

2024 TTABSS Abstracts

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Doctoral Candidate/Post-doctoral Seminar Sessions

Uncovering diverse roles of endophytic microbiomes in wild and cultivated bananas using metatranscriptomics.

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Keywords: Metatranscriptomics, endophytic microbiome, antifungal

Despite endophytic microorganisms playing a vital role in enhancing plant health, our understanding of this mechanism is limited, particularly for diverse banana genotypes. Domesticated bananas face the threat of Fusarium wilt, caused by *Fusarium oxysporum* f.sp. *cubense*. In this study we hypothesized H1: wild (diploid) banana plants would exhibit a more varied range of disease-preventing microbial functions than cultivated (triploid) plants; and H2: the microbiome extracted from wild *Musa balbisiana* (MB) would demonstrate a higher level of antifungal activity against Fusarium wilt (Foc Race 1) in comparison to the cultivated Pisang Awak (PA) microbiome. Investigating H1, RNA sequencing of endophytic microbiomes from four diploid and three triploid banana plants was conducted, analyzing leaf and root tissues via a culture-free enrichment protocol. The SAMSA2 pipeline, with adjustments, assessed the diversity and function of the endophytic microbiome metatranscriptome. For H2, microbiomes from wild *Musa balbisiana* (MB) and domesticated Pisang Awak (PA) were extracted. An in vitro Agar Well Diffusion assay evaluated their antifungal activity against Fusarium (Foc Race 1). Results indicated for H1 that the majority of taxa and gene clusters were genotype-specific, with limited overlap between *Musa* genotypes. Notably, *M. balbisiana* and Thai Black (B-genotypes) each harbored over 500 distinct taxa, showcasing diverse functions. KEGG enrichment analysis highlighted core beneficial functions and novel specialized roles. Processes like energy metabolism, secondary metabolite biosynthesis, and xenobiotics biodegradation shaped plant-microbe interactions. Microbiome interactions involved cellular community dynamics, quorum sensing, and biofilm formation. Surprisingly, the results of H2 showed that the microbiome community from cultivated PA were more effective in inhibiting Fusarium wilt than those from wild MB ($p < 0.5$). These findings provide a valuable dataset for future research involving in planta experiments to study the impact of plant genotypes on microbiome function in a challenging environment.

Dietary protein pH enhancement increases longevity, alters body mass composition, and attenuates metabolic associated disease development in C3H/HeJ mice

Barr, Benjamin (1); Brashears, Mindy (2); Moustaid-Moussa, Naima (3,4); Gollahon, Lauren (1, 4)

Keywords: longevity; diet; pH-enhancement; male; female; ammonium hydroxide

A high fat diet can induce the progressive development of low-grade metabolic acidosis and metabolic syndrome, resulting in tissue damage. Recent studies suggest a more alkaline diet may help mitigate these consequences. Most dietary studies focus on the effects of carbohydrates and lipids, with protein modification an understudied area. This study investigated a novel approach to attenuate metabolic acidosis by modifying protein pH. I hypothesized that increasing pH of the dietary protein with ammonium hydroxide (NH₄OH) supplementation, attenuates the effects of a high fat diet towards inducing chronic diseases. To that end, a long-term (18 month) study was conducted using male and female C3H/HeJ mice, divided into four diet groups of 32; control (11 % fat) (CC), control + NH₄OH (CCN), high fat (46% fat) (HFC), and high fat + NH₄OH (HFCN), where C represents the protein source: casein. Body mass, mass composition, survivorship and tumor incidence were measured monthly. Tissues were collected at cross-sectional time points (6-, 12- and 18-months) for histological, metabolic, and transcriptomic analysis. Three-way ANOVA was performed to identify statistical significance between fat content, NH₄OH supplementation and sex at each time point. A significant effect of dietary fat (C vs HF) was observed on total mass and mass composition in both sexes, with a subtle effect attributable to +NH₄OH. Kaplan-Meier analysis showed marked differences in longevity for females when maintained on +NH₄OH diets. Interestingly, males showed similar longevity between all diets except CC, which was markedly lower. Tumor incidence was similar between sexes. Tumors in males were exclusively liver. Females developed numerous tumor types. Histology indicates attenuation of metabolic associated fatty liver disease in HFCN diets. In summary, our findings indicate that pH enhancement of protein through NH₄OH supplementation extends lifespan, alters body mass composition and attenuates cancer development in a mouse model for obesity.

Graduate Student Oral Presentations

The Population Genetic Structure of American Alligators in the Houston Metro Area

Bollinger, Todd (1), Hruska, Jack (1), Manthey, Joe (1), Densmore, Lou (1)

Population genetics techniques have expanded rapidly over the past fifteen years thanks to advances in sequencing technology and methods for reducing genomic complexity through restriction enzyme digestion. American alligators (*Alligator mississippiensis*) remain arguably the most studied crocodylian in the world, but knowledge of their population genetic structuring, particularly at regional to local scales, is limited and understanding of the effects of game management on their genetic clustering is virtually nonexistent. To discern alligator population structure in an understudied portion of their range, we used genotyping-by-sequencing to analyze single nucleotide polymorphisms in live alligators from a protected state park sanctuary, live alligators captured on private properties, as well as harvested alligators from southeastern Texas. Distance trees, minimum spanning networks, principal components analysis, and Admixture cross-validation showed that animals protected from hunting within the sanctuary population were in fact clustered within the harvested population ($F_{st} = \sim 0.00293$), while grouping individuals by river drainage basin showed somewhat higher yet still small (< 0.10) F_{st} values. Mantel correlation tests showed no significant isolation-by-distance model (Mantel's $r = -0.1529$, $p\text{-value} = 0.937$), while Fast & Flexible Estimation of Migration Surfaces identified several potential gene flow barriers corresponding to human infrastructure around the Houston metropolitan area ($\lambda = 0.0001$). Overall, our results imply that southeastern Texas alligators have minimal population differentiation at the resolution of these genetic markers, indicating that sanctuary animals should not be treated as separate demographic or management units relative to surrounding unprotected animals.

The success of acquisitive plants in grasslands exposed to eutrophication.

Kelley, Monika; Smith, Nick

Keywords: grasslands; plant traits; acquisitive-conservative axis; eutrophication

The need to predict how plant communities will perform under various environmental pressures, such as shifting climate, resource fluctuations, species invasion, interruption to natural disturbances, etc. has increased in urgency as global ecosystems are rapidly shifting due to anthropogenic global change. One proposed “tool” for constructing a global framework for predicting plant responses to global change has been the use of plant functional traits. This research aims to expand on the understanding of plant functional traits along the acquisitive-conservative axis. This axis indicates a level of plant resource acquisition and strategy, with the more acquisitive species having fast investments and returns versus the more conservative species, which tend to have the opposite strategy. This research will focus on the understudied area of grassland species and communities that have been exposed to terrestrial eutrophication events. Four grassland Nutrient Network sites in North America, characterized by similar temperature extremes, and eutrophication events across a precipitation gradient, were utilized for this research. We measured a total of sixteen plant functional morphological and physiological traits in addition to species composition measurements. All measurements were restricted to control plots and plots exposed to eutrophication events (fertilizer applications). The primary objectives are to determine whether (a) more acquisitive species exhibit superior performance concerning species composition and plant physiological responses compared to their conservative counterparts, (b) these trends are consistent across a precipitation gradient, and (c) if phenotypically plastic acquisitive species outperform their counterparts in control plots. Preliminary results align with previous studies, indicating that more acquisitive species in grasslands outperform their conservative counterparts in terms of composition. While the remaining data is still undergoing analysis, our preliminary findings will be prepared for presentation at TTABS.

Phylogeographic patterns of codiversification in *Camponotus laevigatus* and its endosymbiont *Blochmannia*.

(1) Boyane, Swapnil; (2) Behrends, Garrett; (3) Manthey, Joseph

Keywords: California; Phylogeography; Population genomics.

The California Floristic Province (CFP) is a global biodiversity hotspot due to its high endemism rates. Recent phylogeographic studies focusing on invertebrates showed varied geographic patterns of genetic structure in the CFP. The carpenter ant, *Camponotus laevigatus* (Smith, F., 1858), is primarily found in the CFP and has an obligate mutualistic bacterial endosymbiont (*Blochmannia*). In this study, we used whole genome sequencing of 29 individuals from 21 colonies to investigate whether *Camponotus* and its endosymbionts exhibit phylogeographic patterns of codiversification.

Using principal components analysis (PCA) and ADMIXTURE to estimate genetic structure, we found that both *C. laevigatus* and *Blochmannia* possess three distinct genomic clusters. Furthermore, Isolation by distance (IBD) analyses revealed a strong correlation between geographic distance and genetic diversity in both *C. laevigatus* and *Blochmannia*, suggesting limited long-term gene flow across the landscape. Finally, we used estimation of effective migration surfaces (EEMS) to estimate patterns of gene flow; EEMS indicated that the Central Valley in California acts as a major barrier to gene flow between the different populations. Overall, our findings showed congruent patterns of phylogeographic structure in *C. laevigatus* and *Blochmannia* and demonstrated that geographic distance and the role of the Central Valley as a biogeographic barrier shape the genetic structure of codiversification in this mutualism.

The Impact of Land Use and Land Cover on Mitigating the Effects of Extreme Heat on Indian Flying Foxes in Pakistan

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Keywords: Evidence Based Conservation, Extreme Heat Event, Heat Stress, Mass Die-offs, *Pteropus medius*, Thermoregulatory Behaviors.

Extreme heat events have caused mass die-offs of large flying foxes in the genus *Pteropus* in Oceania and parts of the Old World. Despite the realized niche of Indian flying foxes is contracting to avoid rising temperatures, there is still a gap in our understanding of how these rising temperatures are affecting them. This study investigates the impact of extreme heat on Indian flying foxes in Pakistan, specifically focusing on their thermoregulatory behaviors and associated thresholds for temperature and Heat Stress Index. Bridging a crucial knowledge gap, we will evaluate Land Use and Land Cover factors within significant buffer zones using remote sensing techniques, to analyze their impact on behavioral thresholds and local weather conditions at roosts. We collected data from May to August 2021, combining in-situ temperature and humidity measurements at seven roosting sites with video scan sampling for recording thermoregulatory behaviors. We identified sequential thermoregulatory behaviors, and death occurrences after panting, showed a significant positive association with Heat Stress Index ($\beta = 0.3$, $p < 0.01$, $X^2 = 19$). Large forest cover helps maintain a cooler roost environment, promoting better physiological conditions for coping with extreme heat challenges, evident by elevated temperature and Heat Stress Index thresholds for observed behaviors. Similarly, water bodies near roosts positively influenced Heat Stress Index thresholds for panting and wrist licking. The intricate interplay of Land Use and Land Cover with local weather conditions and heat stress thresholds provides valuable insights into the species' adaptation to heat stress. Predicting potential places and times of elevated risk of heat-related die-offs for Indian flying foxes is of great conservation value, by allowing timely mitigation plans, as a conservation priority.

Mimicking the host environment to improve antimicrobial susceptibility testing.

Black, Caroline (1); Wakeman, Catherine (1)

Keywords: antibiotic resistance; polymicrobial communities; infection dynamics

While certain aspects of the host-pathogen interface are common to all sites of infection, other factors can be highly specific to the localized environment. For example, chronic infections are often polymicrobial with the specific microbial consortia present varying greatly between patients. Additionally, nutrient and atmospheric composition shifts between different sites of infection. Herein, we demonstrate that antibiotic susceptibility profiles of pathogens can dramatically shift with changes in the microbial consortium, oxygen levels, or carbon source availability. Specifically, we demonstrate that *Enterococcus faecalis* grown in a polymicrobial community containing other common wound pathogens (*Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*) demonstrated increased susceptibility to gentamicin due to heme cross-feeding allowing more gentamicin to enter the cell via altered proton motive force. However, performing the same AST in anaerobic conditions reversed this phenotype. When *E. faecalis* was grown in community with *A. baumannii*, it exhibited decreased susceptibility to cephalexin as *A. baumannii* likely produces a beta-lactamase allowing for the neutralization of the antibiotic. Further research demonstrated that environmental conditions, like available carbon sources, can also influence antibiotic susceptibilities. *P. aeruginosa* exhibits increased susceptibility to kanamycin when grown in minimal media containing glycerol, as compared to minimal media with malonate, but decreased susceptibility to ciprofloxacin. Overall, these results demonstrate that environmental conditions, such as community members and available nutrient sources, play a role in determining an individual bacterium's antibiotic susceptibility. By accounting for the infection environment when determining antibiotic susceptibilities, we can more effectively treat persistent infections, leading to improved patient outcomes.

Gene expression in *Acinetobacter baumannii* is variably influenced by adult human serum

Ghavanloughajar, Hannaneh(1); Fokar, Mohamed(2); Brown, Amanda(3); Hamood, Abdul(4)

Keywords: *Acinetobacter baumannii*; Adult human serum

Acinetobacter baumannii (Ab) is a Gram-negative multi drug resistant (MDR) pathogen that causes serious nosocomial infections including wound infections, ventilator-associated pneumonia, skeletal muscle and nerve infections, and septicemia. Beyond its MDR phenotype, Ab manifests virulence through iron uptake, cytotoxic production, adhesion, and biofilm formation. In the host's 'nutritional immunity,' metals like iron are withheld to impede bacterial growth, prompting bacteria, including Ab, to employ strategies such as capturing heme-iron and utilizing siderophores like Acinetobactin. In adaptation to exposure to different human fluids and proteins, Ab alters the expression of several virulence genes. During septicemia, blood/serum likely influence the pathogenesis of Ab infection. However, despite numerous studies, the influence of serum on the Ab virulence is not fully characterized. We hypothesized that during Ab septicemia, serum influences Ab pathogenesis by altering the expression of several virulence genes. We examined this possibility by growing Ab strain AB-118 in the nutrient broth Lura Britani (LB) in the presence or absence of 10% pooled human serum. The commercially available serum was obtained from at least 10 healthy adults. The growth curve revealed that Ab-118 in LB-10% serum exhibited significantly enhanced growth compared to LB alone. Further, the transcriptome analysis at 8 hours post-inoculation (HPI) unveiled significant alterations in the expression of 386 genes, with 144 upregulated and 242 downregulated. Notably, the Acinetobactin gene cluster, showed substantial reduction, with 15 out of 18 genes displaying up to -2.3 log₂ fold change. Also, all nine genes present in the *mdc* operon, which are involved in malonate metabolism, were downregulated up to -3.1 log₂ fold change. These results emphasize the dynamic interplay between bacterial virulence and host factors during *A. baumannii*'s septicemia and suggest potential therapeutic targets.

Modifying *Arabidopsis thaliana* model system to maximize drought and salt tolerance

Pokhrel Rakshya

Keywords: *Arabidopsis*; transgenic; co-overexpression; chloride channel; stress tolerance

Plants' response to abiotic stress can be upregulated to increase resilience in areas where water and salinity are the limiting factors for agricultural productivity. The *Arabidopsis* pyrophosphatase protein 1 (AVP1) is a H⁺ translocating proton pump and the *Arabidopsis* chloride channel protein a (AtCLCa) is a membrane transporter that generate proton electrochemical gradients across cell membranes and prevent the accumulation of nitrate ion in cytosol. The objective of this study is to express AVP1 and AtCLCa in the model plant *Arabidopsis thaliana*. The combination of two genes is proposed to work together to tolerate multiple abiotic stresses and overcome the short-term and long-term negative effects upon exposure to these abiotic stress conditions. This study postulates that the transgenic *Arabidopsis* would exhibit better water use efficiency under drought and saline conditions, whereby AVP1 would increase the transport activity of AtCLCa and other tonoplast and plasma membrane localized transporters leading to osmotic homeostasis. Together, the expression of these genes would not only increase photosynthetic activity and carbon assimilation, but also work on metabolic reprogramming to display a robust root and shoot system. According to our preliminary results, after stress treatments the transgenic lines were able to recover from combined stresses of water deficit for 10 days and 250 mM sodium chloride and wild type plants were unable to survive. We observed early flowering, increased root length and distinguished healthier phenotypes in transgenic lines after stress treatment, and the germination rate of the seeds harvested from stress exposed plants was higher. This is a transgenic approach to prevent massive crop failures and operate sustainable agriculture.

A genomic assessment of the Pinyon Deermouse, *Peromyscus truei* (Cricetidae, Neotominae): shedding light into its taxonomy, evolution, and conservation.

Colmenares-Pinzon, Javier (1); Manthey, Joseph (1)

Keywords: *Peromyscus*, Genomics, Structure, Taxonomy, Conservation,

Genomics approaches have become an important part of the toolkit for a basic understanding of wildlife biology. With increasing progress in sequencing capabilities, and the concomitant development of bioinformatic techniques, analyses of large-scale DNA datasets are shedding light into multiple aspects of non-model organisms, such as taxonomy, systematics, evolution, and conservation. Here, we exemplify this by studying from the genomics perspective for the first time the Pinyon Deermouse, *Peromyscus truei*. This is a small neotomine rodent broadly distributed in the western half of the United States, where it occupies rocky slopes with pinyon pine and reaches high abundances. As currently understood, the species comprises a total of 11 subspecies that are phenotypically recognizable. However, beyond subtle differences in color and proportions, there is not clarity about their genetic distinctiveness, relationships, and geographic boundaries, which ultimately is necessary information for the correct assessment of conservation priorities.

By generating the first chromosome level genome assembly and resequencing individuals from the entire distribution, the aim of our work is to get a fine-scale picture of the evolutionary history of the Pinyon Deermouse and interpret it mainly in the contexts of taxonomy and conservation.

