement patterns. Step selection analyses can elucidate why animals move from one place to another and how landscape characteristics and environmental conditions influence their movement behavior. To identify areas that facilitate or inhibit landscape connectivity between tortoise populations, we used step selection analyses to quantify tortoise habitat selection and predict tortoise movement through the landscape.

To document tortoise movements, we outfitted adult tortoises with GPS loggers recording positions at 30-minute intervals. We used hidden Markov models to characterize movements into two behavioral states: sedentary and moving. We fit step selection functions to the movement behavioral state to quantify how tortoises select habitat when traversing the landscape, and to examine how characteristics of the landscape influence their movement. Tortoises selected to move through moderately rugged slopes and vegetated areas near incised desert washes that offer them shelter, but selected against areas of high slope, extreme ruggedness, and dense vegetation. Tortoises also took longer, more directed movements through flat, open desert, and when crossing roads. Our results highlight characteristics of habitat that may be important for tortoise movement and identify a threshold where these characteristics transition from facilitating to inhibiting movement, which should be incorporated in designing effective corridors for the species.

Bat Meat: Preference or Necessity? The Role of Protein Limitation in Driving Bat-Hunting

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KEYWORDS: Bats; overhunting; structural equation modeling; subsistence hunting

Overhunting is one of the leading threats to biodiversity and has driven bat population declines in parts of Africa, Asia, and Oceania. Protein limitation leading to subsistence hunting is one proposed mechanism that drives people to hunt wild meat. This hypothesis posits that areas with decreased access to conventional protein sources, such as livestock and fish, will have the highest incidence of wild meat hunting. However, the role of protein limitation in driving bat hunting is unclear, especially at large spatial scales. Here we use Structural Equation Modeling (SEM) to test whether locations with decreased access to conventional protein sources will have a higher incidence of bat hunting. SEM was used to evaluate a model with over 500 hunting records from across bat-hunting hotspots in Africa, Asia, and Oceania. Locations were collected from scientific literature and social media. We modeled latent constructs hypothesized to drive protein limitation, including access to aquatic protein, access to terrestrial protein, and the ability to purchase protein. We used publicly available remotely sensed raster layers, such as marine trophic index, livestock density, and nighttime light, as indicators for our latent constructs. We found protein limitation has limited power to explain the drivers of bat hunting. Protein limitation and subsistence hunting are often assumed to drive wild meat hunting, yet our work shows this may not be true in many bat-hunting hotspots. Future work will explore the influences of bat ecology, cultural norms, and food insecurity on bat hunting.

Has the lack of fire encouraged shrub encroachment on the Edwards Plateau?

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KEYWORDS: Shrub encroachment; fire

Grasslands are important ecosystems worldwide threatened by the expansion of woody plants. Several environmental changes over the past century may have promoted shrub encroachment: the introduction of livestock and subsequent overgrazing, increased atmospheric carbon dioxide, and decreased fire frequency and intensity. In the grasslands of central Texas, native woody plants, especially *Juniperus ashei*, have increased in density over the past century. Such rapid expansion suggests that source populations may have already been present on the landscape. It is possible that decreased fire frequency, as a result of both livestock grazing reducing fuels and active fire suppression, created conditions necessary for fire-sensitive *Juniperus* to expand into previously frequently burned grasslands. Within a heterogeneous landscape, some regions such as steep slopes and rocky outcrops are relatively protected from fire. My study aims to test if the historical pattern of shrub encroachment is consistent with recent expansion from such fire refugia. Specifically, I will use dendrochronology to determine the age structure of *J. ashei* stands across multiple landscapes throughout central Texas. I will test for a pattern consistent with recent rapid shrub expansion centered on topographically-defined fire refugia which I will identify with fire-hazard mapping. I hypothesize that if *Juniperus* populations have spread from such fire refugia, I will find that older trees are found only in protected parts of the landscape and that maximum tree age declines with distance from putative fire refugia.

