11th TTABSS Poster Abstracts

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Primary Breast Sarcoma: A Retrospective Single Institution Study of Clinicopathologic Features, Treatment and Prognosis

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Primary breast sarcomas (PBS) are a rare and heterogeneous group of cancers with limited research and treatment algorithms. Previous PBS studies showed that the median overall survival (OS) for patients was 108 months. In this study we aim to determine factors associated with the survival of PBS patients and to develop a database of PBS cases from a single institution. We retrospectively reviewed data on 62 patients who underwent surgical treatment for breast sarcoma at MD Anderson Cancer Center from 2000-2020 that were identified from a previous institutional study.). Clinicopathologic factors examined included but were not limited to patient demographics, clinical features, and pathological features. Of the patients studied, 34 had PBS, and 28 had radiation-induced sarcoma from a previously treated breast carcinoma. Final tumor size was the only factor significantly associated with poor prognoses for PBS patients (HR: 1.1, P=0.03). Excisional/incisional biopsy was found to be a significant factor associated with decreased overall survival (P=0.003), and positive margins were found to be significantly associated with increased local regional recurrence (LRR, P=0.02); however, the data is unreliable as the confidence interval is too wide in range as a result of minimal data. No clinicopathological factors were found to be significantly associated with outcomes for breast sarcomas that were radiation-induced. There was no significant difference in OS, disease-specific survival (DSS), or LRR based on different treatment strategies. Preliminary data suggested that neoadjuvant chemotherapy was not effective in patients with PBS, except possibly in the cases of angiosarcoma. Our data confirm that increased tumor size is associated with decreased survival for patients with PBS. Interestingly, our data also suggests that different treatment strategies were not associated with outcomes. However, more patients are needed in the database to make the data more significant.

Responses of Leaf Stomata to 50 Years of CO2 Increase Using Herbarium Specimens

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Herbarium specimens provide a glimpse into various past characteristics of plants, which includes the ways that they interacted and responded to the environment. Plant gas exchange is a key process shaping global hydrological and carbon cycles and is often able to be characterized by plant water use efficiency. Plants are able to balance CO_2 intake with water loss by regulating the stomatal pore aperture and guard cell signaling is regulated by both environmental factors and plant hormones from plant fossil records, it is suggested that plant adaptation to changing atmospheric CO_2 has a correlated evolution in stomatal density and size. Together, stomatal density and size contribute to determining the maximum leaf conductance of CO_2, and in this study we used herbarium specimens to track stomata over time. A collection of over 1500 plant specimens housed in the E.L. Reed Herbarium at Texas Tech is from 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 CO_2 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.

Developing a Codebook Through Inductive Qualitative Analysis of the Biology Teacher-Scholars Program 2022-2023

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The Biology Teacher-Scholars (BTS) Program aims to enhance graduate teaching assistants' (GTA's) instructional training, and therefore improve the overall undergraduate learning experience. This program was created to provide professional development training to GTAs teaching the introductory biology lab course at Texas Tech. Nineteen GTAs participated in a pre-semester boot camp and attended monthly pedagogical meetings throughout the semester. After the boot camp, GTAs provided feedback through exit ticket surveys which allowed us to evaluate any improvements that could be made in the BTS program moving forward. Through inductive qualitative analysis, responses from these surveys were evaluated by our team (individual coding followed by consensus coding) to derive common themes emerging from the collected responses. A codebook was developed to categorize responses into broader themes. Discovered themes include responses about sessions that the GTAs found more useful that relate to undergraduate teaching or personal development for GTAs. Codes such as "relates to assessment writing", "relates to classroom management", "emphasis on session" and others were developed as part of the codebook. Some responses also allowed us to determine whether they related to a certain teaching perspective (Pratt et al., 2001) or to the GTAs self-efficacy (DeChenne et al., 2012). By examining common trends in these responses, our team gained a greater understanding of the effectiveness of the program and what adjustments to make going forward. Additionally, the results from this consensus coding served to guide us in forming interview questions this upcoming semester. This will allow us to delve deeper into the GTAs overall experience as teaching assistants in the Biology department.

Phytomedicine: The Extraction of Chemical Compounds from *Salvia* and *Philadelphus* Herbarium Specimens

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The herbarium is an untapped resource for novel chemical components that may be relevant for phytomedicine and the treatment of ailments. Within the E.L. Reed Herbarium at Texas Tech, two groups of plants with potential for chemical extraction are *Salvia* and *Philadelphus*. The *Salvia* species are versatile in use as teas, oils, and spices and in traditional medicines to decrease ailments from skin, digestive, and throat complications. *Philadelphus* species are known for their sweet scent of orange blossoms or maple and put for decorative purposes in gardens. We aimed to test whether we can identify chemical compounds relevant to phytomedicine from herbarium specimens of *Salvia* and *Philadelphus*. We conducted chemical extraction using dichloromethane and NMR/Mass Spectrometry. By testing specimens from the 1970s and the 2020s, we can determine age is a factor in chemical preservation, whether chemical potency is reduced over time, and whether chemicals differ substantially within species.

Testing for evidence of cryptic species in the widespread moss *Physcomitrium pyriforme*

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According to the biological species concept, species in the same genus should be more genetically distinct than individuals within a species due to reproductive isolation. However, in the widespread moss *Physcomitrium pyriforme*, we have evidence of three distinct genetic clusters unrelated to geographic isolation. We hypothesize that *P. pyriforme* contains cryptic species - taxa that are morphologically indistinguishable but genetically different. We aim to confirm whether the three clades are morphologically distinct in microscopic characteristics including spore and stomatal size. Using a controlled cross-experiment, we also aim to test for reproductive isolation across clades.