This implies at a first glance answering at least six research questions: 1. What is the degree of genetic variation within the species? 2. Is the genetic diversity structured? 3. Is the genetic structure consistent with phenotypic variation? 4. Do the subspecies represent independent evolutionary units? 5. What factors are shaping the genetic variation and structure between populations? 6. Are there genomic signatures of decline within some populations?

Protein Limitation Alone Does Not Drive Hunting in Bat Diversity Hotspots: A Spatial Structural Equation Model

Rutrough, Abigail L. (1); Little, Todd D. (2); Stickley, Zachary L. (3); Kingston, Tigga (1)

Keywords: Bushmeat Hunting, Structural Equation Modeling, Pteropodidae, Conservation social sciences, Large-scale spatial prediction, Behavioral science.

Overhunting is one of the leading threats to biodiversity and has driven bat population declines in parts of Africa, Asia, and Oceania. Protein limitation has been proposed as a driver of wildlife hunting and posits that areas with decreased access to conventional protein sources, such as livestock and fish, will have the highest incidence of wildlife 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 across bat-hunting hotspots, at continental scales. Hunting locations were collected from scientific literature and social media. We modeled latent constructs hypothesized to drive protein limitation, namely access to aquatic protein, access to terrestrial protein, human development, cultural norms, and bat habitat. We used remotely sensed raster layers, including mean annual income, marine trophic index, livestock density, nighttime light, and road density as measured indicators for our latent constructs by extracting raster values at known hunting locations. Our findings show protein limitation contributes to, but does not fully explain, bat hunting and consumption and that there is a significant difference between mainland and island drivers. Protein limitation and subsistence hunting are often assumed to drive wildlife hunting, yet our work shows this may not be true for many bat-hunting hotspots. By modeling the human behavioral drivers of bat hunting, we can better prioritize limited conservation funds, implement more effective interventions, and reduce contact at the human/bat interface to better protect bats and people in a changing world.

Differential gene expression in response to temperature effects antibiotic susceptibility of *Pseudomonas aeruginosa* biofilms

Luecke, Alex (1), Wakeman, Catherine (2)

Keywords: Biofilms, *Pseudomonas aeruginosa*, stress response

As bacteria transition from one environment to another, they must adapt to the ambient temperature. In previous research, we observed that the structure of *Pseudomonas aeruginosa* biofilms change in response to temperature and identified some genes essential for biofilm formation in specific temperature ranges. Additionally, it has been shown that antibiotic tolerance increases as bacteria shift from planktonic to biofilm cell states. Does this change in tolerance also extend to the phenotypic adaptations we observe in response to temperature? To answer these questions, we first conducted an RNAseq analysis of *P. aeruginosa* PA14 biofilms after 48 hours of growth at four different temperatures: 23°, 30°, 37° and 40°C. The mRNA from the biofilms and the remaining planktonic cells were extracted and sequenced, and differential expression analysis was conducted. We also ran an antibiotic susceptibility panel of *P. aeruginosa* PA14 in 96-well plates at the aforementioned temperatures and determined minimal inhibitory concentrations.

We have identified several genes which are differentially expressed in biofilms grown at specific temperatures as well as those which are essential across all temperatures. We have a particular interest in genes associated with the proton motive force, which have been shown to have higher expression in biofilms at warmer temperatures (37° and 40°C) relative to cooler temperatures (23° and 30°C). Additionally, we observed that temperature can impact antibiotic efficacy for therapeutics such as novobiocin and kanamycin. We believe that these changes in antibiotic susceptibility are a result of temperature-dependent changes in the proton motive force. Our findings also suggest that temperature plays a contributing role in antibiotic susceptibility of *P. aeruginosa*. As such, the temperature of a site of an infection could be considered when selecting antibiotic treatment.

Photosynthetic Acclimation of Cotton Plants to Heat and Drought Stress

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Keywords: Cotton Photosynthesis; Temperature Stress; Drought; Photosynthetic acclimation

Cotton production in the Texas High Plains (THP) has declined due to frequent heat and drought events. These extreme climate events impact cotton photosynthesis, subsequently affecting carbon accumulation and crop yield. When cotton plants experience higher growth temperatures, short-term photosynthesis increases until it peaks at the optimum temperature (T_{opt}) and then decreases beyond T_{opt} . Over the long term, the net photosynthesis does not change significantly because plants can adjust to higher temperatures. However, drought and the combination of drought and heat may reduce the net photosynthesis rate by decreasing stomatal conductance and rubisco activity.

This study examined whether cotton leaf photosynthesis can acclimate to concurrent heat and drought stress. Two cotton species, *Gossypium hirsutum* and *Gossypium barbadense*, were exposed to temperatures of 32°C/24°C (max/min) and 40°C/32°C (max/min) after two weeks of growth. Drought-treated plants received irrigation to 40% of field capacity (FC), while well-watered plants were maintained at 80% of FC. Photosynthesis rates were measured at six different temperatures (16°C, 22°C, 28°C, 34°C, 40°C, and 46°C) from the fully expanded fifth leaf.

The results indicate that cotton plants acclimated to higher temperatures and maintained the photosynthesis rate by increasing the maximum rate of rubisco carboxylation (V_{cmax}) and shifting T_{opt} towards the higher growth temperature. Surprisingly, the drought treatment did not affect the cotton photosynthesis rate in our experiment. The study concludes that cotton plants can acclimate to both heat and drought stress, thereby maintaining the net photosynthesis rate under extreme climate conditions.

Phylogeographic patterns of co-diversification of host-microbe interactions in the Galápagos Islands

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Keywords: ants; endosymbiosis; genomics; proteobacteria

Reciprocal selection in symbiotic systems implies that the interacting species' fitness depends on their own genotype and on their partner's genotype, potentially differing among environments. Although evolutionary biologists have investigated how symbiotic microorganisms mediate and constrain host evolution by affecting their genomes and phenotypes, what remains scarcely studied is the co-diversification of hosts and symbionts at a genomic level. Here we combine whole-genome and morphological data to examine what processes shape the evolution of host-microbe interactions under a phylogeographic framework. Specifically, we explore how microbes evolve in concert with their partners across space, and to what extent host ecology mediates co-diversification at micro and macroevolutionary scales. We study the ancient endosymbiosis between carpenter ants from the genus *Camponotus* and their associated *Blochmannia* proteobacteria across the Galápagos Islands. We explore endemic and introduced *Camponotus* species and their multiple dissimilar subspecies, each potentially associated with different bacteria strains across the archipelago. We also include host species from the mainland, as outgroups. First, we implement PacBio HiFi to obtain de novo reference genomes and Illumina resequencing to explore the genomic landscape of divergence for both ant host populations and bacteria strains. We also perform detailed morphometric analysis to delimit hosts at a fine scale and test for host-bacteria specificity. To test for co-diversification, we use whole-genome-based phylogenies to assess whether phylogeographic patterns are congruent. As for the host, preliminary genetic evidence suggests structure among populations, but it seems to be uncoupled from morphological variation. On the bacteria side, preliminary results identify genomic features and functionality variations among bacteria genomes across insular and continental host species. This pioneering study provides insight into short-term ecological and long-term evolutionary mechanisms driving endosymbiosis evolution in yet poorly studied taxa such as those found in the Neotropics.

Characterizing Temporal Changes in Arbuscular Mycorrhizal Diversity in Herbarium Specimens from Guadalupe Mountains National Park

Hosaka, Mara (1); Bullock, Madison (2); Price, Sherese (3); Johnson, Matthew (4)

Keywords: Metabarcoding; mycorrhizae; Guadalupe Mountains National Park; herbaria

Arbuscular mycorrhizal fungi (AMF) are endophytes (an organism that lives inside plant cells), that are understood to play a significant role in the ecology of their plant hosts. However, some studies suggest a loss in phylogenetic diversity of AMF in response to changing environmental factors, though few trends have shown conclusive evidence. Now, the diversity of microbes can be routinely quantified with DNA sequencing, but there is little historical data with which to compare modern findings. Herbarium specimens can provide a historical record of fungal endophyte communities, allowing for study of how AMF communities may have changed over time. In this study we are analyzing changes in endophyte biodiversity over the past 50 years in the Guadalupe Mountains, a biodiversity hotspot in Texas spanning seven ecoregions. We sampled roots and leaves of herbarium specimens from several species collected from Guadalupe Mountains National Park. For each species we took samples from both an older specimen collected from 1973-1977 and from a recent specimen collected in 2022 or 2023. We extracted and sequenced DNA from herbarium specimens and analyzed data using a standard microbiome data processing pipeline. Our characterization of AMF species richness and phylogenetic relatedness will provide proof of concept for characterizing changes in AMF diversity over time using herbarium specimens. Our results will contribute to building a better understanding of the change in composition of AMF communities as a response to climate change.

Is there a relationship between Effective Population Size (N_e) and transposable element diversity? An exploration of the Carrier Subpopulation (CASP) hypothesis.

Hoyos, Manuel (1); Ray, David (2)

Keywords: Effective Population Size (N_e); Transposable Elements; Carrier Subpopulation Hypothesis.

The insertion of transposable elements (TEs) constitutes one of the main components of genomic variation within and among species, with significant consequences for fitness and the evolution of organisms. Despite this, there is still no direct evidence of correlation between speciation events and TE insertions. With this concern in mind, Jerzy Jurka, Weidong Bao, and Kenji Kojima proposed the Carrier Subpopulation (CASP) hypothesis in 2011, suggesting that the impact of TE fixation during periods of demographic bottleneck in a specific lineage is greater due to the action of genetic drift. Since then, the CASP hypothesis has been invoked to explain the fixation of transposable elements but has never been tested in evolutionary terms. This work presents preliminary results from the examination of this hypothesis using bats as model organisms.

Interactive effect of elevated CO₂ and temperature on photosynthetic acclimation of C₃ and C₄ species.

Ezekannagha, Ezinwanne (1); Nick, Smith (2); Kelly Carroll(3)

Keywords: Acclimation, Photosynthetic pathways, Grass species

Plants adjust investment in primary components that determine net carbon dioxide (CO₂) assimilation, namely photosynthetic biochemistry, in response to changing environments. These adjustments, known as acclimation, enable a more efficient use of carbon, available light, and other resources for the plant. The extent to which acclimation occurs depends on the type of environmental change and time since exposure to new growth environment. Plants that use different photosynthetic pathways, such as C₃ and C₄, are expected to acclimate differently across changing environments, but the mechanisms underlying these differences are poorly understood. Here, we assessed how C₃ and C₄ photosynthetic acclimation vary in their response to elevated CO₂ and increased temperatures – key global change factors that will influence the magnitude and direction of the terrestrial carbon sink. To address this, we grew three C₃ perennial grasses (*Pascopyrum smithii*, *Elymus canadensis*, and *Poa pratensis*) and three C₄ perennial grasses (*Bouteloua curtipendula*, *Schizachyrium scoparium*, and *Sorghastrum nutans*) under two temperature regimes (15/20°C and 25/35°C night/day) and two CO₂ concentrations (420 ppm and 1000 ppm) in a full-factorial growth chamber experiment. After ten weeks of growth, we measured photosynthesis, leaf isotopic carbon discrimination, and quantum efficiency of photosystem II. Assimilation responses to internal CO₂ concentration (*A/C_i* curves) were also measured and biochemical process rates that limit photosynthesis were estimated. We expect that C₄ species would exhibit decreased sensitivity to increased CO₂ and temperature compared to the C₃ species, and results to support this expectation are forthcoming. Our findings will provide new insight into plant acclimation response to new growth environments, which can be incorporated into global land surface models in order to improve the accuracy of predictions of ecosystem functions.

Structural equation model to quantify importance of patient factors and wound microbiome on healing.

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Keywords: Microbiome; Chronic Wounds; Predictive Modelling; Structural Equation Modelling

Background: The contribution of microbiome and host factors to driving chronicity and rate of healing in wounds is widely appreciated. However, there is currently little ability to account for the many variables and dynamics influencing differences in healing. Here, with the goal of developing a predictive framework, a novel structural equation modelling (SEM) approach was employed to model the chronic wound environment in relation to healing.

Methods: The dataset consisted of 565 chronic wound microbiomes detected at initial patient visit using 16S sequencing paired with patient medical information. A novel pre-modeling parcel optimization routine was developed to transform the microbiome species table into two latent variables that related to healing time either positively or negatively. These latent constructs in addition to specific species correlating with healing, and patient/wound data were evaluated for model fit in the SEM using backward selection and delta chi-squared testing.

Results: A microbiome latent construct significantly associated with improved healing was validated, and the final SEM included this latent construct plus three species associated with diminished healing (*Anaerococcus vaginalis*, *Finegoldia magna*, *Pseudomonas aeruginosa*), as well as smoking, wound volume, slough, exudate, edema, percent granulation, and wound type. This model explained 49% of variation in healing time with the microbiome contributing the largest proportion of variance explained. Species that formed the latent construct tended to correlate with each other less than did the remaining species ($p < 0.001$), potentially reflecting that species associated with faster healing act individually rather than synergistically.

Conclusions: This study provides a novel pre-modeling approach allowing the integration of microbiome data into SEM. The final model validated the importance of many variables on differences in healing time, with wound microbiome species being the most important. The importance of microbes in this model advocates for the efficacy of guiding treatment based on results of DNA sequencing-based microbiota profiling.

Wide geographic survey with new PCR screen reveals plant-parasitic nematodes host diverse hidden endosymbionts.

Kaur, Amandeep (1); Brown, Amanda (1)

Keywords: PCR survey; plant-parasitic nematodes; endosymbionts; community genome skimming; Wolbachia; Cardinium

Wolbachia and Cardinium, two endosymbionts harbored by plant-parasitic nematodes (PPNs), exhibit diverse roles ranging from mutualists to reproductive manipulators in different hosts. Despite their various functions observed in non-PPN hosts, their distribution, prevalence, diversity and roles in PPNs remain unknown. The scarcity of fully sequenced representative genomes and difficulties in culturing PPNs on the media plates under laboratory conditions is a limitation in understanding their roles in PPN hosts. In this study, nematode communities were sampled from different locations covering grasslands, forests, and farms across 23 U.S. states with an aim to investigate the endosymbionts hidden within nematode communities. To determine the presence/absence of Wolbachia and Cardinium in PPN communities, a novel PCR assay was developed using primers specific to PPN-type Wolbachia and Cardinium. The primers were designed using Geneious Prime with alignments to PPN-type strains recently discovered or extracted from database mining. Out of 310 PPN communities screened, 35% and 45% tested positive for Wolbachia and Cardinium respectively. Primer specificity was further confirmed by Sanger sequencing of the PCR products followed by phylogenetic analysis. Sequences clustered with known PPN-type Wolbachia and Cardinium, but also formed numerous other deep branches, basal to all other known strains. This high prevalence was unexpected but suggests a hidden world of endosymbionts yet to be discovered. Despite being more prevalent than Wolbachia, Cardinium exhibited a negative co-occurrence, indicating exclusion. Future work will focus on whole genome sequencing of these endosymbiont-hosting communities and from polished genomes conducting functional enrichment analyses across genes and pathways to infer the potential roles of these mysterious endosymbionts.

Transcriptomic assessment of sorghum root exudate, sorgoleone, on root-lesion nematode gene expression.

Kaur, Taranjot (1); Brown, Amanda M.V (1)

Keywords: Transcriptomics; sorghum; root exudates; sorgoleone; root-lesion nematodes

Management of root-lesion nematodes (*Pratylenchus penetrans*) poses a major challenge. To help protect against *P. penetrans*, various cover crops such as carrot, oats, onion, radish, and marigold have been tested, but their beneficial effects were short-term. As an alternative strategy, this study investigated anti-nematode effects of sorghum. Sorghum as a green manure was shown to be effective in protecting against root-knot nematodes. Such benefits may be due to compounds released from plant roots. Some root exudates facilitate infection and damage by plant parasitic nematodes, whereas others indirectly or directly reduce this damage. The compound sorgoleone is a well-studied exudate from sorghum root hair which is known to suppress the growth of plants in the surrounding area due to its allelopathic properties. Furthermore, a wide range of bacterial taxa across the rhizosphere are known to be either inhibited or promoted by sorgoleone. Allelopathic compound research may therefore be an essential component of nematological research. Our analysis focused on evaluating the effects of sorgoleone on *P. penetrans*. We extracted sorgoleone from *Sorghum bicolor* roots and exposed the field-sampled mixed population of *P. penetrans* to this compound. Nematode RNA was extracted to analyze the changes in gene expression in response to sorgoleone exposure. Differential gene expression was calculated using DeSeq2. In future, combining analyses of gene expression changes and behavioral changes in *P. penetrans* in response to sorgoleone will help clarify mechanisms underlying the effectiveness of sorghum as cover crop against *P. penetrans* and provide potential avenues for breeding enhanced sorgoleone-secreting varieties of crops.

A SINE-based method to reconstruct concordant phylogenies across Chiroptera.

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Keywords: retrophylogenomics; non-autonomous transposons; low-homoplasy; bat taxonomy

Chiropteran taxonomy has been a historical challenge, with traditional methods relying on morphological and karyotypic features. Recent advancements in DNA sequencing technologies have improved phylogenetic hypotheses, yet uncertainties persist. This work introduces a large-scale analysis of Short INterspersed Elements (SINEs) in bat genomes as phylogenetically informative markers. I recovered over 1 million SINEs and performed a proof-of-concept retrophylogenetic analysis of 10 vespertilionid species and used 100 thousand ortholog SINEs for tree inference. Two trees were reconstructed, both of which support introgression events between certain bat lineages, especially in the genus *Myotis*. I also reaffirm the placement of *M. brandtii* as a sister clade of the New World myotines and propose a novel relationship between *M. myotis* and *Eptesicus fuscus*. This SINE-based approach concurs with previous studies that make use of UCEs and quartet based methodologies, despite our use of a very limited subset of taxa. These findings have implications for understanding the relationships among Vespertilionidae tribes and showcase the potential of SINE-based methods in phylogenetics in the genomics era.