Pulmonary Smooth Muscle Cells as Cellular Sources of HIV in the Vasculature: Implications for HIV Reservoirs

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Human Immunodeficiency Virus (HIV) is a retrovirus that infects CD4⁺ cells. People living with HIV can now live longer due to AntiRetroviral Therapy (ART); however, ART does not cure HIV infection. The existence of HIV reservoirs challenges current efforts to eradicate HIV. HIV reservoirs are cells or anatomical sites that contain replication-competent virus. Over the years, the study of immune cells like lymphocytes and macrophages have dominated the field, as important sources of HIV under ART. However, theoretically, any CD4⁺ cell may act as an HIV reservoir. The expression of CD4 receptors has been confirmed in non-immune cells such as vascular Smooth Muscle Cells (vSMC). Previous studies by others have demonstrated that vSMC express the CD4 receptor as well as CCR5 and CXCR4, which allow HIV entry. Moreover, vSMC are associated with vascular pathologies associated with chronic HIV infection. Our hypothesis is that pulmonary vSMC may serve as an HIV reservoir under ART. To prove our hypothesis, pulmonary arterial SMC were purchased from Lonza and cultured in the presence of cell-free or cell-associated HIV reporter virus tagged to DsRed (pNL43-AD8). This allowed us to use red fluorescence as a marker of active viral replication. vSMC were exposed to HIV and treated with/without Tenofovir (~0.4 ug/mL) at different timepoints and analyzed by fluorescent microscopy. Treatments of vSMC with HIV and Tenofovir simultaneously showed no red fluorescence even after 72 hours. vSMC treated with HIV for 48 hours prior to treatment with Tenofovir showed red fluorescence at 48 hours and 72 hours. A potential implication of these findings is that vSMC could be acting as an HIV reservoir in the pulmonary vasculature under ART that may challenge the eradication of HIV infection. Future directions will confirm vSMC as a reservoir by additional methods and in the presence of ART.

Testing dynamic connectivity: Seasonal differences help determine connectivity for lesser prairie-chickens (*Tympanuchus pallidicinctus*) in New Mexico and Texas

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KEYWORDS: landscape change; connectivity; conservation; woody species encroachment; energy infrastructure

Land-cover conversion to agriculture, energy infrastructure development, and the encroachment of honey mesquite (*Prosopis glandulosa*) is fragmenting habitat for the endangered lesser prairie-chicken (*Tympanuchus pallidicinctus*) in the southernmost part of its range. As a result of these structural changes, connectivity between breeding areas (leks) has likely been greatly reduced, with implications on population size and gene flow. Lesser prairie-chickens exhibit avoidance/tolerance behaviors to physical landscape features as a response to potential predation risk. This response varies in strength through the breeding and non-breeding seasons: during the breeding season, they avoid tall vertical structures and vegetation with a density >10 per km², but during the non-breeding (dispersal) season, they do not exhibit such an avoidance. Because of these differences, we predicted that functional connectivity would vary between breeding and non-breeding seasons. Identifying portions of the landscape where functional connectivity is stably congruent across seasons would be useful in informing management decisions. We used habitat-occupancy data from 2019, known dispersal distances, and classified imagery from 2015 and 2022 to generate resistance surfaces for these times. We then used Circuitscape to map functional connectivity between leks during breeding and non-breeding seasons. Raster math was used to compare differences in corridor and pinchpoint (areas of channelized flow) current as well as to find areas of overlap between seasons. Preliminary results show an increase in connectivity between leks during the non-breeding season due to increased permeability associated with changes in habitat use. We also found a critical threshold in the combined effects of energy infrastructure development and honey mesquite encroachment on losses of connectivity in the southernmost portions of our study area. Despite finding greater potential connectivity during the non-breeding season, our results suggest managing for woody species encroachment may help preserve functional movement corridors among lesser prairie-chicken leks.

Optimal resource investment to photosynthetic capacity controls leaf and whole plant acclimation responses to CO₂

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KEYWORDS: photosynthesis, whole plant growth, nitrogen-water use tradeoffs, nitrogen acquisition strategy, global change

Plants acclimate to increasing CO₂ by reducing leaf nitrogen allocation and photosynthetic capacity at the leaf level, a response that often occurs alongside growth stimulation at the whole plant level. Nitrogen limitation has been hypothesized to be the primary mechanism driving leaf and whole plant acclimation responses to elevated CO₂. However, recent work indicates that these responses may instead be the result of optimal resource investment to photosynthetic capacity, which maximizes nitrogen allocation to whole plant growth. Acclimation responses to CO₂ may also vary in species with different nitrogen acquisition strategies, but few studies have examined responses of plant acclimation to CO₂ across soil nitrogen availability thresholds in individuals with different acquisition strategies. To test mechanisms driving leaf and whole plant acclimation responses to CO₂, we grew *Glycine max* L. (Merr) seedlings under two atmospheric CO₂ levels, with and without inoculation with *Bradyrhizobium japonicum*, and across nine nitrogen fertilization treatments in a full factorial growth chamber experiment. After seven weeks, *G. max* demonstrated strong reductions in leaf nitrogen, V_{cmax25}, and J_{max25} under elevated CO₂ independent of changes in fertilization or inoculation. Leaf acclimation responses to CO₂ corresponded with strong increases in total leaf area and total biomass, a pattern that was stronger with increasing fertilization, but was not modified by inoculation treatment. Whole plant acclimation responses to CO₂ were driven by reductions in the cost of acquiring nitrogen with increasing fertilization. Overall, results provide strong support suggesting that optimal resource investment is the primary mechanism governing *G. max* acclimation responses to CO₂. Results also indicate that fertilization played a relatively more important role in modifying whole plant responses to CO₂ than inoculation treatment, perhaps due to a reduction in nodulation across the fertilization gradient.