Analyzing hidden symbionts in sequence archives using a novel database mining software tool “SRAMiner”.

Sharma, Era; Brown, Amanda M. V.

Keywords: Computational Biology, Wolbachia, Bioinformatics, Novel bioinformatic tool, Python

Wolbachia is a widespread bacterial endosymbiont of arthropods and nematodes that plays a range of important functions in its hosts. This endosymbiont is best known for its ability in many insect hosts to manipulate host reproduction by inducing cytoplasmic incompatibility (CI) wherein infected males mate with uninfected females and produce failed progeny. The discovery of Wolbachia in plant-parasitic nematodes (PPNs), which cause over \$100 billion in crop loss annually, has become a focus of ongoing genomic studies. However, to date, the distribution and role of Wolbachia in PPNs remains unclear. Current investigations seek to address the question of whether Wolbachia plays a beneficial role in PPNs such that a disruption of this symbiosis could release the PPN parasitism burden on the plant. The goal of the present study was to develop a novel, highly computationally efficient software tool to rapidly search for hidden PPN Wolbachia sequences in the hundreds of thousands of Top 10 PPN, rhizosphere datasets in public sequence repositories (i.e. in the National Center for Biotechnology Information’s Sequence Read Archive, SRA), then extract and comparatively analyze resulting data from amplicon sequencing data, whole genome shotgun sequencing data, and metatranscriptomics data. For this, a data mining software tool was created with an easy command-line interface that takes user keywords (e.g., sequencing method, target species, sampling type, etc.) and rapidly mines associated SRA files to discover and analyze endosymbiont genomes. The Python code narrows the input read file size by an iterative blast before engaging in an intensive computational analysis, including a custom iterative re-assembly. Additionally, this software can be used for similar data mining screens for any other target genes, genomes, or taxa from SRA databases.

Occupancy, activity patterns and relative abundance of the lowland tapir (*Tapirus terrestris*) in Arauca, Colombia.

Alviz, Ángela (1); Stevens, Richard (2); Salazar-Bravo, Jorge (3).

Keywords: Occupancy, habitat loss, lowland tapir, conservation strategies.

The lowland tapir has the broadest geographic range of all tapir species. Populations have decreased by approximately 33% over the last three generations due to habitat loss, forest fragmentation, and poaching. Despite available information, studies on tapirs in the Colombian Orinoquia are fragmented. The project aimed to estimate the tapir's occupation, activity patterns, and relative abundance in Arauquita, Puerto Rondón, and Cravo Norte (Arauca). The highest probability of occupation was found in Puerto Rondón, which is influenced by deforestation processes and the availability of food. The area with the highest concentration of individuals is believed to be here, due to the well-preserved forest cover. In contrast, the likelihood of occupation in Cravo Norte is influenced by fires and the availability of food. Lastly, in Arauquita, the results vary significantly, with roads and the presence of water being the main determining factors. The municipality is under pressure, which is endangering the tapirs. Over the last 30 years, 70% of the forest cover has been lost. The results provide insight into the factors affecting the tapirs, which is crucial for developing conservation strategies in the area.

Lipophosphoglycan shields Leishmanial GPI-anchored proteins from the pore-forming toxin aerolysin.

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Keywords: Aerolysin, Leishmania, GPI anchored proteins, sphingolipids, sterols ,small pore forming toxin, Aeromonas hydrophila

One neglected tropical disease that affects over 12 million people and puts 367 million people at risk is Leishmaniasis. Leishmaniasis is caused by *Leishmania major*. *L. major* is spread via sandfly bites. The site of the sandfly bite forms a lesion that is exacerbated by secondary bacterial infections. Bacteria involved in secondary infections include Gram-negative *Aeromonas* and *Pseudomonas* spp. How bacteria compete with *L. major* in lesions for limited nutrients is unknown. *Aeromonads* can produce the beta pore-forming toxin aerolysin, which binds to GPI anchored proteins. Two major GPI anchored Leishmanial virulence factors are LipoPhosphoGlycan (LPG) and gp63, which promote infectivity and survival of the parasite respectively. Prior data suggests the GPI anchor of gp63 failed to bind aerolysin in *L. major* promastigotes, yet bound aerolysin when gp63 was expressed in hamster cells. In contrast to these findings, we observed binding of aerolysin to *L. major* promastigotes and killing of promastigotes. We tested the hypothesis that *L. major* uses LPG to prevent the oligomerization of the GPI anchored proteins needed for aerolysin pore formation. Using flow cytometry, we found that aerolysin bound to the Leishmanial plasma membrane independent of gp63 or LPG. Loss of LPG or gp63 altered cell killing. Loss of LPG enhanced aerolysin cytotoxicity, suggesting LPG shields the Leishmania plasma membrane from agents that bind GPI-anchored proteins. Interestingly, loss of gp63 removed the ability of *L. major* to activate aerolysin but conferred no resistance on activated aerolysin. This suggests that the metalloprotease activity of gp63 can activate aerolysin, like furin. Domain analysis of aerolysin suggests the GPI-anchor binding large lobe was more important for killing *L. major* promastigotes than the glycan-binding small lobe. In contrast to LPG and gp63, loss of sterols or sphingolipids failed to alter *L. major* sensitivity to aerolysin. Based on these results, we suggest LPG protects *L. major* from competition by *Aeromonads* and other bacteria using pore-forming toxins like aerolysin.

Identifying Solutions to Local and Landscape-Scale Connectivity Loss for the Sonoran Desert Tortoise.

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Keywords: connectivity; habitat selection; animal movement; GPS telemetry; desert tortoise

Wildfire, the invasion of non-native grasses, human development, and linear barriers like roads are replacing habitat and reducing landscape connectivity for the Sonoran desert tortoise (*Gopherus morafkai*). These processes are largely driven by anthropogenic activities and are increasing in severity throughout the Sonoran Desert. Studies examining landscape connectivity, habitat use, and disturbance that may inform management plans specific to the tortoise are few. Denied listing under the Endangered Species Act (ESA) in 2022, management plans for *G. morafkai* are largely dependent on our knowledge of other North American tortoises protected under the ESA. We used graph-theoretical models to quantify habitat patch importance for facilitating landscape connectivity, and to estimate changes in structural connectivity throughout *G. morafkai*'s range. We used integrated step-selection analyses (iSSA) to quantify fine-scale habitat selection by *G. morafkai* and to examine how their movement behavior is influenced by roads. On the landscape scale, we found that structural connectivity is most compromised in the northern half of the species' range and that the effects were most severe for dispersal distances under 10 kilometers. On a localized scale, we found that areas of moderate terrain ruggedness and vegetation cover, and areas near desert washes may facilitate tortoise movement. Tortoises avoided areas close to low-traffic roads and dense vegetation, which may constrain movement. Together, our results suggest that local management actions (e.g., restoring unused roads and preventing the invasion of non-native grasses) may enhance landscape connectivity for the species.

Pilot study for future non-invasive population genomic study of black bears (*Ursus americanus*) in West Texas.

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Keywords: Population genomics, *Ursus americanus*, shotgun sequencing, pilot study, enrichment

American Black Bears (*Ursus americanus*) are diurnal, solitary, wide-ranging carnivores and are considered a keystone species in North American ecosystems. Black bears, which were believed to have been exterminated from Texas by the mid-1900s due to habitat destruction and hunting, are now recolonizing parts of their former range in West Texas. Most bear population genetics studies have been concentrated in the northern and southeastern regions of North America, with a few additional studies in southwestern Texas. Although earlier work provided a hypothesis of bear genetic structure in West Texas, these investigations relied on either examining mitochondrial DNA sequences or a limited number of microsatellite markers. Accurately inferring demographic characteristics and genetic variability of populations requires whole-genome sequencing data. This study aims to explore the feasibility of a population genomics study of black bears using shotgun sequencing from scat. For this pilot study, we used fecal samples from six black bears. Samples were homogenized, and divided into subsamples, and some of them underwent selective methylation enrichment for eukaryotic DNA and were subsequently sequenced using 2×150 bp sequencing on an Illumina NovaSeq 6000. Reads were then aligned to the reference genome using bowtie2. Enrichment samples exhibited a significantly higher proportion of bear DNA and read length distributions reveal that bear DNA was significantly more degraded than non-bear DNA in the sample. Read mapping showed that on average across samples about 10% of reads were aligned to the bear genome. This study establishes the groundwork for sample processing and sequencing analysis expectations and informs the protocol for a larger forthcoming study.

Comparison of phylogenetic analysis for resolving IAV subtypes.

Rowell, Austen (1), Bono, Lisa (2)

Keywords: Bayesian; Influenza; Phylogenetics

Bats are known to harbor a variety of viruses. While influenza A (IAV) is known to infect a broad host range, such as birds and mammals, they have been under sampled in bats. New IAV subtypes (H17/H18) were discovered in South American bats. These novel strains are important due to the receptor used for attachment. The standard receptor for IAV is α 2,3 sialic acid in birds or α 2,6 in human infection. H17/H18 subtypes are unique by attaching to major-histocompatibility complex class II (MHC-II). To better understand the evolutionary relationship, we compared H17/H18 to IAV subtypes. We selected 60 representative nucleotide sequences for each of the 8 genomic segments from NCBI's RefSeq database. A maximum likelihood phylogeny (IQ-Tree) and Bayesian time constrained model (BEAST) were produced to compare the relationship of H17 and H18 to IAV strains. A comparison of the trees overlaid by isolated host and subtype yielded no consistent pattern that would indicate the strains arose from a single subtype of IAV. Most trees from both pipelines support early divergence of H17 and H18 from other IAV subtypes forming distinct clades. The tree analysis of the attachment protein hemagglutinin (HA) supports the IAV subtyping as well as the Bayesian approach for the polymerase protein (pb2) segment. The most important finding came from the polymerase subunit (pb1) segment that placed H17/H18 within the influenza B (IVB) outgroup. This suggests that H17/H18 certain segments share a more recent common ancestor with IVB than IAV subtypes resulting from a genetic exchange event.

Combinatorial chlorogenic acid and cinnamaldehyde demonstrated anti-metastasis and apoptosis induction in MCF7 and MDA-MB-231 breast cancer cells.

Olayiwola Yusuff; Lauren Gollahon

Keywords: Natural compounds; Chlorogenic acid; Cinnamaldehyde; Breast cancer; Metastasis.

The majority of reported breast cancer-associated deaths are directly associated with metastatic disease. Furthermore, the nature of current metastatic cancer treatments detrimentally impacts all organ systems. Thus, there remains the need for more effective and safer strategies to treat metastatic breast cancer at a systemic level. Recently, more attention has been given to Natural Products as candidate anticancer approaches. This study is aimed at investigating the synergistic impact of two such natural compounds, chlorogenic acid and cinnamaldehyde (CGA and CA). We hypothesize that CGA and CA in combination, will decrease metastatic potential of breast cancer cells by suppressing their invasive and migratory abilities by restoring E-cadherin expression and concurrent downregulation of N-cadherin, and MMP-9. We also hypothesize that cell death will occur through downregulation of Akt activation pathway. To test this hypothesis, wound healing and Boyden Chamber assays were conducted to examine the impact of the combination on the migratory and invasive ability of the cells. Western blotting was conducted to investigate the effect of the natural products on expression-cadherin, N-cadherin, AKT, caspase 3 and BCL2. Apoptosis was determined by Annexin V /propidium iodide fluorescence microscopy and FACSsort.

Results showed that CGA and CA significantly inhibited cancer cells growth and induced apoptosis. The anticancer effect of the compounds was mediated via downregulation of Akt activation as evidenced by decreased phosphorylated Akt expression. The expression levels of caspase 3 and Bcl2- α were increased and decreased respectively, thus promoting apoptosis in the cancer cells. Inhibition of metastasis was evidenced by restoration of epithelial characteristics such as increased expression of E-cadherin and downregulation of N-cadherin, and MMP-9 expression was attenuated. Overall, the present study demonstrated that CGA and CA combination downregulates Akt pathway and arrests the malignancy and metastasis of both triple-positive and triple-negative breast cancer cell lines.

A Tale of Two Plants: Comparing the genetic diversity of two endemic and widespread congeneric pairs.

Bullock, Madison (1); Johnson, Matt (1)

Keywords: *Chaetopappa*; *Salvia*; endemic species; conservation genetics; Angiosperms353; microhaplotypes; evolutionary potential

Though there has been some headway into research of specific species or ecosystems, it is still largely unknown why certain species have incredibly narrow ranges while their close relatives are able to exist across vast distributions of habitats. Endemic species can be highly adapted to narrow geographic areas and are limited by restricted distributions, smaller effective population sizes, lower genetic diversity, and lower reproductive capacity. Though not necessarily always rare, endemic species can possess important evolutionary potential, or the capacity of a population to evolve in response to environmental change, within an ecosystem that could be lost upon extinction. Widespread species, on the other hand, are generally thought to occupy more generalized distributions, have larger total and effective population sizes as well as relatively higher genetic diversity at the population level. Some closely related species share many life history traits that make them particularly interesting in studying the causes of genetic diversity and susceptibility to ecological threats, though this is not always the case. Therefore, if the goal is to protect evolutionary potential, then it is possible that conservation management focused on rare species alone might not protect the most evolutionary potential in a population or ecosystem. Here, we use case studies of two endemic plant species from the Guadalupe Mountains National Park (*Chaetopappa hersheyi* and *Salvia summa*) and compare their population genetic demographics to their widespread congeners (*C. ericoides* and *S. farinacea*) to understand the conservation implications of endemism with special focus on the development of a new bioinformatic pipeline using microhaplotypes.

Elucidating the roles of phosphatidylserine synthase and phosphatidylserine decarboxylase in the lipid homeostasis of Leishmania parasites.

Ossai, Chioma (1); Bhakta, Om (2); Zhang, Kai (3)

Keywords: "leishmania" "lipid synthesis" "phosphatidylserine"
"phosphatidylethanolamine"

Leishmania is a protozoan parasite and the causative agent of leishmaniasis which is an infectious disease affecting 12 million people worldwide, mainly in parts of the tropics, subtropics, and southern Europe. The common forms of leishmaniasis are cutaneous, mucocutaneous, and visceral and the most common clinical symptoms in people who develop the disease are sores on their skin. Available treatments used to treat leishmaniasis are becoming ineffective with increasing resistance. Moreover, there are gaps in the current knowledge of the cellular mechanisms important to the parasite. One major component of most cells is the different lipids important to their membrane structure, energy metabolism, and cellular signaling. Leishmania parasites synthesize lipids that are different from those produced in mammalian cells, thus presenting an opportunity to utilize lipids as important potential drug targets. By understanding the function and essentiality of the enzymes involved in lipid synthesis, we can discover the key enzymes that could be potentially inhibited to hinder parasitic growth. My project is to investigate the essentiality and role of phosphatidylserine synthase (PSS2) and phosphatidylserine decarboxylase (PSD) in Leishmania major parasites. These two enzymes, PSS2 and PSD are involved in the synthesis of phosphatidylserine and phosphatidylethanolamine which make up a significant percent of lipids in the parasite. Previous research has shown that in other trypanosomatids, these enzymes are essential and play a crucial role in maintaining mitochondrial function. Understanding the function of these enzymes can give insight into the biology of Leishmania parasites and offer potential novel strategies for treating leishmaniasis.

Using machine learning techniques to assist in predicting the location of mesquite on the Southern Plains.

Dawsey, Justin (1); McIntyre, Nancy (1)

Keywords: machine learning; classification algorithms; conservation; woody species encroachment

Honey mesquite (*Prosopis glandulosa*) encroachment is problematic on the Southern Plains due to its tendency to reduce the amount and quality of habitat for wildlife and grazing animals through both space and water use. Once the species has established itself, it is difficult to reduce, showing resistance to fire, disking, and grazing. Increased carbon emissions and elevated temperatures have also allowed the species to compete more effectively against other natives, causing it to become an increasingly noxious weed. Together these issues raise the importance of being able to effectively identify where it occurs on the landscape as well as where it may potentially encroach next. We used Google Earth Engine to run X-means clustering on National Aerial Imagery Program data randomly selected 314 sq km circular areas in New Mexico and Texas. Accuracy assessment points were generated for each area to confirm locations of clusters deemed “mesquite.” Soils data (percent clay, water-holding capacity, organic carbon content) from OpenLandMap and Bioclim data (mean annual precipitation, annual mean temperature, and annual temperature range) were added to each of these points. A logistic regression was then created to measure the log-odds of mesquite presence. We found that mesquite presence showed significant negative associations with mean annual precipitation, organic carbon content at 30 cm depth, and soil water-holding capacity at 30 cm depth, and was positively associated with clay content at the surface. These methods provide an easily reproducible and scalable way to assist with image classification of plants from remotely sensed imagery. The results from this study will also be useful in predicting where mesquite encroachment is likely to occur in the future on the Southern Plains.

Association between mindset and study strategies is mediated by undergraduates' error reactions.

Chouvalova, Anatasia (1), Navlekar, Anisha (1), Adams, Mikayla (1), Daye, Sami (1), De Anda Fatima (1), Limeri, Lisa (1)

Keywords: "mindset"; "implicit theories of intelligence"; "lay theories"; "study strategies"

Various study strategies are employed by undergraduate STEM students. Furthermore, study strategies widely differ in their effectiveness in promoting deep content mastery. For example, efficient study strategies include self-testing and spacing out study sessions while inefficient study strategies include using flashcards and rereading material. Study strategy interventions also differ widely in their efficacy in promoting the use of efficient study strategies to students; telling students that a given strategy is effective does not guarantee they will adopt it. While it is well-known that the cost (time, psychological, resources, effort) associated with a given strategy often determines how likely a student is to use it (Rea et al., 2022), there are multiple other factors impacting students' decisions about how to study and prepare for assessments. We hypothesized that students' beliefs about errors and reactions to errors mediate the association between their lay theories of intelligence (i.e., mindset, universality, and brilliance beliefs) and their study strategy use. This hypothesis was tested by collecting survey responses from 345 undergraduate introductory biology students attending a northwestern American institution. We found that only one implicit belief, mindset (not universality or brilliance), predicts beliefs about errors as well as reactions to errors. Adaptive error reactions predict the use of effective study strategies and use of spacing. A significant indirect relationship was noted between a growth mindset and use of spacing. This indicates that study strategy interventions should consider including modules promoting a growth mindset and modules promoting positive and adaptive responses to errors.

Bats amidst declining forests: unravelling the impact of land-use changes on bat assemblage structure in northeast Bangladesh.

Ul Hasan, Md Ashraf (1); Kingston, Tigga (1)

Keywords: Bangladesh; bat assemblage; species diversity; land-use change; conservation

Bangladesh's forest ecosystem is rapidly declining due to extensive human population growth and anthropic activities. Bats play a pivotal role within forest ecosystems, serving as indicators of biodiversity health and exhibiting sensitivity to land-use changes. However, there is a need for data on bat species diversity and their response to land-use changes in Bangladesh, a country lacking bat research. Our goal was to assess the impact of land-use changes on bat assemblages in 3 protected areas (PAs) of northeast Bangladesh. We categorized PAs into two land-uses: forest and degraded based on the level of habitat modification. Each PA contained two localities representing differing land-uses in proximity, establishing a paired design for comparison. We captured bats using four-bank harp traps and mist nets in the summers of 2022 and 2023, dedicating a total of 62 nights of trapping efforts. This involved 6201 hours of mist netting (net length in meters x hours deployed) and 779 hours of harp trapping (total hours dedicated to trapping). Our captures yielded 892 individuals across 17 species within 5 families. Species richness was neither significantly different between land-uses, nor among the localities, species abundance varied significantly between land-uses, and across different localities, showing a higher proportion of captured individuals in degraded habitats compared to forests. This might indicate that changes to natural habitats could be affecting the population of individual species without affecting the overall diversity. Beta diversity between the land-uses showed no significant differences. This finding suggests both land-uses support comparable species composition. Conclusively, while natural forests and degraded habitats within the PAs continue to serve as refuges for bat assemblages in northeast Bangladesh, our study emphasizes the need for further research on the adaptability of bats persisting in both natural and degraded habitats and identify conservation approach that optimizes the conservation value of degraded habitats.

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

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Keywords: *Pseudomonas aeruginosa*, Antibiotic resistance trade-off

Random mutations in the bacterial genome can provide evolutionary advantages 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 has been observed with antibiotic sensitivity, in which resistance to a particular antibiotic can make bacteria sensitive to other antibiotics, a process known as collateral sensitivity. This research aims to identify potential vulnerabilities in drug-resistant *P. aeruginosa* to treat infection and restrict the emergence of antibiotic resistance. 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.

Does habitat association predict patterns of genetic diversity, differentiation, and divergence in co-distributed species?

(1) Hruska, Jack; (1) Manthey, Joseph.

Keywords: phylogeography, population genetics, genomics, community assembly

How natural communities assemble is a central goal of evolutionary biology. A popular approach to test the tempo and mode of community assembly is comparative phylogeography, wherein the population genetic patterns of co-distributed species across geographical or ecological barriers are examined to evaluate the historical drivers of community assembly. Historically, the divergence of species across barriers was assumed to be governed by vicariant events, such as the orogeny of geographical features or the spatial reconfiguration of habitat. In a comparative phylogeographic framework this model leads to the prediction that species will show concordance in divergence times that is temporally aligned with the emergence of a geographic or ecological barrier. Alternatively, discordance in this case would result from stochasticity in how species interact with barriers through time. One of the factors that can mediate the interaction of species to barriers are species-specific traits that govern dispersal propensity and persistence across landscapes. One such trait that is predicted to affect patterns of population genetic isolation, through differences in the amount of gene flow, is the degree of specificity in habitat preference. For example, in accordance with the specialist-generalist variation hypothesis (SVGH), habitat specialists (those restricted to one or a few habitat types) are anticipated to show reduced rates of gene flow between populations, increased population structure, decreased genetic diversity, and concordant divergence times. Here, we test if genetic diversity and divergence across geographic and ecological barriers is predicted by degree of specificity on pine-oak habitat. In particular, we sample five species of co-distributed birds (three specialists, two generalists), and ask whether these patterns manifest as expected across barriers. We find mixed support for the SVGH: habitat specialists showed increased genetic diversity, but also demonstrate evidence of greater population structure.

Structure-function studies on Grapevine Red Blotch Virus to elucidate disease etiology.

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Keywords: Grapevine red blotch disease; Grapevine Red Blotch Virus; Geminiviruses; Post-transcriptional gene silencing; small RNAs.

Grapevine red blotch disease (GRBD), first identified in 2008 in California has now become a major threat to viticulture across U.S., and around the globe, because of its secondary spread by insect vectors such as alfalfa hopper and erstwhile nursery propagation of infected materials, respectively. The causal organism of this disease was identified to be Grapevine Red Blotch Virus (GRBV), which has a monopartite, ssDNA genome belonging to the Geminiviridae family of plant viruses. GRBD leads to economic losses to vineyards once infected, and there is no known cure against GRBV or convincing evidence to date that rouging (removal of infected and neighbor vines) prevents spread. My PhD dissertation focuses on understanding mechanisms by which GRBV establishes successful host infection, particularly its impact on host post-transcriptional gene silencing (PTGS) pathways, resulting in symptoms like leaf anthocyanin accumulation and altered gene expression. As geminiviruses are the triggers and as well as targets of host PTGS, viruses have developed counter-defense mechanisms such as viral suppressors of RNA silencing (VSR). Previous work in the lab identified C2 and V2 proteins as VSRs. I am proposing to test further the known spliced GRBV mRNAs V1:V3, C1:C2 and V0:V2 translated proteins in a facile transient Agroinfection assay in 16c GFP marker *Nicotiana benthamiana* for their host PTGS suppressing activities. In addition, I plan to identify the host sRNA targets of the putative VSRs by degradome sequencing and additionally performing protein-protein yeast-two-hybrid interaction and sRNA binding studies. I will test by Agroinfection of GRBV partial dimer construct the resistance to GRBV replication and disease symptoms of available C2 and V2- hairpin-expressing transgenic grapevine plants. Thus, my work can result in new information about molecular mechanisms of GRBV etiology relevant to practical applications for breeding/engineering grapevine resistance against GRBV to benefit viticulture and industry stakeholders.

Cancer cells fool immune dendritic cells via the secretion of asymmetric dimethylarginine.

Pearce, Lilly; Chen, Ethan.

Keywords: Prolactin, ADMA, Dendritic cells, Tumor immunity

Tumor microenvironment plays a pivotal role in cancer growth and metastasis, and is immunosuppressive. Small molecules secreted by tumor cells contribute to immune evasion. Two molecules, prolactin and asymmetric dimethylarginine (ADMA), are significantly produced and secreted by tumor cells. While prolactin is a well-known lactating hormone and is produced by anterior pituitary gland, its expression outside the scope of pituitary and lactation has far less discussed. ADMA is a metabolite generated by proteolysis of methylated proteins, and its impact on tumor progression and tumor immunity remains unclear. To investigate the effects of prolactin and ADMA on the modulation of dendritic cell functionality, we utilized mouse triple negative breast cancer cells (EO771 and Py230) and mouse dendritic cells (DC2.4) as a model system. Dendritic cells are important immune cells that bridge between innate and adaptive immune responses through phagocytosis, antigen presentation (either direct or cross priming), and T cell activation by co-stimulatory ligand expression. In this study, we show prolactin, but not ADMA, promotes dendritic cell proliferation. To examine the phagocytic capacity of dendritic cells, tumor antigens are labelled with pHrodo dye which fluoresces only when tumor antigens are consumed and present in the low pH phagolysosomes. Both prolactin and ADMA increase phagocytosis of tumor antigens by dendritic cells. However, ADMA reduces surface tumor antigen presentation indicating a negative impact of ADMA in the antigen processing and loading pathways. Additionally, it is interesting to show that most tumor antigens are cross-presented by MHC I rather than MHC II, and dendritic cells treated by ADMA have a trend with lower expression level of co-stimulatory ligand, CD80. In summary, the tumor derived ADMA negatively regulates dendritic cell functions including antigen presentation and co-stimulatory ligand expression. Future investigation on the mechanistic actions of ADMA could foster the development of novel therapeutics for cancer treatment.

Tick spatial distribution: unravelling the landscape of cCHF risk in Uganda's cattle corridor.

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Keywords: Ticks; Spatial temporal distribution; CCHFV

Background: Ticks are obligate ecto-parasites of wild and domestic animals. They transmit various pathogens which cause diseases including zoonotic infections such as Lyme disease, babesiosis and Crimean-Congo hemorrhagic fever (CCHF). CCHFV, is an RNA virus which causes a severe infection with a fatality rate of 30% and more. Primarily transmitted by *Hyalomma marginatum*, this disease has been reported in Africa, Middle East, Southern and Eastern Europe. However, knowledge gaps exist on vector distribution, virus ecology and risk factors driving CCHF outbreaks. Understanding the dynamics of tick species populations and associated risk factors is therefore crucial for effective CCHF prevention and control.

Method: A survey was conducted in 6 districts to determine tick species abundance, distribution, and acaricide use in Uganda. Ticks were sampled from 218 domestic animals. Morphological and molecular analysis (16S rRNA amplicon sequencing) was used for species identification. In addition, the impact of the frequency of acaricide treatment on tick abundance on animals was assessed.

Results: A total of 10,725 ticks were collected comprising seven species. *Rhipicephalus lunulatus* which had not previously been documented in Uganda was identified in this study. There was significant variation ($P < 0.05$) in species diversity across the six districts with the highest diversity in North-East. *R. appendiculatus* was the most wide spread and had the highest abundance and accounted for 62% of the total tick collection. Despite the recurrent CCHF outbreak in the cattle corridor, *Hyalomma* species was not recovered throughout the districts surveyed. Acaricide use varied significantly ($P < 0.05$) across the districts with households in North East reporting lowest use.

Conclusion: This study indicates that *Hyalomma spp.* may not be the primary vector of CCHFV in Uganda. Results from this study contributes vital information for the development of evidence-based strategies for CCHF prevention and control including tailored acaricide application and targeted surveillance programs.

Loss of Dnase1L3 triggers lupus-like phenotypes and neurological degeneration in mice.

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Keywords: Lupus; SLE; autoimmunity; neurology; NPSLE; neurobiology; immunology; behavior

One leading cause of death in women is the chronic autoimmune disease Systemic lupus erythematosus (SLE). Out of all people with SLE, 40% have brain, nerve, or spinal cord complications, causing neuropsychiatric systemic lupus erythematosus (NPSLE) and increased risk of vascular dementia. Neuropsychiatric symptoms can be caused in part by the targeting of NMDA receptors by anti-dsDNA antibodies. Destruction of DNA could represent a new therapeutic target for NPSLE, but the contribution of DNA to NPSLE is poorly understood. The endonuclease Dnase1L3 is secreted by myeloid cells, and digests antibody-DNA complexes. While absence of Dnase1L3 in humans causes pediatric-onset SLE, and moderate lupus-like symptoms in mice, its role in NPSLE remains poorly defined. Here, we hypothesized that loss of Dnase1L3 causes phenotypes representative of NPSLE through the accumulation of anti-dsDNA antibodies and polarization of microglia to M1 phenotypes in the central nervous system. To test this hypothesis, we measured behavior, immunophenotype, brain histology, and brain immunohistochemistry in Dnase1L3^{-/-} mice. Initial behavioral analyses using the Open Field Maze suggest anxiety-like phenotypes in old Dnase1L3^{-/-} mice. Analysis of brain immunohistochemistry showed a significant increase of glial fibrillary acidic protein (GFAP) surrounding the hippocampus in Dnase1L3^{-/-} mice. GFAP is upregulated in response to CNS injury such as a traumatic brain injury, and increased expression is indicative of hippocampal neurodegeneration. Dnase1L3^{-/-} mice further showed an increase in MAP2 expression in the hippocampus, suggesting a compensatory effect of damaged neurons. These data suggest loss of Dnase1L3 contributes to NPSLE-like phenotypes in mice. Therefore, attempts to restore Dnase1L3 expression, such as Dnase1L3 replacement therapy, may represent an effective novel treatment to reduce neuropsychiatric complications of SLE.

Melanoma antigen (Mage proteins) in spermatogenesis during fasting: A single-cell transcriptomic perspective.

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Keywords: Spermatogenesis; Nutrient stress; Single-cell RNA-sequencing.

Melanoma antigens (MAGEs) are tumor antigens that serve as ubiquitin ligase regulators; however, their physiological function is not yet known. We recently showed that melanoma antigen A (MAGEA) genes protect male germline in times of food scarcity. However, the underlying molecular mechanisms are not understood. Here, we investigated the impact of food restriction and the role of Mage proteins during nutritional stress on a single-cell level.

12-months-old wild-type (WT) and MAGEA knock-out (KO) mice were exposed to 4 months of nutrient restriction (80% of initial body weight). To address the effect of caloric restriction on spermatogenesis, we performed single-cell analysis.

We observed a significant increase in corticosterone serum levels in fasted mice, suggesting that food restriction is stressful. Fasted animals had a slight decrease in sperm concentration, although the testis weights were not significantly changed. In contrast, when we performed single-cell RNA-sequencing of testicular cells, we found that although fasting has limited effect in WT mice, germ cells and Sertoli cells from KO mice exposed to fasting showed significant differences. In WT fasted animals, we found a very limited number of differentially expressed genes (DEG), suggesting the existence of yet to be discovered protective mechanisms that enable shielding of the germline against environmental stress. In contrast, spermatogonia, meiotic spermatocytes and haploid spermatids show several DEGs in KO mice when exposed to fasting. DEGs are involved in gluconeogenesis, AMPK signaling, and ubiquitination, pathways that may be regulated by MAGEA genes to enable the protection of spermatogenesis during nutritional stress.

Our findings will shed light on the function of MAGEA genes in spermatogenesis in normal conditions and during stress. Intriguingly, our data suggest that the exposure to nutrient stress in the absence of MAGEA genes deregulates ubiquitination networks, suggesting that MAGEA function as ubiquitination regulators may be conserved in humans and mice.

Community Disassembly in Response to Forest Fragmentation Leads to An Expansion of Functional Volume and Niche Space.

Azhar, Isham (1); Sihaloho, Hendra (1); Senawi, Juliana (2); Phillips, Caleb (1); Kingston, Tigga (1)

Keywords: Assembly, Community processes, Disassembly, Functional diversity, Fragmentation, Niche

Deforestation is occurring globally and advancing at alarming rates, particularly in the tropics. This pervasive trend results in the loss of habitats, transforming extensive forested areas into fragmented isolated patches. In this study, we aimed to explore the underlying mechanisms driving the disassembly of assemblages in response to habitat fragmentation. With forest interior insectivorous bats as the focal organisms, we surveyed six continuous forest sites and 27 forest fragments of varying sizes to assess the impact of fragmentation on their functional diversity. We quantified five functional diversity metrics that have been recommended as the most suitable measure for assessing assembly mechanisms. These metrics include functional richness (FRic), functional evenness (FEve), functional divergence (FDiv), functional dispersion (FDis), and mean nearest neighbor distance among coexisting species within the functional space (FNND). The null model analyses indicated that assemblages in the continuous forests were assembled through dual mechanisms: environmental filtering and niche packing. Although assemblages in the fragments exhibited patterns resembling random species loss, we observed an expansion of trait space and decreased trait packing within the fragments. We also found that assemblages characterized by lower taxonomic richness were nested subsets of those with higher taxonomic richness. Although, the nested patterns were not associated with fragmentation. Our findings highlighted the distinctive conservation values of continuous forests, challenging previous notions that they are comparable to larger fragments. We also demonstrated how functional diversity can serve as a tool in identifying priority fragments to maintain diversity at the landscape scale, moving beyond emphasizing fragment sizes and empirical measurements of taxonomic diversity.

Translational Dysregulation of Hypothalamic Hormones in the MAGEL2- KO Mouse Model.

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Keywords: Prader- Willi, MAGEL2, Translation

Introduction: Our objective is to investigate the potential involvement of melanoma antigen L2 (Magel2) in translational regulation within the hypothalamus and pituitary of the Prader-Willi syndrome (PWS) mouse model. We want to know if Magel2 contributes to proper hypothalamic endocrine function also on the translational level, particularly during stress. Translational regulation of gene expression occurs on polysomes and is critical for proper cellular stress response. Dysregulation of protein translation contributes to human diseases. However, if and how it contributes to PWS pathogenesis is not known. Several PWS clinical symptoms suggest hypothalamic endocrine dysfunction. Previous work eluted that Magel2 is critical for proper hormonal secretion of several hypothalamic hormones, including oxytocin, however, the underlying mechanisms are still enigmatic (Chen et al, 20120). **Methodology:** In this project, we performed polysome profiling analysis of hypothalamic and pituitary translatoome of wild type and *Magel2*^{p4/m+} mice exposed to 24h-fasting-induced stress to determine genes whose translation depends on Magel2. We first optimized the polysome fractionation of the hypothalamus and pituitary tissues and then performed the analysis, pooling pituitaries from 3 animals and individual hypothalamus. **Results, conclusions, and future directions:** Our data will provide the first insight into potential role of Magel2 in translational regulation.