The small Rho GTPase Rac is essential for plasma membrane repair during Necrotizing Soft Tissue Infections

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KEYWORDS: rho GTPases; Rac; membrane repair; bacterial pore-forming toxins; Necrotizing soft tissue infections; Streptolysin O (SLO); Perfringolysin O (PFO)

Necrotizing soft tissue infections (NSTIs) exhibit a rapid disease progression characterized by substantial local tissue loss, which causes human morbidity and mortality rates of up to 40% despite optimal treatment. The causative agents of NSTIs are *Streptococcus pyogenes* and *Clostridium perfringens*. These bacteria produce the bacterial pore-forming toxins (PFTs), Streptolysin O (SLO) and Perfringolysin O (PFO), respectively, as virulence factors. Recent work in our lab found that the plasma membrane damage caused by these bacterial PFTs is repaired via Mixed-Lineage Kinase 3 (MLK3) and Mitogen-activated protein kinase kinase (MEK) signaling. However, the upstream mediator that activates MLK3-MEK membrane repair to these bacterial toxins remains unknown. Here, we tested the role of Rho-family small GTPases (cdc42, Rac, or Rho) as upstream mediators in membrane repair to these bacterial PFTs using selective GTPase inhibitors. Inhibition of cdc42 did not increase HeLa sensitivity to SLO or PFO while Rho inhibition had a minor impact on membrane repair to SLO but not PFO. Rac inhibition significantly increased sensitivity to both SLO and PFO. These findings were also confirmed via Western blotting because Rac inhibition blocked downstream activation of MEK. Rac-mediated membrane repair is also conserved in other cell types, such as HEK 293 and mouse fibroblast cells. Therefore, we conclude that Rac is an essential upstream activator of the MLK3-MEK membrane repair to bacterial PFTs (SLO and PFO). This pathway represents a potential therapeutic target to aid necrotizing soft tissue infections.

RAM Evaluation Using a *Carollia* Genome

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KEYWORDS: Transposable elements (TEs); *Carollia perspicillata*; RepeatModeler; RepeatAfterMe (RAM); manual curation; LINEs

Transposable elements (TEs) are repetitive and ubiquitous DNA sequences abundant in vertebrate genomes, sometimes occupying more than half of mammalian genomes. Their de novo identification has been enabled by RepeatModeler, one of the most common bioinformatics tools to produce libraries of TE families. However, RepeatModeler often needs to produce more accurate or complete consensus sequences, potentially falsely increasing the observed number of TE families and insertions and requiring extensive manual curation. This process takes some weeks for a de novo genome assembly, and longer for several. To overcome these issues, the software RepeatAfterMe (RAM) was designed. We use RAM to examine TE diversity in *Carollia perspicillata* in comparison to the previously described manual curation method. A total of 860 TE consensus sequences were obtained, of which 493 were considered “complete” (TEs with a clear random sequence in both flanks). The total proportion of TEs obtained in the *C. perspicillata* genome was approximately 30% of the genome, with a high proportion of LINEs. Unlike manual curation methods, the RAM analysis was completed in a few hours, compared to several days using manual curation. The resulting TE library was highly accurate, with minimal manual corrections required. Unlike other mammals, many chiropteran genomes contain recently active DNA transposons. The diversity of TEs found in this Phyllostomid species is lower in relation to TE diversity in Vespertilionid bats, showing a reduced TE accumulation in the recent past, similar to several other bats but distinct from vesper bats.