Feeding Identity and Wing Morphology: Phenotypic Variability Within the Family Phyllostomidae

Albrecht, Katelyn (1); Thompson, Cody (2); Bradley, Robert (3); Stevens, Richard (4)

Keywords: bats, allometry, modularity, phenotype, variability, morphology

Phenotypic variability among Chiropterans is pervasive across a multitude of geographical, physiological, behavioral, and ecological parameters. This diversity is evident especially within the Family Phyllostomidae (New World leaf-nosed bats), which occur across broad environmental and latitudinal gradients and contain species with high degrees of specialization, particularly with respect to feeding guild identity ranging from sanguivory to insectivory. The inherent variability across Phyllostomids may indicate differential expression of morphological elements related to functional elements that, when compared, may align to ecological radiation or be driven by phylogenetic relationships between species or other taxonomic subunits. Full body micro-CT scans were obtained for 114 species of alcohol preserved specimens from both the Texas Tech University Natural Science Research Laboratory (NSRL) and the University of Michigan Museum of Zoology (UMMZ). Four genera per feeding identity were then selected for analysis, excluding sanguivores with three representative species, with adult males and females represented by two samples each to account for sexual dimorphism. Isolation and measurement of elements, performed using segmentation tools in the imaging softwares Dragonfly and 3DSlicer, include all bones composing the right forelimb from the humerus to distal phalanges, excluding the carpals. Regression and covariation models were used to quantify variance among characters and assess possible allometric and modular components of the skeletal components of the wings at a clade level. Additionally, matrix decomposition was performed to partition variability to describe the relevant contributions of ecological variability and evolutionary trajectory towards phenotypic diversity. Allometric and modular relationships are expected to align to feeding behavior and phenotypic radiation that could be responsible for specialized morphological changes seen in such a large, highly diverse taxa. This analysis, paired with the creation of a comprehensive digital data base, promotes the advancement of highly detailed, expansive morphological analysis in highly expressive, even cryptic, species and functional groups.

Streamlining workflows and generating interactive risk maps for mosquito borne diseases in Connecticut, USA.

Champion Jr, Jerry (1); McMillan, Joseph (1); Armstrong, Philip (2)

Keywords: Risk Mapping; Mosquitos; Arboviruses; Vector-Borne Disease; Epidemiology

In 1999 West Nile Virus (WNV) was first discovered in America, and since then, mosquito surveillance has become the gold standard for monitoring epidemic and epizootic transmission. Despite the prevalence and importance of WNV surveillance programs in the US, there remains critical gaps to communicating risk of WNV, and many other mosquito-borne diseases, to the public, particularly when creating risk maps. To address this common limitation of mosquito surveillance programs, we synthesized results from a series of published investigations using The Connecticut Agricultural Experiment Station (CAES) mosquito and arbovirus surveillance system. We utilized this information from the CAES and made use of a mapping program that is interactive, web-based, and user friendly. Utilizing R, we can rapidly create visual displays of up to 9 mosquito-borne viruses across Connecticut over any chosen timeframe. These visual displays are projected onto a map, and each site has a built-in, interactive table with site-specific data relevant to the public. Sites testing positive are additionally highlighted with a 5km red buffer that communicates the estimated spatial extent of risk surrounding a positive site. While these maps create a targeted view of epidemic risk for public use, more studies are needed to assess how communities understand and utilize risk maps of mosquito borne diseases.

Canopy traits drive plant flammability: shoot flammability of Texas shrubs.

(1) Azaj, Mahmud (2); Dylan, W, Schwilk

Keywords: Shoot flammability; Canopy traits; Leaf traits; Temperature integration; Ignition delay time

Flammability is a trait of land plants, and an understanding of this trait is important for understanding the ecological and evolutionary consequences of fire on plant species in fire-prone ecosystems. Although many studies have examined the flammability of individual leaves, fewer have examined how entire canopies behave as fuel. Therefore, it is still not well understood how the plant traits flammability relationship scales up from the individual to ecosystem level. In this study, we burned branches of 16 native shrubs of Texas and measured four canopy traits: total dry mass per 70 cm branch, canopy bulk density per 70 cm branch, leaf stem mass ratio per 70 cm branch (on dry mass basis) and canopy moisture content and four common leaf traits: leaf mass per area (LMA), leaf area per leaf, leaf length per leaf and leaf moisture content. We used these data to answer two questions: 1) Canopy or leaf traits are better at predicting shoot flammability? 2) What are the dimensions of shoot flammability? We found that canopy traits are more important in determining shoot flammability than leaf traits; total dry mass per 70 cm branch was the best predictor of temperature integration. Furthermore, we found that shoot flammability in shrubs is mostly described by a single axis of variation represented by metrics related to flame duration.

This finding illustrates the potential for incorporating canopy traits in fire behavior models, canopy traits in fire behavior models, and might help forest and fire managers in making well-informed decisions about fuel management. This study represents a significant step towards enhancing our understanding of the fire-fuel feedback in crown fire ecosystems.

Expression of CD44 spliced variants in the regulation of epithelial to mesenchymal transition and metastatic characteristics in breast tumor stem cells.

Pascuzzi, Nicholas (1); Chen, Ethan (2)

Keywords: epithelial to mesenchymal transition; labile iron pool; CD44; prolactin

Epithelial to mesenchymal transition (EMT) is considered as one of the early events in tumor invasion and metastasis. With more deciphering of the tumor microenvironment (TME), the mechanistic actions of molecules and/or stromal cells within the TME to initiate EMT needs to be elucidated. Within the TME, tumor cells secrete prolactin as an autocrine survival loop and the prolactin levels in cancer patients are positively correlated to tumor progression. In our previous study, we discovered prolactin induces CD44 expression which drives intracellular labile iron accumulation in breast cancer cells. CD44 is a cell surface glycoprotein and has been implicated in the regulation of EMT process. However, there are more than 20 different spliced variants of CD44, and the specific spliced variant that involves in EMT is unknown. Additionally, there is no study that links the intracellular labile iron pool to the EMT status. Thus, we aim to investigate the correlations between the intracellular iron level and the mesenchymal transition of tumor cells, and to identify the specific CD44 spliced variant that leads to EMT. Tested by human MCF7 (luminal A breast cancer) and MDAMB468 (triple negative breast cancer) and mouse triple negative breast cancer cells (EO771 and Py230), we show a positive correlation of intracellular iron level and mesenchymal transition of tumor cells (examined by the mesenchymal markers, vimentin, and fibronectin expression). Interestingly, when examining the expression of CD44 spliced variants in breast cancer cells, we find no difference across all spliced variants in non-metastatic bulk tumor cells, but the spliced variant, V3 and V5, are specifically upregulated in the metastatic tumor stem cells. In summary, our results depict a potential new role of iron in tumor metastasis, and the identification of the specific CD44 variants (V3/V5) could ignite new hope for therapeutics development that targets tumor metastasis.

Microbial modulation of γ -Aminobutyric acid in crickets changes territorial-related aggression.

Guerrero, Christian R. (1), Brown, Amanda M. V. (1)

Keywords: gut; brain; cricket; aggression

Guts across all animal life host diverse microbiomes that can communicate with the host's brain to modulate behavior, but how these microbiomes modulate male aggression is unclear. Guts communicate with the brain through the gut-brain-axis (GBA) in a bidirectional manner, whereby gut microbiota and the neuroactive compounds they synthesize send signals to the host's brain through the central nervous system, and signals are sent back to modify gut microbiota function. We hypothesize that microbial-derived metabolites impact behaviors in insects such as aggression consistently to mammals. We developed a novel behavioral paradigm to test our hypothesis using the Mediterranean house cricket, *Acheta domestica*, and a local cricket species, *Gryllus texensis*, which are ideally suited for studying GBA effects on male aggression due to their natural territorial behaviors. The paradigm is based on Chinese cricket fighting where crickets are fought and their chirps, in response to their opponent, are counted. This behavioral assay provides quantitative scales to measure minute behavioral changes in males' aggressive tendencies when afflicted with dysbiosis. Large sample sizes to overcome high variance in behavior and microbiome are achieved using crickets. We predicted that probiotic treatment with *Bifidobacterium longum* BB536 would increase expression of the neurotransmitter γ -Aminobutyric acid (GABA), reducing neuronal excitability within the cricket and reducing male aggression measured as chirp counts. Inversely, we predicted that treatment with vancomycin would deplete endogenous *Bifidobacteria* spp., increasing male aggression and chirp counts. Shotgun sequencing and Hi-C sequencing were performed to uncover details of the microbiota interacting at the host gut, and ongoing analyses such as RNAseq will be performed to assess changes in microbiome and host gene expression to infer GBA functions driving changes in aggression. Complementary experiments changing serotonin (5-HT) transport and measuring metabolite concentrations will be performed next to understand how host-derived-5-HT-secreting cells modify the microbial communities in a manner that also contributes to male aggression.

Variation in reproductive traits among wild rodents along an elevational gradient in the Bolivian Andes.

Revollo-Cadima, Susana (1); Rico-Cernohorska, Adriana (2); Salazar-Bravo, Jorge (1,3)

Keywords: Reproductive season; Litter size; Sigmodontine rodents; Testicular size.

In several rodent species, reproduction is regulated by environmental characteristics. From this perspective, in tropical environments elevation can be an important variable, as resources at higher elevations fluctuate and become more seasonal. Seasonal breeding in mammals synchronize the energetically expensive reproductive activities to coincide with the most favorable annual environmental conditions. Reproductive characteristics are expected to adjust to these conditions (i.e., seasonality), becoming more seasonal at higher elevations because of the energetic cost that reproduction represents. In this contribution, we test this hypothesis by analyzing the reproductive patterns of two genera of sigmodontine rodents (*Akodon* and *Oligoryzomys*) co-distributed along a 3000 m elevation transect along the escarpments of the eastern cordillera in central Bolivia. Reproductive data analyzed for females include the number of pregnant females per site/species and litter size. In males, the variable analyzed was testis size, as a proxy for sexual maturity. Data were analyzed with a Generalized Linear Model (GLM). For both genera, there were more pregnant females in the transition period (*Akodon*: $\chi^2=6.26$, g.l.= 1, $p = 0.01$; *Oligoryzomys*: $\chi^2=8.10$, g.l.= 1, $p = 0.004$). *Akodon* exhibited larger testicles in the transition period at higher elevations ($W = 239$, $p = 0.02$), whereas in *Oligoryzomys*, testicles were larger at lower elevations ($W = 256$, $p = 0.01$). Litter size was larger in the dry season at lower elevations, only in *Oligoryzomys* ($W = 60.5$, $p = 0.01$). Elevation and time of year affect reproductive patterns, and their effects varied among the groups studied. These differences must be related to the plasticity of the species in responding to variations in food resource availability and species-specific energetic requirements.

Diversity and composition of the ectoparasitic and phoretic arthropods associated with small mammal assemblages along an elevational gradient in the Andes.

Bernal Hoverud, Nuria(1)(2)(3); Mollericona, Jose Luis (2); Ramos, Vanessa (4); Sempertegui, Alba (4) & Salazar-Bravo, Jorge (1)(3)

Keywords: community ecology; small mammals; ectoparasites; phoresis

Parasites are useful indicators of environmental stress, food web structure, and play an important role in the regulation and evolution of host populations and communities. However, the mechanisms that shape within host-parasite communities remain unclear, with environmental conditions, the characteristics of their life cycles, and host traits parameters implicated in the distribution, abundance, and composition.

The aims of this study are to (i) determine the species diversity of ectoparasites on the small non-volant mammals (rodents and marsupials) along a 4000m elevational transect in Madidi National Park (Bolivia, 2015 to 2017); (ii) to investigate the effect of host species and trapping location on the infestation of small mammals with ectoparasites; and (iii) to assess the factors influencing the abundance of the most abundant ectoparasites on mice and marsupials. Data from the literature was used to complement our field data. We expect that environmental variables (e.g., temperature) and life-cycle will emerge as the main mechanisms that shape within host-parasite communities.

Using a standardized protocol on every host analyzed (n= 660 individuals) we found fleas (n = 450, 12 genera, 23 species), mites (n = 11,750, 5 genera, 45 species), ticks (n = 68, 2 genera, unidentified species), lice (n = 5, 2 genera, unidentified species), and two different phoretic arthropods, pseudoscorpions or Chelonethida (n = 15, 1 genus, unidentified species), and rove beetles (n = 149, 2 genera, unidentified species).

Prevalence (percentage of infested hosts among all screened hosts) will be reported together with confidence intervals (95% confidence level). Mean intensity (total number of ectoparasites divided by all infested hosts) will be reported together with the standard error of the mean (SEM). Prevalence and mean intensity will be combined to obtain mean abundance by multiplication as a quantitative descriptor of the ectoparasite population.

Characterizing inter and intra-host plaque variants and growth fitness of global zika virus lineages.

Sifuna M, Ciota At, Onyango MG

Keywords: Zika lineages, plaque variants, replicative fitness

Background: Zika virus (ZIKV), (Flavivirus; Flaviviridae) has two primary lineages, namely the African and Asian/American. The Asian/American lineage can be divided into three distinct sub-types: American, Pacific, and Southeast Asian subtypes. To date, the African ZIKV lineage has not been identified beyond the confines of the African continent, not been linked to epidemic transmission, congenital malformations, or neurological pathologies. Despite this, several in vitro and in vivo studies demonstrate a higher transmissibility and pathogenicity of the African ZIKV lineage. We hypothesize that intra-host variation of ZIKV exists, and this may assist in understanding the biology of virus-host interaction that contributes to differences in viral replicative fitness and pathology observed across the ZIKV lineages.

Method: Using vertebrate and invertebrate cell lines, we examined the in vitro growth of global ZIKV lineages. Virus titers were determined by RT-qPCR targeting the ZIKV NS1 region for the quantification of copies of the ZIKV genome present in samples. Utilizing plaque assays, we characterized the plaque morphology of global ZIKV lineages.

Results: The in vitro replicative fitness demonstrated the highest growth potential in both American and Southeast Asian ZIKV subtypes, whereas the African strains showed the lowest proliferative capacity. Moreover, the African lineage had uniform intrahost plaque morphology while we observed a diverse intrahost plaque morphology in the American and Southeast Asian ZIKV subtypes. The Nigerian strain had unique plaque morphology and a slower replication rate compared to the rest of the strains belonging to the African lineage studied.

Conclusion: Our results provide important information on lineage-specific viral biological characteristics and growth capacities which may inform the geographical disparities in the manifestations of disease caused by ZIKV. The intra-host plaque variants we observed could result in immune barrier escape which may complicate ZIKV vaccine development and cause public health concern.

Determining the timescale of acclimation to light between previously and newly developed leaves in *Glycine max*.

Gray, Eve(1) Perkowski, Evan(1), Smith, Nick(1)

Keywords: Photosynthetic acclimation, Plant physiology, Ecology

Light is the driving force behind photosynthesis and is critical in calculating gross primary production (GPP). The fraction of light that reaches plants is assumed to increase GPP linearly. However, the natural environment is highly variable and can change drastically through seasons and with human disturbance. This can lead to plants being exposed to suboptimal conditions where the linear relationship of light and increased GPP may not hold true. Fortunately, plants are dynamic, able to modify the morphology or biochemistry of leaves to acclimate to new conditions. Considering acclimation may lead to more reliable estimates of GPP which helps to predict global change in models. A fully-factorial high and low light acclimation experiment was conducted at Texas Tech University to quantify the timescale of acclimation to light using soybean (*Glycine max*). Soybean plants were divided into two groups to germinate in one of two starting treatments in two controlled growth chambers. Treatment one maintained low light at (450 PAR) and treatment two maintained high light at (1200 PAR) while both kept CO₂ and humidity consistent. Morphological and biochemical traits were measured on the third fully expanded trifoliolate leaf to establish a baseline measurement before swapping plants into their contrasting light treatment while some plants remained as a control. While continuing to measure the baseline leaf on a daily basis for stomatal conductance and fluorescence, and bi-weekly for photosynthesis and respiration measurements, a new leaf developed in the second condition will be subjected to the same measurement regime. All morphological data will be collected at the completion of the experiment along with chlorophyll content and carbon and nitrogen ratios. Through measuring the old and new leaf, acclimation dynamics within the same plant can be measured for insight on how GPP estimates may change within a plant canopy in addition to disturbance.

Poster Presentations

The sex hormone, prolactin, and its novel sexy role in the regulation of iron redistribution between tumor and macrophages.

Farrell, Reagan (1); Pascuzzi, Nicholas (1); Kim, Mary (2); Torres, Miguel (2); Pearce, Lilly (2); Gollahon, Lauren (3); Chen, Kuan-Hui E. (3)

Keywords: Prolactin; ferric and ferrous uptake; CD44; iron transfer; macrophage

Iron is an essential element for human health. In humans, dysregulated iron homeostasis can result in a variety of neurological disorders as diverse as multiple sclerosis, stroke, Parkinson's disease and the development of cancers. Enhanced uptake, redistribution, and retention of irons in cancer cells have been noted and suggest an “iron addiction” pattern of cancer cells. However, the source of irons and the mechanisms cancer cells adopt to actively acquire iron is not well understood. In the present study, we discovered the peptide hormone, prolactin, exhibits a novel function to regulate iron distribution on top of its well-known pro-lactating role. When stimulated by prolactin, breast cancer cells increase CD44, a surface receptor mediating the endocytosis of hyauronate-bound iron, and hepcidin, a molecule that inhibits the export of iron from ferroportin, thus resulting in the accumulation of iron in tumor cells. In contrast, macrophages when treated by prolactin, express more ferroportin, resulting in net iron output. The increased iron in cancer cells positively correlates to rapid tumor growth and the epithelial-to-mesenchymal transition which forms the basis for later tumor metastasis. Interestingly, when co-culturing of macrophages with pre-stained labile iron pool and tumor cells without any iron staining in an iron free condition, we demonstrate a direct iron flow from macrophages to tumor cells. As most irons in human are stored in erythrocytes, macrophages are the next major iron-storage cells and it is known that macrophages infiltrate tumors and facilitate tumor progression. Thus, our work presents a novel regulatory role of prolactin to drive iron flow which provides new information on fine-tuning immune responses in tumor microenvironment and could potentially benefit the development of novel therapeutics.

Exploring the Role of Optic Tectum CRF Receptors in Feeding Behavior.

Murtuza, M.Ghufran (1); Kolli, Sreevalli (1); Carr, James A. (1); Harris, Breanna N. (1)

Keyword: CRF, Stress, Feeding, Xenopus, Optic Tectum, Prey

In order to survive prey animals must balance feeding and fleeing behaviors. Prey animals rely on multisensory cues to detect both food and predators. This decision making takes place in a brain region called the optic tectum (OT). Although the neuronal mechanisms maintaining this balance are not fully understood, research suggests that corticotropin-releasing factor (CRF) in the OT plays a role in inhibiting feeding behaviors in the African clawed frog, *Xenopus laevis*. To further understand the interplay between CRF and the OT in feeding behaviors, we investigated whether the microinjection of CRF at varying doses into the OT of juvenile *X. laevis* alters behavioral responses to live prey cues, such as earthworms and crickets. Frogs were assigned to a treatment group (n = 12-16): one of four doses of CRF, saline, CRFR1 antagonist, gauged, or left unmanipulated. One hour after injection into the OT, frogs were exposed to a live prey stimulus (earthworm or cricket, respectively); feeding-related behaviors were recorded. We found that CRF presence in the OT subtly decreases but does not abolish responses to live prey cues. When treated with 0.001ug or 0.01ug doses of CRF, the juvenile *X. laevis* took longer to contact and put the earthworm in their mouth. The juvenile frogs treated with CRF as opposed to unmanipulated responded less often to the cricket. Data scoring for frog's responses and analysis are still pending. However, we predict that when injected with doses 0.001ug or 0.01ug of CRF, the frogs will take longer to contact the cricket and put the cricket in their mouth. Our data will aid in understanding the neuroendocrine mechanisms of feeding and fleeing behaviors, as well as probing the role of supra-hypothalamic CRF as a novel regulator of feeding in response to stressors. NSF Funded (Grant No.1656734).

Creating multi-antibiofilm therapeutics with cellulase based carbon dots.

Sawant, Vikram; Gordon, Christopher

Keywords: *Pseudomonas aeruginosa*, Biofilm, Microrheology, Carbon dots, Antibacterial

Pseudomonas aeruginosa biofilms can cause chronic and serious wound infections. Treatment of wound biofilms is difficult, and often requires multiple rounds of antimicrobial therapy and debridement. There is a need to create topical therapeutic treatments with multiple antibiofilm effects. In this work, we explore the potential of cellulase based carbon dots as a potential therapeutic. Cellulase is a glycoside hydrolase that has already been shown to be effective in causing biofilm dispersal as well as reduction in biofilm stiffness and elasticity. By synthesizing the cellulase into a carbon dot, we hypothesize that the molecule can retain some of those capabilities, because carbon dots are known to retain some of the effects of their precursor proteins and increase the bactericidal effect and penetration of the cellulase. Carbon dots are synthesized from both cellulase and citric acid using a one-step hydrothermal carbonization method, and then characterized for surface properties, size, roughness, compositions, and emission spectra. *P. aeruginosa* biofilms were grown in a microfluidic environment for 24 hours and then treated with these carbon dots at a range of concentrations. Using microrheology, it was seen that biofilms treated with the cellulase based carbon dots were more viscous and less stiff compared to those treated with citric acid-based carbon dots. This appears to be because the cellulase carbon dots impact PSL within the biofilm based on microrheology studies examining bacteria strains with specific EPS component removed. This is consistent with the impact of molecular cellulase on biofilms. The penetration of the carbon dots into the biofilms is being examined via confocal microscopy. In general, initial studies suggest that the cellulase based carbon dots have the potential to act as an excellent multi-antibiofilm therapeutic in the future.

Shotgun metagenomics for the assessment of diet of American black bears (*Ursus americanus*).

Prew, Christopher (1); Neha, Sufia Akter (1); McKinney, Bonnie (2); Bradley, Robert(1,3); Manthey, Joseph (1); Phillips, Caleb (1,3).

Keywords: Shotgun Metagenomics; *Ursus americanus*; Enrichment; Diet; Feces

Understanding the dietary requirements of species is critical to elucidate their trophic interactions, can also inform conservation strategies, as well as human wildlife interactions in some instances. Understanding diets of wild animals from direct observation is challenging, but non-invasively collected fecal samples can provide valuable ecological information about species including diet, host genetics, microbiota, and parasites. In this pilot study, using shotgun DNA sequencing we reconstructed diet from six black bear scat samples collected in the Trans-Pecos ecoregion. Samples were homogenized and split into subsamples, some of which were selectively enriched for eukaryotic DNA then 2×150 bp sequenced on an Illumina NovaSeq 6000. Bear genomic reads were first identified by mapping to a reference bear genome, and remaining reads were aligned against the NCBI representative eukaryotic species database using BLAST. Eukaryotic DNA enriched samples showed a higher proportion of bear DNA, which will be useful for genotyping individual bears from scat samples. Enriched and non-enriched subsamples differed in their dietary species proportions, indicating that non-enrichment is better for providing an unbiased assessment of dietary composition. Sequencing effort was assessed through dietary species detection rarefaction curves, which plateaued around 40,000 reads and indicated that samples had been adequately sequenced to characterize diet. The relative abundance of dietary items showed that the top five most prevalent taxa found in the feces of black bears were *Triticum aestivum*, *Gryllus bimaculatus*, *Sorghum bicolor*, *Digitaria exilis* and *Gossypium hirsutum*. The results indicate a significant deviation in the dietary composition of black bears from wild species, with a notable shift towards incorporating a substantial portion of human-processed products (e.g., grain and cotton supplements used to augment bird and deer feeders). This study provides a sample processing and analysis framework upon which larger studies of black bear ecology in the Trans-Pecos will be based.

Microbial March Madness: a Course- based Undergraduate Research Experience for student research opportunities.

Miralles-Salazar Jacqueline (1) , Walker Nina (2) , Molinar Dessiree (1) , Reid Joshua (1) , Wakeman Catherine (1)

Keywords: microbiology, bacteria interactions, CURE

To gain research experience, undergraduates typically attempt to apply to the research programs of their professors. However, demand for these spots is high and the number of positions is limited. To solve this problem, a new modality of teaching has been implemented in multiple universities: “the Course-based Undergraduate Research Experience (CURE)”. Through CUREs, students are introduced to the research process in a classroom setting, build their critical thinking skills, and master lab techniques. The proven benefits of CUREs include enhancing the student’s awareness of what it means to be a researcher, increasing their likeness to stay in STEM careers, and pursuing graduate school. With the CURE developed herein, we anticipate that we will additionally observe an increased understanding of the more complex topics associated with the upper-level microbiology courses offered by our department. The Microbial March Madness CURE embraces the TTU love of NCAA basketball by allowing the students to prepare and experimentally test an NCAA-style March Madness bracket of microbes pitted against each other in different environments. The students will learn about the specific environmental adaptations of the different microbes to develop and test their hypotheses about the environmental fitness of individual microbes. If their hypotheses are proven incorrect, they can reevaluate the reasons for their experimental findings to improve their critical thinking skills. As a pilot study, we had 3 students working in the course, A high schooler, a community college student, and a senior from Biology.

Unraveling Autophagy's Role in Bone Health and Osteoporosis: Insights from Molecular Pathways to Therapeutic Strategies.

Mian, Maamoon (1) Tahiri, Jihane (2)

Keywords: Bone Health; Osteoporosis; Autophagy; Optineurin; Homeostasis; Antiaging; Bone-related Disorders; Dysregulation

Osteoporosis and bone-related disorders are widely prevalent in the elderly and are associated with a plethora of negative physical consequences. We conducted a literature review to assess the role of molecular autophagy in bone health with preventing or prolonging bone-related disorders in old age with different therapeutic strategies and prophylactic methods. Our review includes synthesizing current knowledge from randomized controlled studies, systematic reviews, and clinical articles focusing on the role of autophagy in osteoporosis, therapeutic strategies to counteract molecular degeneration, and prophylactic methods to help achieve healthy bone aging. Review of the literature found autophagy as an antiaging process and dysregulation of this cellular process is associated with bone loss, especially in the elderly as age-related autophagy deficiency is a natural process that occurs. It was also found that certain autophagy receptors, such as optineurin, play pivotal roles in coupling autophagy and bone metabolism, and underexpression of these receptors disrupts bone homeostasis. These findings were consistent with the results of the literature that was reviewed over autophagy and osteoporosis, highlighting the potential for therapeutic and prophylactic interventions, such as receptor targeted drugs and a healthy lifestyle, to modify and prevent disease progression.

Measuring the cultural strengths of diverse students in higher education.

Tijerina, Rose Marie (1); Dr. Marroquin-Flores, Rosario (1); Tedeschi, Mason (1); McFather, Luke (1); Casas, Zianna (1); Banjara, Sofia (1); Warmsley, Redmon (1); Dr. Limeri, Lisa (1)

Keywords: Community Cultural Wealth; STEM Education; Measurement Development; QuantCrit Methodology

Students who hold minoritized identities are underrepresented in STEM fields and often have disproportionate outcomes when compared to students from the cultural majority. Educational institutions often attribute these disproportionate outcomes to a lack of cultural capital, the knowledge, skills, and experiences valued by the privileged majority. Community Cultural Wealth (CCW) is an asset-based framework that focuses on the cultural strengths that diverse students use to be successful. CCW consists of 6 forms of capital: aspirational, navigational, social, linguistic, familial, and resistant. This presentation focuses on linguistic, resistant, and aspirational capital. Linguistic capital refers to the skills that students develop through spoken language, storytelling, and other modes of communication. Resistant capital refers to the knowledge and skills required to challenge oppressive systems and seek reformation. Aspirational capital refers to the ability to maintain hopes and dreams for the future, despite existing barriers. Using a QuantCrit approach, we are developing and collecting evidence of validity for the first complete measure of CCW. QuantCrit is a methodology that centers the research around the lived experiences of the people under study and challenges researchers to critically reflect on potential biases. We are currently collecting evidence of validity based on response process using cognitive interviews. We are using purposeful sampling, the practice of selecting information-rich participants with unique insights and experiences, to recruit undergraduate participants. We are specifically recruiting students with experiences that differ from the majority culture in race/ethnicity, gender identity, financial hardship, neurodiversity, and the intersectionality between these identities. We hope to use our measure of CCW to better understand the forms of capital that minority students use to be successful and to challenge deficit perspectives that exist within educational institutions.

Reef Fish Assemblages of the Mesoamerican Barrier Reef in Roatán, Honduras.

Mowry, Annie (1); Kennedy, Ashlyn(2); Knauss, Madelyn(3); Randell, Stephanie(2); Flores, Morena(2); Gomez, Racheal(2); Hicks, Matthew(2); Robertson, Traesha(4); Lockwood, Stephanie(1)

Keywords: Fish; Species Diversity; Coral Reef; Foodweb; Conservation

Global fish populations are declining rapidly due to anthropogenic climate change and human activities. Frequent disturbances are causing reef specialists to be replaced by generalist species who continually adopt original functions, resulting in an overall trend of reef homogenization. Over the last three decades, the Mesoamerican Barrier Reef (MBR) has experienced multiple stressors which have contributed to a rise in depauperate reefs and shifts in fish assemblages. Frequent surveys are needed to assess reef function and apply appropriate management strategies. This study aimed to assess the species diversity of shallow reef fishes of the MBR in Roatán, Honduras. A team of three divers followed a modified Reef Life Survey method and recorded all fishes observed along a 25 m transect. Seventy-two species of fish were observed across five dive sites. The diversity indices ranged from 1.78–2.73. Roatán's reef specialists made up 62% of the fish species observed, and 78% of the reef fish abundance. Our results also demonstrate that while the Roatán Marine Park hosts sustainable communities of herbivorous fish, its commercial fish abundance is in critical condition. Currently the reef is in a depauperate state where algal species are more dominant than coral. However, 51% of the fishes observed are, to some extent, algivorous, and this high herbivorous activity can decrease macroalgal concentrations and create space for juvenile coral recruitment. Additional surveys are needed in this area to track potential shifts from reef specialists to generalist fish species.

Phylogenomic Analysis of *Xanthisma* (Asteraceae) And Assessment of Ploidal Variation Using Herbarium Specimens.

Shodipo, Oluwaseun (1) Johnson, Matt(2)

Keywords: *Xanthisma*; Ploidy variation; Monophyly; Allopolyploidy; Autopolyploidy; Speciation; Angiosperm 353; Reproductive Isolation

The Asteraceae (Compositae) family is the largest family in plant taxonomy and is known for its rapid evolution, polyploidy ancestry, and convergent morphology which made its classification quite challenging. *Xanthisma*, *Machaeranthera*, and *Haplopappus* are genera in Asteraceae tribe Macherantherinae that have posed incongruence in species classification. *Xanthisma* was expanded in the early 2000s to accommodate 16 more species with similar morphological characters, but there has been no update to its molecular phylogeny since. My research aims to carry out a phylogenomic analysis of this genus to 1) reconfirm the monophyly of *Xanthisma* 2) determine whether ploidy variation in *Xanthisma* is allopolyploid or autopolyploid 3) determine whether ploidy variation is associated with historical reproductive isolation in *Xanthisma*.

Methods: Ray Jackson, former TTU professor, collected these species in the 1900s and identified chromosome numbers on herbarium specimens in the E.L. Reed Herbarium. I will use Angiosperms 353, a target capture probe set of orthologous genes to reconfirm the monophyly of *Xanthisma* and determine whether the genetic divergence among populations suggests speciation.

We will use gene clustering and principal coordinate analysis of variants at the 353 genes to determine if the ploidy variation is associated with historical reproductive isolation in *Xanthisma*.

Potential Results: Our phylogenetic inference will determine whether *Xanthisma* is monophyletic in North America or needs further subdivision if it is non-monophyletic. If we observe separate genetic clusters associated with ploidy levels, it may suggest reproductive isolation and an indicator of cryptic speciation. If historical reproductive isolation is not associated with ploidy variation, we will follow up by studying introgression among ploidy levels.

Conclusion: This research will provide the essential fundamentals to explore further research such as the comparison between geographic distribution and diversity of populations in the 1900s and now, and the impact of polyploidy on gene expression.

Annotation of Novel Bacteriophage Genomes Recovered from Soil Samples in Lubbock, TX.

Block, Natalie (1); Dickens, Whitney (1); Miller, Laurissa (1); Mosharraf, Fahareen (1), Rowell, Austen(1), Smith, Allie (2), Bono, Lisa M. (1)

Keywords: genome annotation; novel bacteriophage; phage isolation; Actinobacteria

The HHMI Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program is a course-based undergraduate research experience (CURE) curriculum recently implemented at Texas Tech University through the TrUE Scholars Undergraduate Research Program. Originally developed by Graham Hatfull's group at the University of Pittsburgh, the aim of the SEA-PHAGES curriculum is to isolate novel bacteriophage (bacteria-infecting viruses) from soil samples and characterize them. Over the Fall 2023 semester, we isolated phage from local soil samples that can infect *Arthrobacter globiformis* 2979 and *Gordonia rubripertincta*, went through multiple rounds of purification and amplification, and harvested high titer lysates of phage. Through this workflow, we were able to recover five novel phages. We then extracted DNA from these phages and submitted them for whole-genome sequencing. Our current project is to complete both positional and functional annotation of the entire genomes of these novel phages. These annotations will be used to further understand the biological function and lineage of our novel phage. This will contribute to our understanding of the phages that infect Actinobacteria.

Exploring the correlation between cockroach habitat and microbiome.

Owusu Ntim,Rhoda(1); Nanyonga, S. Linda(1); Anyango, Victor(1); Onyango Maria(1)

Keyword: Cockroach ; Microbiome; Sequencing.

Introduction: Cockroaches (Phylum Arthropoda; Order Blattodea) are resilient insects and capable of surviving in extreme environments and conditions¹. Microbiome constitutes a key determinant of individual variation, combined with genes and environment, these factors shape an individual's physiology and fitness². The microbial composition of an organism is driven by the habitat, and this may influence the host phenotype as well as drive the evolutionary processes³. This study aimed to assess the diversity and composition of cockroach populations associated with different habitats: Kitchen freezers; sewers and pristine laboratories.

Methodology: Samples were collected from each habitat and the 16S V3-V4 hypervariable rRNA region of the cockroach genomic DNA was sequenced on Illumina sequencing platform. The microbial abundance and profile of cockroach populations associated with the different habitats were compared.

Results: The freezer cockroach population had a more diverse microbial species composition than the sewerage and lab-reared cockroach populations (Chao1, p-value: 0.028278; [ANOVA] F-value: 4.5652). In addition, though there were microbial species common across all the populations, the freezer cockroach population displayed unique microbial species absent in the other two populations ([PERMANOVA] F-value: 3.3779; R-squared: 0.31053; p-value: 0.014). Both sewer and lab-reared cockroach populations contained enriched levels of *Blattabacterium* spp. while the freezer populations had decreased levels of *Blattabacterium* spp. Cockroaches utilize *Blattabacterium* spp. to synthesize amino acids from urea, especially under extreme deprivation. Interestingly, bacteria belonging to the *Rickettsiella* genus were present in lab-reared cockroaches while bacteria belonging to the *Coxiella* genus were identified in lab-reared and sewer cockroaches.