IMPACTS OF FOREST FRAGMENTATION ON PALEOTROPICAL INSECTIVOROUS BATS FUNCTIONAL DIVERSITY

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KEYWORDS: Conservation value, Ensemble, Functional diversity, Habitat fragmentation, Insectivorous bats

Habitat loss and fragmentation are the primary causes of biodiversity loss in the Anthropocene. It is well established that a negative relationship exists between taxonomic diversity and the disturbance of various taxa, including bats. However, understanding the complex mechanisms that contribute to species coexistence and maintenance in severely disturbed ecosystems remains limited. To fill this gap, we used bat species traits related to species clutter negotiating ability and resource acquisition to measure changes in the functional diversity of forest interior insectivorous bat ensemble in response to habitat fragmentation. The study was undertaken at Tengku Hasanal Wildlife Reserve and the forest fragments embedded within the surrounding landscape in Malaysia. We quantified the functional diversity of bat assemblages from six continuous forests, and 24 forest fragments that were categorized into large, medium, and small fragments. We found that functional richness was significantly different between continuous forests and forest fragments. We also found that the nearest neighbor distance between coexisting species in the functional space significantly differed between the continuous forest and the small fragment. We observed that the nearest neighbor distance of co-existing species in fragments is greater relative to continuous forests in response to fragment area, distance to the nearest continuous forests, and distance to the nearest forest fragments. Functional dispersion in fragments for forest specialists was also greater relative to continuous forests. Overall, we found that fragment area, distance to the nearest continuous forest, and forest fragments were poor predictors of functional diversity. Our findings suggest that forest fragments may have added value in maintaining functional diversity at the landscape scale, but large tracts of forest are important for maintaining forest interior insectivorous bat assemblages.

Genetic diversity and demography of highland birds in the Bale Mountains National Park, Ethiopia

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KEYWORDS: Birds; Genetic Diversity; Demography; Genomics; Africa; Biodiversity Hotspots

The Ethiopian Highlands are known for their complex topography that drove diversification in a variety of taxa. The exceptional species diversity of the region under significant anthropogenic threats qualified the highlands as a global target for conservation within the Eastern Afromontane Biodiversity Hotspot (EABH). Genetic diversity is a key constituent of biodiversity in these hotspots as it is the raw material for species to adapt to changing environments and serves to delineate population scale conservation targets. Unfortunately, the genetic diversity of the EABH is disproportionately underestimated relative to hotspots elsewhere. Here we characterize the genetic diversity of 17 birds in the Afromontane Forests of the Bale Mountains National Park using whole genome resequencing and explore how species traits, demography, and paleoclimatic factors shaped the birds' contemporary genetic diversity patterns.

Population structure of the giant otter (*Pteronura brasiliensis*) in Tauramena (Casanare, Colombia) and conservation challenges.

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KEYWORDS: Ecology; Orinoquia; Mammals; Bioindicators

Giant otter is one of the most endangered mammals in the Orinoquia, as its populations suffered a rapid reduction due to habitat loss and poaching pressure during the 1970's. They mainly inhabit large rivers, streams, lagoons, and wetlands, concentrating in specific habitats as a response to resource availability. Knowing the population status of this species is fundamental for the conservation of riparian ecosystems due to its role as a mesopredator. The otter is considered an umbrella and flagship species. Despite this, population trends in the Orinoquia are still unknown, with available fragmented information in Arauca and the Amazon region. The work sought to generate information on the population structure, distribution, and behavior of the species in Tauramena. Periodic monitoring was carried out for one year along the Tua sub-basin where the species was considered extinct. In total, approximately 250 km were covered, and 4 family groups were recorded. Of the total number of otters documented, 19 were identified, of which it is estimated that there may be 7 males and 11 females according to the behavior they exhibited during the sightings. Despite its strong presence in the area, the species is facing anthropogenic pressures related to deforestation, retaliatory hunting, and oil pollution. For effective management and conservation of the species, it is important to work with local communities and generate baseline ecological information.