Conclusions: Our results suggest that habitat may shape the microbial composition of cockroaches as well as their abundance. Cockroaches are considered a health risk due to their capacity to disseminate pathogens in their feces which spread through consumption or contact with infected feces⁴ yet the role of cockroaches in human infections is poorly understood. Our findings demonstrate the need for the study of the contribution of cockroaches to vector-borne diseases of public health concerns.

Presence of Superbugs and the Impact of Biofilms on Antibiotic Resistance of Commonly Found Bacteria.

Jones, Emily (1); Heifetz, Kimberly (2); Wahl, Christian (2)

Keywords: Superbugs; bacteria; antibiotics; resistance; biofilm

Antibiotics are drugs that are used and prescribed in the hospital setting to treat bacterial infections. However, overexposure and evolutionary adaptations are leading to the exacerbated rise of multi-drug resistant antibiotic bacteria, also known as superbugs.

In a previous study performed in 2020, samples were collected from Texas Tech University students from the front and back of their face mask, headphones, and cell phones. In this study, we examine which bacteria found can be classified as a superbug as well as test the efficiency of antibiotics with three different mechanisms of action against these bacteria and the impact of the presence of a biofilm on the efficiency of the antibiotics. The bacteria were streaked and grown on Tryptic Soy Agar (TSA) plates for a 24-hour period. These plates were challenged with eight different antibiotics: Ampicillin, Bacitracin, Cefotaxime, Doxycycline, Lincomycin, Neomycin, Novobiocin, and Vancomycin. The susceptibility of bacteria was determined by measuring the zone of inhibition of the antibiotic disk. Lincomycin, which targets protein synthesis, was the least effective antibiotic. Novobiocin, which targets DNA synthesis, was the most effective. In reference to our experimental design, we have defined a superbug as a bacterium that has become resistant to more than four of the antibiotics to which it was subjected to. Our results showed that 8.06% of the samples tested were classified as low resistance (resistant to one-two antibiotics) and 41.94% of the samples tested were classified as superbugs or strong superbugs (resistant to five-eight antibiotics). *Staphylococcus* spp. and *Bacillus* spp. were identified as the most prominent bacteria found and showed to have similar resistance levels to all antibiotics tested except Novobiocin. Our results also indicated that the presence of a biofilm did not affect the resistance to most antibiotics tested, only increasing the resistance against Vancomycin and Novobiocin.

Electron Microscopy for Characterization of Novel Bacteriophage Recovered from Soil in Lubbock, TX.

Miller, Laurissa (1), Rowell, Austen (1); Block, Natalie (1); Dickens, Whitney (1); Smith, Allie (2), Bono, Lisa (1)

Keywords: Transmission Electron Microscopy; environmental bacteriophage; characterization; novel phage

The HHMI Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES) program has been recently implemented at Texas Tech University through the TrUE Scholars Program, and provides a discovery-based research experience for undergraduate students. Through this curriculum, students work to recover novel phage from locally sampled soil and perform rounds of isolation, purification, and amplification; this process recovered five novel phages. After generating a high titer lysate for each phage, samples were submitted to the College of Arts and Sciences Imaging Core facility for Transmission Electron Microscopy (TEM) to obtain high-resolution images of the phage virion particles. These TEM images will be used, alongside genetic characterization, to further understand the ecology and biology of our novel phages, and how they fit in to the larger phylogenetic lineage of environmental bacteriophage.

Assessing the influence of nutrient addition on diversity in a semi-arid grassland over a five-year period.

German, Hannah (1), Smith, Nicolas (1)

Keywords: diversity; community composition; nutrient addition; long-term; short-term

Plant community composition plays an integral role in ecosystem net productivity and stability. Over time, community composition can change due to climate, the introduction of new species, and changes in resource availability such as light, water, and nutrients. Nitrogen (N), phosphorus (P), and potassium (K) are key macronutrients that plants acquire and use for the production and maintenance of structural compounds, photosynthetic structures, and vascular transport networks. Increased productivity has been observed in plant communities that are exposed to short-term nutrient addition, while long-term experiments document decreased plant diversity due to the emergence of dominant species that occupy plant community niche space. However, our understanding of how nutrient addition relates to biodiversity and productivity could be skewed due to the majority of sampling being done in temperate climates where nutrient and water availability is not a limiting factor. In this study, we used annual species composition and biomass data collected from a five-year full factorial N*P*K field experiment in a semi-arid grassland to assess how nutrient addition changes biodiversity. We also used local weather station data to assess possible interactions between nutrient addition and climate on species composition since the rate of nutrient acquisition changes as water becomes more available. Preliminary results indicate that nutrient addition had no significant effect on species diversity regardless of nutrient addition treatment or annual weather pattern. This unexpected null effect of nutrient addition could be a consequence of timescale, where species replacement and changes in species composition occur along broader timescales than a five-year experiment. However, this could also be a pattern driven by low precipitation in the region. Future work is needed to investigate whether nutrient addition treatments modify plant biomass as well as diversity and to assess whether biomass and diversity vary inter-annually due to seasonal weather patterns.

Identifying abiotic drivers of *Aedes aegypti* and *Aedes albopictus* population dynamics in the DFW metroplex.

O'Dell, Nathaniel (1); McMillan, Joseph (2)

Keywords: Mosquito surveillance; high-risk populations; *Aedes aegypti*; *Aedes albopictus*; Aedes-borne disease; DFW

Climatic and socioeconomic conditions are historically among the most influential explanatory abiotic factors of the distribution of *Aedes aegypti* and *Aedes albopictus* at fine spatial and temporal scales. While these species are considered ecological competitors since each species occupies similar urban microhabitats as both larvae and adults, mosquito surveillance data from throughout the southern US indicates these species often co-occur at the scale of individual surveillance sites. To better define the influence of abiotic factors – such as climate, land cover, and socioeconomics – on spatiotemporal patterns of *Ae. aegypti* and *Ae. albopictus* abundance and coexistence, we examined a longitudinal mosquito surveillance data set from Tarrant and Dallas Counties, Texas, United States, spanning from 2015 to 2022 using spatial regression models and random forest algorithms. We hypothesized that temperature best explains temporal patterns of each species' abundance, while socioeconomic variables such as mean home income and percentage of households below the poverty line best explain spatial patterns. We further hypothesized that periods of higher mean temperature favor a proportional dominance of *Ae. aegypti*, especially in low socioeconomic status regions. By defining the influence of these variables on *Aedes* spp. mosquito population dynamics, we can better define high-risk scenarios for Aedes-borne disease transmission as well as guide improved surveillance strategies for these two medically important mosquito species.

The Role of Tectal CRF in Lateral Line Related Feeding Behaviors.

Sreevalli Kolli¹, Ghufran Murtuza¹, James. A. Carr¹, Breanna N. Harris¹

Keywords: Stress; Corticotropin releasing factor; *Xenopus laevis*; lateral line; behavior; optic tectum

One of the most important decisions that an animal must make for survival is when to flee and when to feed. Animals must use sensory and situational information to assess the level of importance between hiding from predation and hunting for prey. In the species *Xenopus laevis*, the optic tectum is responsible for consolidating visual and lateral line information, and this brain region is also involved in making decisions relating to the feed vs flee tradeoff. Previous research in our lab shows corticotropin-releasing factor (CRF) inhibits feeding on multisensory prey by binding to CRF R1 receptors of the optic tectum. While we do know that CRF reduces feeding behaviors, we do not know which sensory modality CRF impacts, hence leading us to test how CRF affects *Xenopus laevis*' response to lateral line cues. Here we will subject *Xenopus laevis* to tectal CRF injection and measure how CRF affects prey capture. Data collection is currently underway, however, we predict that CRF will reduce feeding-related behaviors in response to lateral line or live prey cues. To test this hypothesis, frogs are injected with one of four doses of CRF, or are in one of three control conditions (unmanipulated, saline, and antagonist) and one hour later, we expose frogs to lateral line stimuli (air puffs), followed by a live prey (cricket) trial. Our results will help us determine not only how *Xenopus laevis* responds to multisensory cues when injected with CRF, but will also illustrate whether or not CRF alters the way that *Xenopus laevis* responds to discrete lateral line cues. NSF Funded (Grant No. 1656734)

Transcriptomic analysis of novel proteins essential for *Pseudomonas aeruginosa* biofilms at environmental temperatures.

Salinas, Adolph (1); Lueke, Alex (1); Wakeman, Catherine (1)

Keywords: *Pseudomonas aeruginosa*, Thermal regulation, Transcriptomics, RNAseq

Pseudomonas aeruginosa, is a ubiquitous microorganism that can be found in various environmental habitats such as soil and bodies of water, and is also a known plant and human pathogen. Given the opportunity, this bacterium can infect immunocompromised individuals such as those with open wounds, burn victims, medical implants, and cystic fibrosis patients. *P. aeruginosa* typically forms biofilms, which is a community of cells encased in a sticky substance called the extracellular polymeric substance (EPS) matrix. In its motile free-living form (planktonic cells), *P. aeruginosa* is most susceptible to known antibiotics; however, once encased in an EPS matrix, this bacterium can exhibit antibiotic tolerance upwards of 1000 times the original inhibitory concentration after biofilm formation. Given its wide variety of environments, how does the biofilm and planktonic phenotypes change as it transitions from one environment to another, and can we exploit these differences to better control its growth?

In previous research, we established that two novel proteins, PA14_50070, PA14_67750, play a key role in creating an EPS matrix that is compositionally unique at environmental temperatures (23° and 30°C) but not at host temperatures (37° and 40°C). Our current efforts are to illuminate the functionality of these two hypothetical proteins because of their observed significance in biofilm formation at lower environmental temperatures. We hypothesize that biofilm formation of *P. aeruginosa* would be notably impacted if either PA14_50070 or PA14_67750 are nonfunctional, thus creating a downstream effect during the production of other proteins at environmental temperatures. The characterization of these hypothetical proteins may provide us with a better understanding of biofilm formation, as well as demonstrate that there are novel drug targets that may be unique to environmentally grown biofilms that are not present in clinical biofilms.

Testing the acclimation of plants to midday or average conditions.

Vanginault, Christine (1); Smith, Nick (2)

Keywords: photosynthetic acclimation; environmental variability

Photosynthetic acclimation is a process in which plants undergo a biochemical change following a long-term environmental change. The environmental conditions to which plants acclimate are still not fully understood. Learning more about how plants acclimate will help us to improve the projections of Earth System Models. To test what conditions plants acclimate to, a study will be conducted to see whether plants acclimate to average daily conditions or midday (variable) conditions. This experiment will be set up in growth chambers and completed at Texas Tech University in 2024. The growth chambers will have the same average conditions but vary in diurnal conditions. Coupled A/Ci curves and fluorescence will be measured. In addition, V_{max} , maximum Rubisco carboxylation, J_{max} , maximum rate of electron transport, and ϕ , quantum efficiency of photosystem II, will be determined. At the end of the experiment, higher biochemical rates and higher leaf nitrogen will be found in plants acclimated to a particular treatment.

Responses of Leaf Stomata to 50 Years of CO₂ Increase Using Herbarium Specimens.
Salazar, Jazlyn; Bullock Madison; Johnson, Matthew

Keywords: Stomata; Herbaria; Stomatal density; CO₂ intake; Climate change

Herbarium specimens provide a glimpse into various past characteristics of plants, which includes the ways that they interacted and responded to the environment. Plants are able to balance CO₂ intake with water loss by regulating the stomatal pore aperture. Guard cell signaling is regulated by both environmental factors and plant hormones. From plant fossil records, it is suggested that plant acclimation to changing atmospheric CO₂ has a correlated evolution in stomatal density and size. Plants are able to balance CO₂ intake with water loss by regulating the stomatal pore aperture. Guard cell signaling is regulated by both environmental factors and plant hormones. From plant fossil records, it is suggested that plant acclimation to changing atmospheric CO₂ has a correlated evolution in stomatal density and size. Together, stomatal density and size contribute to determining the maximum leaf conductance of CO₂, and in this study we used herbarium specimens to track stomata over time. The objective of the study is to calculate potential changes in stomatal size and density over time to understand temporal differentiation in resource investment in stomata. Based on similar reasoning as previous research, I expect there will be a decrease in stomatal conductance, which could mean increased photosynthetic efficiency when combined with the higher water-use efficiency predicted as increased atmospheric CO₂, temperature as well as decreased precipitation in the last 100 years will have led to increased leaf ¹³C natural abundance. Within the E.L. Reed Herbarium at Texas Tech is a collection of over 1500 plant specimens housed in the E.L. Reed Herbarium at Texas Tech is a survey of Guadalupe National Park in the 1970s. From this collection to modern specimens of the same species, we identify how plants responded to over 50 years of CO₂ addition. Our results can use a look into the past in the floristic biological diversity to predict how plant communities will respond to future climate changes.

Effect of Nutrient Source and Rearing Temperature on Interspecific Larval Competition between *Aedes aegypti* and *Aedes albopictus*

Bennett, Samuel; Chavez, Alexa; Laubmeier Amanda; Boluwatife, Awoyemi; Dina, Nusrat; McMillan, JR

Keywords: Ecology; nutrition; mosquito, medical entomology

Aedes aegypti (L.) and *Aedes albopictus* (Skuse) are two medically important mosquito species in the United States. Because their spatiotemporal ranges overlap, they are often considered ecological competitors. Competition between the two is traditionally studied during the larval stage, with asymmetric survival outcomes in favor of *A. albopictus* being attributed to the species' status as a superior competitor. Although many factors can influence competitive outcomes, few studies have investigated the effect diet source has on competitive outcomes, with even fewer studies investigating the added influence of rearing temperature on survivorship. To explore the interaction between nutrient source and temperature on the competitive outcomes between these two species, we measured the survivorship of *A. aegypti* and *A. albopictus* in two different nutrient-limited environments at various interspecific ratios across a range of temperatures from 20 to 35C. Two types of bovine liver powder were used – “Liver Concentrate NF XI Powder,” a nutrient rich, molecular-grade liver powder manufactured by MP Biomedicals, and a general liver health supplement manufactured by NOW – and were provided as 2 mg per larva in all replicate containers. We found evidence of higher survival to adulthood for *A. albopictus* at lower temperatures and when provided the Liver Concentrate by MP Biomedicals as a nutrient source. At higher temperatures, and in the presence of the general liver supplement by NOW, the inverse was seen, and *A. Aegypti* demonstrated higher survival rates compared to *A. albopictus*. Since nutrient content and availability are rarely uniform in field settings, these preliminary results provide a potential mechanism of *A. aegypti* coexistence where populations are sympatric.

A Comparison of Biology Student's Awareness, Usage Patterns, and Perceptions of ChatGPT.

Syed, Shifath Bin; Reid, Josh

Keywords: ChatGPT; Generative AI; artificial intelligence; biology education

In recent years, generative artificial intelligence (AI) tools, such as ChatGPT, have witnessed remarkable advancements, enabling their integration into classrooms by students. Nevertheless, the incorporation of such tools in education raises concerns centered around issues of academic integrity, data security, and the impact on educational outcomes. Investigating the usage patterns of ChatGPT by students and faculty is essential for informed decision-making and effective integration within educational contexts. Our research aims to investigate how graduate and undergraduate students in a biology department utilize ChatGPT in their biology coursework, as well as the perceived advantages and disadvantages of using ChatGPT in an educational setting.

A mixed-methods approach was employed, combining quantitative and qualitative data collection and analysis methods. Employing a mixed-methods approach ensures a holistic understanding, blending quantitative survey data with qualitative insights gained from interviews. Data was collected via a comprehensive survey and semi-structured interviews. The comprehensive survey assessed the frequency of ChatGPT tool usage, the specific tasks they utilize the tool for, and their perceptions of the usage of the tool in biology education settings. The semi-structured interviews provide deeper insights into participants' experiences, perceptions, and potential challenges in employing generative AI tools in this educational context. The qualitative data obtained will complement the survey findings, providing a comprehensive understanding of the factors influencing AI tool adoption.

In this poster, we will disseminate our findings from this study and share current recommendations for ChatGPT integration. In conclusion, this research delves into the evolving landscape of generative AI tools like ChatGPT in education. By investigating their utilization patterns in educational practices in biology courses, this study provides insights vital for well-informed decision-making on the integration of ChatGPT into the classroom. The findings will aid educators, students, and policymakers in navigating the dynamic interplay between AI technology and biology education.

Abundance and Disease Status for Starlet Corals in the Bay Islands, Honduras.

Dominguez, Gloria (1); Garza, Xaile (1); Quintanilla, Ana (1); Lockwood, Stephanie (3); Hicks, Matthew (1); Gomez, Racheal (1); Traesha Robertson (2); Stephanie Randell (1)

Keywords: Disease; Corals

Coral reefs support fish, hard corals, and plants. Starlet corals are a group of hermatypic corals that are a primary reef building species. Coral reefs are declining due to infectious diseases that are increasing at alarming rates. Two of the most prominent diseases affecting starlet corals are Dark Spot Syndrome (DSS) and the newly emerging Stony Coral Tissue Loss Disease (SCTLD). DSS is a disease that affects the symbiotic zooxanthellae, most commonly within the starlet corals, *Siderastrea siderea*, *Stephanocoecia intersepta*, and *Siderastrea radians*. DSS is known to cause nonlethal dark lesions that can persist on a coral colony for years, weakening the immune system and the CaCO₃ skeleton. SCTLD produces lethal lesions on stony corals, resulting in rapid tissue decay and becoming the deadliest coral disease. This study was conducted to assess starlet coral abundance and disease status on the Mesoamerican Barrier Reef in Roatán, Honduras. Field sampling was conducted using the Randell-Robertson Marine Survey Technique to locate starlet coral species on the reef. Once identified, species, health status, and disease coverage were recorded. 86% of *Siderastrea siderea* and 53% of *Siderastrea radians* observed were affected by DSS. Only one *Stephanocoecia intersepta* was recorded and was found to be healthy. Bears Den had the most *Siderastraea siderea* and *Siderastraea radians* diseased with DSS. Mandy's Eel Garden had the highest percentage of healthy *Siderastraea radians*. No starlet coral species were observed with active SCTLD, though 13 total were found dead. In future studies, researchers should investigate environmental factors that could lead to DSS.