Scale-dependent habitat selection by a habitat generalist bat in a mosaic landscape: a proposal

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KEYWORDS: Bats, Bangladesh; habitat selection; land-sharing conservation; *Lyroderma lyra*; radio tracking; resource selection function

A land-sharing conservation strategy is one that works to optimize the conservation value of human-modified landscapes and support those species that provide ecosystem services. As a result of the rapid expansion of the human population in Bangladesh, natural land covers have been converted to agricultural lands and left only 6% of the total land area unmodified. Optimizing and sustaining biodiversity through land-sharing needs to be central to Bangladesh's conservation strategies but has received little attention. Kalenga Wildlife Sanctuary (KWS) in Bangladesh is an example of a mosaic landscape comprised of natural and human-modified habitats. At KWS, the greater false vampire bat (*Lyroderma lyra*, Family: Megadermatidae) occurs in both natural and human-modified landscapes, predated largely on insects and small rodents, and plays an ecological role in pest suppression. Therefore, it raises the question of whether this generalist species optimizes the use of this mosaic landscape at non-random for resource acquisition. In this study, it is predicted that *L. lyra* selects human-modified habitats over natural habitats. This proposed study will evaluate how *L. lyra* respond to landscape modification at the population and individual level at KWS. To identify scale-level habitat selection, individuals will be tracked using VHF radio telemetry. The location of tagged bats will be collected every 10 minutes to analyze habitat selection within the home range on a second (total home range) and third-order (home range of each individual) scale. Available habitat for both second and third orders will be defined by generating random locations within the home range of all studied bats, and each individual bat, respectively. Finally, habitat selection will be estimated by comparing the disproportionate use of the habitat type with the available habitat. This finding will address the relative contribution of individual (third-order) versus population level (second-order) plasticity to persistence in a modified, shared landscape.

Bioinformatic analysis reveals diverse genomes of *Cardinium* endosymbiont in soybean cyst nematode

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KEYWORDS: soybean cyst nematode; endosymbionts; *Cardinium*

Analysis of hologenomes – genomes of hosts together with their symbionts – is a promising, under-explored approach in the field of population genomics. Furthermore, many existing public population genomic datasets from plants and animals contain hidden microbial symbionts whose population genomics have yet to be examined. This study sought to discover and analyze symbionts in plant-parasitic nematodes (PPNs), which are a substantial problem for agricultural production worldwide. Existing chemical and biological controls for PPNs are often insufficient due to their wide plant host ranges and prolonged survival environmentally. Although PPNs harbor endosymbionts such as *Wolbachia*, *Cardinium*, *Xiphinematobacter*, and others, which are thought to be important players in some of the most significant nematode pests, few have been characterized. We assembled and analyzed *Cardinium* endosymbiont genomes extracted from publicly available sequence reads from a previous population genomics study of 15 different populations of soybean cyst nematode (SCN), *Heterodera glycines*. Analyses used custom in-house pipeline which generated nearly complete genomes of *Cardinium* in one-third of the SCN populations. Remaining populations had short *Cardinium* DNA fragments suggesting past horizontal gene transfers. Among five *Cardinium* genomes assembled from SCN in this study, ~53% (632 out of 1201) genes were conserved with 375 genes being unique to the pangenome of these *Cardinium* isolates as compared to previously sequenced *Cardinium* strain from SCN, cHgTN10, suggesting significant population-level divergence among these symbionts. Pangenome analysis revealed only 301 out of 5249 (5.7%) genes were conserved between *Cardinium* from SCN and *Cardinium* from non-SCN hosts including arthropods, root-lesion nematode, and outgroup *Amoebophilus asiaticus*; from 701 genes not occurring in these non-SCN *Cardinium*, just 78 were annotated beyond hypothetical proteins indicating significant evolutionary specialization of the PPN symbionts. Further pathway and population genomic analyses should provide insights into the role of this distinct clade of *Cardinium* symbionts in this important nematode pest.

Uncovering replacement symbionts using metagenome assembly for treehoppers from Brazil

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KEYWORDS: endosymbionts; metagenomics; hemipteran

In multipartite endosymbioses between eukaryotic hosts and diverse consortia of microbes, it is unclear which microbes play important roles in the host. The multipartite endosymbiotic community within the bacteriome organ of auchenorrhynchan treehoppers provides a system to explore these complex interactions. According to a study from the 1940s, some treehoppers may harbor up to 6 symbionts working closely together to coordinate essential nutritional supplementation. However, a recent study by Salazar et al. discovered up to 8 microbes including the usual *Sulcia* (Bacteroidetes) and *Nasuia* (Betaproteobacteria) in 13 treehopper species from Brazil. Surprisingly, the normally obligate partner, *Nasuia*, was sometimes missing. The function of these additional microbes is unknown and whether one or more of these additional microbes fills the role of the lost *Nasuia* is of special interest. To address this question, we performed shotgun metagenomics for 30 additional treehopper species including nymphs and adults. Nine of these species were found to be missing *Nasuia*, while *Sulcia* and a *Sodalis*-like symbiont were detected in all 30 species. *Arsenophonus* and *Wolbachia* were detected in 18 and 29 species, respectively. Finally, a yeast-like symbiont, found in 7 species, appeared to be phylogenetically similar to *Ophiocordyceps*, which has been shown in other auchenorrhynchans to sometimes replace the primary symbiont. We assembled complete and nearly complete metagenome assembled genomes (MAGs) of the symbionts for comparative genomic analysis. Completeness was assessed based on similarity to NCBI references and CheckM values of 100% (complete) or ~20-40% for *Sulcia* and *Nasuia* or >80% for all other microbes (near complete). Quality assemblies were obtained for 20 *Sulcia*, 13 *Nasuia*, 4 *Bombella*, 4 *Sodalis*, 6 *Arsenophonus*, and 8 *Wolbachia*. Ongoing investigations include FISH microscopy to localize symbionts and confirm bioinformatic predictions, phylogenomics to assess evolutionary transitions, and comparative genomics and pseudogene analysis of MAGs to test for metabolic complementarity that would confirm our hypothesis of symbiont replacement.

A preliminary analysis of terrestrial small mammal communities along an altitudinal gradient in the central Andes of Bolivia

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KEYWORDS: Central Andes; rodents; marsupials; distribution

Understanding the patterns of distribution and variation of biodiversity is a fundamental goal of biodiversity science. However, issues associated with scale of analysis and sampling effort tend to challenge perceived observed patterns. Studies that concentrate on small non-volant mammals are advantageous because these taxa tend to show low vagility and are often locally abundant, which in combination permits the identification of discrete communities in the landscape. Consequently, they can be used to test for patterns of distribution along gradients such as elevations, which summarize historical and current processes. The Andean mountains are considered a cradle for speciation, consequently, the central Andes of Bolivia, a tropical hotspot is considered a key area to test for distribution patterns. We collected terrestrial small mammals along a 4-km high altitudinal gradient (190 to 4800 m) over a 3-year period (17 months), at 100-meter intervals within 15 different vegetation types. In this contribution we present preliminary analyses of the taxonomic diversity (alpha and beta diversity) within these 15 vegetation belts. We detected a mid-domain effect at around 1300 m. From the ca. 75 species present in the area, four species seem to be restricted to high elevation (above 3800 m) vegetation belt only: *Calomys lepidus*, *Phyllotis xanthopygus*, *Chinchillula sahamae* and *Neotomys ebriosus*, and 4 species are restricted to lowlands (below 200 m): *Cerradomys maracajuensis*, *Monodelphis peruviana* gr., *Cavia aperea*, and *Pseudoryzomys simplex*. Sites between 200 and 2.600 were the most diverse (11 species), and sites between 1.200 and 2.650 had assemblages with the most unique species. Our preliminary analyses indicate that four new species to science (one rodent and three marsupials) are present between 1200 and 2560m. A general non parametric analysis for and between sites show that the low and mid mountain vegetation belts have the highest diversity and lowest similarity.

Using small mammal patterns of distribution and phylogenetic diversity to identify conservation areas in the Puna bioregion

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KEYWORDS: Puna, Small mammals, diversity, conservation

The Puna bioregion, an amalgam of arid to semi-humid high-elevation grasslands, peatlands, barren soils, and shrublands occurs in the high Andes of Argentina, Bolivia, Chile, and Peru. The Puna has a unique diversity of environments which determines a highly diverse and endemic biota. Unfortunately, the region suffers from many human-induced pressures, from the expansion of the agricultural frontier to increased desertification due to climate change and global warming. These pressures are negatively impacting this fragile ecosystem and altering the community structure of many taxa. My research aims to identify areas of conservation importance in the Puna bioregion of the central Andes of South America. This will be accomplished by identifying patterns of ecological and phylogenetic diversity and endemism in the most diverse group of South American vertebrates: non-volant small mammals. Because of their high levels of endemism, turnover rate across the landscape and the ecosystem functions they provide in the Puna, this group represents an interesting model for biogeographic and macroecological exploration. To date, I constructed: (a) a list of species present in the study area, (b) georeferenced species data points, and (c) a phylogenetic tree for the species of interest. These data were used to construct two diversity and two phylogenetic distance indices which in combination indicate that the most important area for conservation is the geographic center of the Puna. This region includes the largest lake in South America and the highest body of water in the world: Lake Titicaca. These patterns are mirrored by groups of other vertebrates (fish and birds), plants, and invertebrates. Importantly, the area identified currently harbors no conservation units of any importance. Therefore, it is fundamental that countries bordering the identified region join efforts to protect this area.