The genome sequence of lytic *Pseudomonas aeruginosa* bacteriophages BL1, BL2, and BL3 isolated from the environment.

Marpa, Christopher Keith (1); Mosharraf, Fahareen B. (1); Rojas, Karagen (1); Bernard, Jeffrey (1); Rowell, Austen (1); Bono, Lisa M. (1)

Keywords: Bacteriophages; *Pseudomonas aeruginosa*; Genomics

In a complex community of bacteriophages, we methodically isolated and sequenced a group of phages demonstrating the ability to infect the *Pseudomonas aeruginosa* PAO1 strain. Our comprehensive analysis of these phages is driven by the key objective of identifying their inherent characteristics and potential, paving the way for prospective applications, particularly in phage therapy. Samples were collected from bodies of water and enriched against the *P. aeruginosa* PAO1 strain to get our desired phages. We used the standard agar-overlay technique from the collected community sample to isolate and purify specific phages to obtain triple-purified plaques in a controlled laboratory environment. High-titer lysates were prepared, and DNA was extracted and sequenced using Illumina NextSeq 2000. Data acquired underwent processing steps involving trimming, purification, and assembly using specific computational methodologies. The phages exhibited a singular contig surpassing 5000 bp, indicating that they belong within the unassigned Caudoviricetes family. No tRNA sequences, virulence genes, or antibiotic resistance genes were detected during the analysis. This research contributes comprehensive insights into the genomic characteristics of the isolated phages, providing a foundation for potential applications in combating antibiotic-resistant *P. aeruginosa* PAO1 infections.

Isolation and Characterization of Novel Bacteriophages Recovered from Soil Samples in Lubbock, TX.

Dickens, Whitney (1); Block, Natalie (1); Miller, Laurissa (1); Mosharraf, Fahareen (1); Smith, Allie (2); Bono, Lisa (1)

Keywords: bacteriophages, DNA extraction, restriction endonuclease digestion, gel electrophoresis

Bacteriophages are of increasing interest in modern scientific research, especially in their applications to medicine. In collaboration with the ongoing initiative started by the Howard Hughes' Medical Institute, the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program (SEA-PHAGES) curriculum was implemented at Texas Tech University through the TrUE Scholars Undergraduate Research Program. Environmental soil samples were collected from various locations across Lubbock, TX, and we worked to isolate, purify, and amplify phage virus from these samples; we were able to recover five novel phages from this process. We then extracted the DNA from these phages and performed restriction endonuclease digestion and gel electrophoresis to further characterize the genomes of these novel phages. The goal of characterizing these novel phages, alongside electron microscopy and sequencing and annotation of the genomes, is to further contribute to global efforts to identify novel phages for future research applications.

Physiological role of MAGEL2 protein in Prader-Willi and Schaaf-Yang Syndromes.

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Keywords: Prader-Willi Syndrome ;Schaaf-Yang Syndrome; Proteomics; Neurobiology; Western blot; Immunoprecipitation; Mass Spectrometry; TEM microscopy, Phylogenetics

MAGEL2 represents one of the biggest MAGE proteins, which are coded on the critical region of chromosome 15 (15q11-q13). The region is key in the occurrence of the Prader-Willi Syndrome (PWS), a genetic, multisystem neurodevelopmental disorder. Genes coded on the critical or PWS region of chromosome 15 are expressed only on paternally inherited chromosomes, with the loss of their expression leading to PWS. Besides the deletion of the whole region of the chromosome, which is common in PWS patients, the mutations in the gene MAGEL2 lead to the occurrence of the Schaaf-Yang Syndrome (SYS), a sister syndrome when it comes to symptoms. Even though scientists have elucidated many of the molecular characteristics of these diseases, the mechanisms of their development still elude exact interrogation, as do potential therapy targets for patients. Previous research has shown that MAGEL2 regulates retromer dependent intracellular recycling and excretion of protein in the hypothalamus, but the molecular mechanisms of the physiological function of MAGEL2 and the pathological consequences of its absence are still not clear. Recently a polyclonal antibody against Magel2 was developed, which will for the first time allow us to study the localization and the binding partners of the protein in tissue where it is expressed. METHODOLOGY: We have characterized the expression of MAGEL2 using publicly available databases. Then, we performed phylogenetic analyses of the MAGEL2 protein and all its thus far known binding partners to better understand their co-evolution. To determine novel binding partners, we plan to use immunoprecipitation with mass-spectrometry of endogenous Magel2 from mouse brain tissue. We have optimized the protocols for immunoprecipitation and plan to perform experiment on wild type and Magel2pΔ/m+ mice. Our results will help advance the understanding of Magel2 physiological function, its binding partners and pathological consequences when MAGEL2 is deleted in PWS and SYS patients.

Expression of oleosin increases fatty acids production in *Yarrowia lipolytica*.

Boafo, Kwesi (1); Cabrales-Arellano, Patricia (2); Delgado, Efren (3)

Keywords: *Yarrowia lipolytica*, Oleosin, heterologous expression, lipid bodies, fatty acids.

Oleosins are key elements in the lipid droplets from plants, their production has been related to lipid accumulation. This work developed several modifications in the pINA1269 expression plasmid to evaluate the best arrangement for oleosin production from cotton in the oleaginous yeast *Yarrowia lipolytica*. Diverse oleosin gene copies under hp4d and hp8d promoters were evaluated. The hp8d promoter showed higher oleosin expression by real-time PCR. Furthermore, yeast transformants under this promoter displayed higher lipid content especially Palmitic C16, Palmitoleic C16:1, Stearic C18, Oleic C18:1, and Linoleic C18:2 fatty acids compared with the wild-type Po1g strain. Oleosin expressed was targeted to the intracellular lipid droplets. These results evidence the importance of customizing vectors to obtain the highest level of interest protein and the role of protein constituents of lipid droplets, such as oleosin, as intracellular lipid recruiters.

Identification of genes essential for temperature-dependent biofilm formation in *Pseudomonas aeruginosa* using Transposon sequencing (Tn-seq).

Mercado, Vincent J. (1), Luecke, Alex R. (1), Wakeman, Catherine A. (1)

Keywords: Biofilm; Transposon; Genes

Mesophilic bacteria such as *Pseudomonas aeruginosa* can be isolated from a variety of locations such as soil, bodies of water and even within chronic and acute infections in plants and animals. Furthermore, *P. aeruginosa* is known to form biofilms, which are microbial cells housed within a sticky matrix called the extracellular polymeric substance (EPS). These biofilms are especially pragmatic in the context of chronic infections due to a significant increase in antibiotic tolerance. As microorganisms transition from one ecological niche to another, how does the physiology of both the free-living cells and biofilms change? Can we exploit these phenotypic adaptations to optimize our methods of microbial growth in both biotic and abiotic niches?

To answer these questions, we conducted a transposon sequencing (Tn-seq) analysis to identify mutants that are less fit in either biofilms or free-living cells of *P. aeruginosa* PA14 due to temperature stress. Each mutant has a single nonfunctional gene from an insertion event of a transposon into its genome. The mutants (~6,000 in total) were then pooled, and cultured at 23°, 30°, 37° and 40° C for 48-hours. In this pooled culture, mutants that do not survive or are less abundant after the 48-hour growth period will be sequencing less and thus the corresponding genes can be considered necessary for survival. From this analysis, we have been able to characterize essential genes for growth in both environmentally and clinically relevant temperatures. Even though *P. aeruginosa* can be found in various ecological niches, our methods for the eradication of biofilms remain limited; as such, identifying novel drug targets unique to environmental and clinical infections is paramount. Further studies of our genes of interest may aid in the development of new drug targets to better combat microbial growth in a range of infections.

Using QuantCrit as a methodological approach to measurement development.

Casas, Zianna & McFather, Luke; Rosario Marroquin-Flores; Tijerina, Rose Marie; Tedeschi, Mason; Banjara, Sophia; Warmesley, Redmon; Lisa, Limeri

Keywords: Community Culture Wealth, QuantCrit, measurement development, validity evidence

Students from minoritized communities are often viewed using deficit perspectives, where data focuses on the shortcomings that students have and how those shortcomings influence academic outcomes, rather than focusing on students' strengths. Community Cultural Wealth (CCW) is an asset-based framework that can be used to understand the collective strengths that minoritized students use to find academic success. CCW consists of six forms of capital: linguistic, familial, social, resistant, navigational, and aspirational capital. This presentation focuses on familial, navigational, and social capital. Familial capital refers to the cultural knowledge and moral consciousness established between a person and members of their family. Navigational capital refers to the skills that people develop as they maneuver through oppressive systems. Social capital refers to the network of people and community resources that are used to create support systems. While quantitative methods are frequently used to answer questions related to social inequity, they are often applied without considering their contribution to oppressive systems. QuantCrit is a methodological approach to data analysis, collection, and interpretation that can be used to conduct quantitative research more equitably. We are using a QuantCrit approach to develop and collect validity evidence for the first comprehensive measure of CCW. We are currently collecting evidence of validity based on response process by conducting cognitive interviews with STEM undergraduates. Data from the cognitive interviews are used to ensure that respondents from our target population understand the drafted items, respond to entire questions, and that our items are eliciting the expected responses. We specifically recruit undergraduates from a range of backgrounds, identities, and cultures because their strengths and experiential knowledge best situate them to contribute to the research. We hope our research can be used to challenge deficit perspectives and highlight how diverse students maximize their success in STEM fields.

Exploring the Role of Optic Tectum CRF Receptors in Feeding Behavior.

Murtuza, M.Ghufran (1); Kolli, Sreevalli (1); Carr, James A. (1); Harris, Breanna N. (1)

Keywords: CRF, Stress, Feeding, Xenopus, Optic Tectum, Prey

In order to survive prey animals must balance feeding and fleeing behaviors. Prey animals rely on multisensory cues to detect both food and predators. This decision-making takes place in a brain region called the optic tectum (OT). Although the neuronal mechanisms maintaining this balance are not fully understood, research suggests that corticotropin-releasing factor (CRF) in the OT plays a role in inhibiting feeding behaviors in the African clawed frog, *Xenopus laevis*. To further understand the interplay between CRF and the OT in feeding behaviors, we investigated whether the microinjection of CRF at varying doses into the OT of juvenile *X. laevis* alters behavioral responses to live prey cues, such as earthworms and crickets. Frogs were assigned to a treatment group (n = 12-16): one of four doses of CRF, saline, CRFR1 antagonist, gauged, or left unmanipulated. One hour after injection into the OT, frogs were exposed to a live prey stimulus (earthworm or cricket, respectively); feeding-related behaviors were recorded. We found that CRF presence in the OT subtly decreases but does not abolish responses to live prey cues. When treated with 0.001ug or 0.01ug doses of CRF, the juvenile *X. laevis* took longer to contact and put the earthworm in their mouth. The juvenile frogs treated with CRF as opposed to unmanipulated responded less often to the cricket. Data scoring for frog's responses and analysis are still pending. However, we predict that when injected with doses 0.001ug or 0.01ug of CRF, the frogs will take longer to contact the cricket and put the cricket in their mouth. Our data will aid in understanding the neuroendocrine mechanisms of feeding and fleeing behaviors, as well as probing the role of supra-hypothalamic CRF as a novel regulator of feeding in response to stressors. NSF Funded (Grant No.1656734)."

Phylogenomic analyses clarify the position of a divergent lineage of free-living and fecal associated protists (Sainouroidea, Rhizaria).

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Keyword: evolution; protistology; biodiversity; transcriptomics

Sainouroidids exhibit remarkable genetic and phenotypic heterogeneity. Members can be flagellates or amoeboid organisms; some are strictly unicellular, while others can be facultatively multicellular, and one member even utilizes an alternative nuclear genetic code. Sainouroidids can be found in marine, freshwater, and terrestrial environments, as well as the gut contents and feces of various animals. This divergent clade of protists, Sainouroidea, belongs to the eukaryotic assemblage Rhizaria. A well-resolved phylogeny of the group is a crucial first step in developing hypotheses regarding the evolutionary history of diverse traits and lifestyles exhibited by sainouroidids. The small subunit ribosomal RNA (SSU RNA) gene is the most used single gene marker for molecular phylogenetic studies in protists. While phylogenies based on the SSU rRNA gene support a home for sainouroidids in Rhizaria within the Cercozoa, its exact location is obscured by the highly divergent nature of this marker in members of this clade and the gene's limited ability to resolve ancient divergences within the tree of eukaryotes. To date, multigene phylogenies have done little to resolve this issue due to limited genomic data from sainouroidids and close relatives. To help resolve the position of sainouroidea within Rhizaria as well as the internal relationships between members of the group, we generated novel transcriptomic data from five sainouroidid taxa and three cercozoan relatives. We use these data to perform multigene phylogenomic analyses of Rhizaria, including sainouroidea. We discuss our results in the context of the macroevolutionary patterns in Sainouroidea and Rhizaria as a whole.

Measuring Asian Social Media Sentiments Towards Bat Exploitation.

Batrice, Amir (1)

Keywords: Attitudes; Social Media; Bats; Human-Animal Interaction; Sentiment analysis

As human activities continue to negatively affect bat populations, bat conservation efforts continue to rely on questionnaires to understand human actions towards bats; however, the use of questionnaires constrains understanding by limiting the sample size to those who choose to participate, being subject to selection bias, and overall may not be the most efficient way of understanding sentiments and behaviors towards bats. We used social media to analyze sentiment towards bat exploitation behaviors in Asia and evaluated the influence that these posts have on users in the region. We gathered and analyzed a total of 458 social media posts and 2581 comments throughout Asia utilizing keywords and hashtags in 16 languages. We found that nearly 90% of posts discussing bat exploitation were discussed in an acceptive way. Posts from Southeast and South Asia showed more acceptance to bat exploitation than East Asia. Comments from Southeast Asia, particularly the Philippines and Indonesia, were acceptive of bat exploitation for food and medicine, whereas comments from South and East Asia were rejective of bat exploitation. In contrast, South Asian posts were more acceptive of persecution of bats. Studying online sentiments towards these behaviors may provide us with important ethnic-cultural information alongside Bat Attitude Questionnaires. We recommend using social media platforms to promote messages that reject bat exploitation and encourage bat conservation efforts, as our results indicate that positive messages receive mostly positive comments, reinforcing the importance of protecting bats. Moreover, we suggest future work be conducted using social media to further understand region-specific narratives for and against bat exploitation.

Enhancing the Bryophyte Herbarium at Texas Tech University using Focus-stacked specimen images.

Mackey, Anij; Homoya, Hannah; Johnson, Matt

Keywords: Bryophyte; Focus-stacked; Photography; Macrophotography; Digitization; Herbaria

Despite the worldwide expansion of digitizing herbarium specimens in the 21st century, many bryophyte herbaria are under-digitized. Vascular plant herbaria tend to have high-resolution images of specimens, but nonvascular plants often only have an image of a label. The main objective of this project is to complete the digitization efforts of our bryophyte herbarium at Texas Tech University. Using a Macropod Pro 3D, we can create high-definition focus-stacked macro images of our bryophyte specimens. Partnering with the Symbiota support hub at Arizona State University, we can then upload the images to the Consortium of Bryophyte Herbaria, which is free for public use. These images will help support and further biodiversity studies, such as phenological data that wouldn't be transcribed on a label. The goal is to provide high-quality images for bryophyte specimens in the E.L. Reed Herbarium, which currently has 345 specimens, and to design a workflow for adding new focus-stacked images in the future.

Impacts of pyoverdine expression in *Pseudomonas* spp. during bacteriophage infection.

Bernard, J & Makilan, F; Rowell, A; Bono LM.

Keywords: Microbiology; Phage; Pyoverdine; Evolutionary arms race

Virus-host interactions are an evolutionary arms race where constant competition necessitates adaptation. One adaptation found in bacteria are virulence factors that have antiviral properties such as CRISPR or in this study a pigment. *Pseudomonas aeruginosa* is of clinical relevance due to being an ESKAPE pathogen known for its increased mortality and resistance to antibiotics. *P. aeruginosa* expresses the fluorescent pigment pyoverdine when placed under nutrient starved conditions and pyoverdine has been linked to increases in virulence, antibiotic resistance, and mortality during infection. Pyoverdine is expressed in most *Pseudomonas* spp. in different conformations and acts a signaling molecule for biofilm formation. We observed that increases in pyoverdine are also linked to an increase in resistance to bacteriophages. To determine if this relationship is found in all pyoverdine expressing species we tested susceptibility to bacteriophage in *P. aeruginosa*, *P. syringae*, and *P. pseudoalcaligenes*. By using species with different conformations of pyoverdine we can discern whether this is a universal mechanism or if there are species specific modifications that increase viral resistance. This will eventually allow us to identify factors in pyoverdine production that cause these antiviral properties. In *P. aeruginosa*, the bacteriophage were inoculated under standard or starved conditions and planktonic or biofilm for a total of four environmental conditions for 18 hours in a plate reader. This was replicated in different pathovar strains of *P. syringae*, *P. pseudoalcaligenes* using bacteriophage phi6. The plate reader measures absorbance (growth) and fluorescence (pyoverdine expression). We found that when pyoverdine expression was high the phage had less of an impact on bacterial growth suggesting increased resistance. Phage therapy has been suggested as an alternative to modern antibiotics, but in order to produce more effective therapies we must understand virus-host interactions.