Microplastic ingestion perturbs the microbiome of *Aedes albopictus* and *Aedes aegypti*

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KEYWORDS: vector biology, microbiome, toxicology

Plastic pollution remains one of the most ubiquitous and menacing ecological threats worldwide. Though larger plastics have been known to cause ecological impact, little is known about the effects of much smaller microplastics, which can be formed by the degradation of plastics such as UV light and abrasion. Microplastics the size of few microns or less are difficult to remove from the environment and are easily ingested by animals, particularly invertebrates and their biological effects are unclear. While these previous studies have focused on the ecotoxicology of microplastics on other insects and animals, no studies have examined the effects of microplastics on the microbiome and the ecology of disease transmission by container inhabiting mosquitoes such as *Aedes albopictus* (Asian tiger mosquito) and the *Aedes aegypti* (yellow fever mosquito). The goal of this study was to examine if varying concentrations of microplastics will have an impact on the composition of the microbiota of *Ae. albopictus* and Fluorescent polystyrene beads of 1 μm diameter were fed to *Ae. albopictus* and *Ae. aegypti* as larvae at varying concentrations, and 16s and ITS2 high through Illumina sequencing was used to identify changes in bacterial and fungal microbiome composition. Our results demonstrate that ingestion of microplastics results in dysbiosis of the bacterial microbiota but has little impact on the fungal microbiota composition in *Ae. aegypti* and *Ae. albopictus*. Understanding the effects of microplastics on microbiota composition is crucial for predicting and effectively mitigating the potential effects of microplastics exposure in mosquitoes in relation to vector competence of arboviruses and other insects.

A story told through plant functional traits: a perspective from the Grasslands.

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KEYWORDS: Community; Ecology; Conservation; Climate Change.

Grasslands are particularly important to mitigate CO₂ concentrations, sequestering 20% of atmospheric carbon. However, these ecosystems are usually underestimated because of their open areas that at first impression seem only suitable for cattle ranching, monocrops, and oil exploration, without considering that they can be transformed. Land use change, including deforestation, habitat fragmentation and increased nutrient inputs from crops, increases biodiversity loss and thus potentially reduces its ecosystem functions. Nutrient addition can cause community shifting in composition and structure and those changes can be tracing with functional traits. Therefore, environmental changes driven by humans has the potential to alter ecosystem processes such as the carbon storage. Since it has been shown that plant functional traits vary according to environmental conditions at different scales, it is possible to recognize changes in species abundances that are related to alterations in ecosystem functions. Therefore, the objective of this proposal is to compare changes in aboveground and belowground traits to quantify their effects on biological carbon storage. The study area will be defined in the Nutrient Network site in Lubbock, which has experienced nutrient additions in the last 5 years. Measurements of leaf and root traits are expected to be made in the different plots previously established, as well as C and N content in the plant tissues. The addition of nutrients is expected to decrease the community composition and, therefore, to reduce the ecosystem process performance.

Understanding how the gut-brain axis modulates male aggression using a novel invertebrate model

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KEYWORDS: gut-brain axis; *Gryllus*; probiotic; behavioral paradigm

Guts across all animal life host diverse microbiomes that can communicate with the host's central nervous system to modulate brain function and behavior. This gut-brain axis (GBA) communication involves the vagus nerve, neurotransmitters, and hormones, but how they work together is unclear. Based on several recent studies, we hypothesize that vagal pathways are the primary and most critical route by which psychoactive compounds from gut microbiota impact behaviors such as male aggression. We developed a novel behavioral paradigm to test our hypothesis using the banded cricket, *Gryllus sigillatus*, and a local cricket species, *Gryllus texensis* which are ideally suited for studying GBA effects on male aggression. The paradigm is based on Chinese cricket fighting with timing intervals and discrete behaviors that will provide quantitative scales to measure minute behavioral changes in males' territorial and aggressive tendencies when supplemented with probiotics or amino acids. We predict that probiotic treatment with *Bifidobacterium longum* BB536 will alter neurotransmitter subunit expression in the cricket brain and reduce aggression. Here, we use our behavioral paradigm on both vagotomized and non-vagotomized crickets with and without treatment with the probiotic. We will measure behavioral changes in each treatment group compared to the control and perform RNAseq on guts in each treatment to assess changes in total microbiome and host gene expression to infer GBA functions driving changes in aggression. We will then perform a similar experiment using two crucial enzymes in dopamine synthesis, TH (tyrosine hydroxylase) and DDC (DOPA decarboxylase), which *B. longum* produces, to test whether these compounds alone drive aggression patterns, or if more complex factors are at play, such as shifts in composition and activity of endogenous microbiomes.

Understanding neurodivergent STEM student outcomes using lay theories

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KEYWORDS: lay theories of intelligence; disability; neurodivergent; STEM education; college students

Though students with learning disabilities, also known as neurodivergent students, are equally likely as their peers to select a STEM major, they are underrepresented when it comes to undergraduate retention (Lee, 2022). Often the structure of courses in higher education reflects pervasively held social beliefs in the inferiority of neurodivergent students (Clouder et al., 2020), and exclusionary beliefs about who can be successful are especially prevalent in STEM fields (Leslie et al., 2015). Beliefs about students' abilities or intelligence are also called lay theories, and include mindset, whether one believes intelligence can change over time (Dweck, 1999), universality, whether one believes anyone can achieve the highest level of intellectual ability (Savani et al., 2017), and brilliance, whether one believes preexisting talent is necessary for one's success in a particular field (Leslie et al., 2015). I will investigate whether lay theories are an effective tool for understanding the success of neurodivergent students, first by conducting interviews to assess how lay theories resonate with these students. I will follow that with a survey to assess the relationship between neurodivergent students' lay theories and their academic outcomes. These outcomes include intent to persist, sense of belonging, and science identity (Limeri et al., 2022). The findings of this study will be useful to determine how neurodivergent STEM undergraduate students find success despite the challenges presented by classes that often overlook their ways of learning, and can ultimately be used to support their success.

Membrane repair response against sterol specific toxins in *Leishmania* is calcium independent but ionic strength dependent

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KEYWORDS: Membrane Repair, *Leishmania*, Cholesterol dependent cytolysins, Membrane Model system

Plasma membrane in mammalian cells is important for providing a barrier to the external environment, protection against toxic substances and maintenance of cellular morphology. Sterol specific toxins such as Streptolysin O(SLO) and Perfringolysin O(PFO) compromise plasma membrane integrity and trigger toxic calcium influx and potassium efflux. This ionic flux activates membrane repair responses such as patching, clogging and ESCRT III mediated microvesicle shedding in mammalian cells to restore plasma membrane integrity. However, evolutionary related yet pathogenically relevant parasites such as *Leishmania* are not well understood in terms of their repair response to membrane perturbing agents such as SLO and PFO. *Leishmania* are known to possess orthologous mammalian ESCRT III components such as Chmp3, Chmp4b and alix, however if these proteins also share similar roles as their mammalian counterparts in microvesicle shedding is unknown. As a result of limited repertoire of Leishmanial repair proteins such as Chmp3, chmp4b and alix, the project aims to develop *Leishmania* as a pathogenically relevant membrane model system to study repair response to membrane perturbing agents such as SLO and PFO. Our hypothesis is that repair response in *Leishmania* is mediated by microvesicle shedding via its orthologous ESCRT III components and shows calcium and or ionic strength dependence. Using flow cytometry, we found that Leishmanial repair response to SLO and PFO is calcium independent whilst showing chloride ion dependence. Furthermore, a dose dependent chloride ion protection is shown in *Leishmania*. Using ultracentrifugation and western blotting, we also found that there is minimal shedding of SLO on microvesicles shed by *Leishmania* on SLO challenge. Overall, development of *Leishmania* as a pathogenic membrane model system will enable better understanding of repair mechanics in other similar protozoan parasites.

Floral compounds activate mediate olfaction in *Aedes aegypti*

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Plants and animals emit several biochemical compounds as byproducts of their metabolic pathways. These volatiles are detected by insect olfactory receptors and directly affect their survival in their niche environments. They serve as signals to insects to the presence of nectar sources and potential sources of bloodmeals and alert the insects to the presence of predators. In this study, we utilize a heterologous expression system to investigate a clade of conserved olfactory receptors in *Aedes aegypti*, one of the most common species of mosquitoes in the United States. We expect to identify a group of volatiles that activates these receptors, understand the similarities in their structure and function, and predict the impact these compounds will have on the fitness of *Aedes aegypti*. The knowledge gleaned could have potential applications in integrated pest management practices currently in place to control vectors of diseases.