Our study uses the cultivation of moss species *P. pyriforme* from different geographical locations to see if there is any relationship between genetic clusters and reproductive isolation or geography. We crossbred three clades from eastern North America in a growth chamber to test for production of hybrid offspring. The lack of offspring would suggest that *P. pyriforme* has cryptic species under its genus. In the likelihood that an offspring is produced and makes it to the maturation stage of its lifecycle, we would test the fertility of the sporophytes and gametophytes.

An alternative explanation is that species are not cryptic but are instead defined by microscopic characters. Our expected findings include differences in spore and stomatal characteristics between the clades of *P. pyriforme*. Each genetic cluster having different stomatal characteristics of size, density, and count would support the description of new species of the common bladder moss.

CSI Plant: A New Way to ID Plants in Mixtures

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The objective of this experiment is to detect plants using their DNA in mixed samples. This cannot be done already due to the large size of plant genomes. The traditional plant DNA barcoding methods that have been used over the past 15 years are only sensitive enough to detect plant genus. By using Angiosperms353, there is a larger available DNA window and it could be possible to detect specific plant species in mixtures. It is crucial for people to know what is in mixtures they purchase in order to protect endangered species, provide environmental safety, and protect consumers.

This experiment uses a seed mixture from known species. Known vouchers from the same species were from enriched DNA sequences created using Angiosperms353. The idea is to develop and evaluate a new bioinformatics method to identify whether it is possible to identify known species in a mixed sample. Success of this project has implications for detecting plant species in other unknown situations such as correct identification of species in herbal supplements and helping monitor for the presence of endangered or invasive species.

They're Around Here Somewhere: The Search for Phage

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Pseudomonas aeruginosa is a known pathogen that chronically infects patients suffering from cystic fibrosis. The purpose of our research is to isolate bacteriophage from various freshwater lakes around Lubbock, TX and see how human disturbance correlates to the presence of *P. aeruginosa*-infecting bacteriophage in these lakes. We hypothesize that phage collected from more disturbed lakes would tend to infect *P. aeruginosa* strains associated with human infection while the host range of phage from less disturbed water sources would contain environmental host strains. We identified a series of playa lakes that varied in distance from human activities, including parks, hospitals, etc. These samples underwent a series of dilutions and filtration steps, and afterwards they were then triple plaque purified. Phage host range was assessed by spotting on a variety of *P. aeruginosa* hosts, including clinical samples collected from hospital patients and environmental isolates. We incubated these plates over a range of temperatures from room temperature to human body temperature. Additionally, the morphology of the phage were characterized using TEM. In the future, the phage will be assessed as candidates for phage therapy.

Chromosomal Inversions in Brown Creepers (*Certhia americana*) Along an Environmental Gradient

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Genotype-environment associations are a crucial part of studying how organisms evolve and adapt to their environments. Here, we are investigating whether the frequencies of chromosomal inversions in populations of a songbird (Brown Creeper; *Certhia americana*) are associated with environmental characteristics. Brown Creepers have populations extending from Alaska to Honduras, where they occur in coniferous forests and forage for invertebrates and seeds by scaling tree trunks. Chromosomal inversions are large-scale mutations present as a result of a segment of a chromosome breaking off and reattaching in the reverse direction and may impact evolutionary processes. Between temperate and subtropical habitats in the transition from the Rocky Mountains to the Sierra Madre Occidental in western North America, Brown Creepers occupy vastly different environments and possess different combinations of inversions. We want to discover whether these inversions are associated with environmental factors along this environmental gradient. We therefore obtained tissue samples of Brown Creepers on a transect from central Mexico to Utah and are conducting a polymerase chain reaction restriction site fragment length polymorphism (PCR-RFLP) molecular analysis to measure chromosomal inversion frequencies across populations. Following the PCR-RFLP analysis, we will use regression and ANOVA statistical tests to understand the type of association between environmental factors and frequencies of the inversions. We will test inversion associations with three environmental factors: mean annual temperature, precipitation during the summer (breeding season), and vegetation type. Though we do not yet know which Brown Creeper populations between Utah and Mexico will possess inversions on certain chromosomes, we anticipate that we will find a stronger correlation between frequencies of certain inversions and vegetation than the remaining two environmental factors (mean temperature and precipitation). By performing this study, we hope to shed light on how large-scale genetic variants such as inversions are tied to organisms' evolutionary processes and adaptation to different environments.

A Second Chance for Industrial Hemp in Texas: Ecological Issues for the Semi-Arid Southern High Plains

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KEYWORDS: Hemp; Arbuscular Mycorrhizae; No-till Agriculture; Southern High Plains Soil

Until recently, *Cannabis*, or more commonly known as weed or marijuana, was banned in the United States as many viewed its only purpose was for high content of Δ9-tetrahydrocannabinol. However, *Cannabis*, or hemp, can be utilized in many ways than simply the production of Δ9-tetrahydrocannabinol. In recent years, Texas legislatures have recognized the potential of industrial hemp production and have legalized such production. However, the arid and drought-prone climate of West Texas may deter farmers from experimenting with this new crop. Currently, producers are using *Cannabis indica* for commercial production in the semi-arid, drought-stricken climate of Southern High Plains. The goals of this research are to evaluate the capacity of several varieties of *C. indica* to form arbuscular mycorrhizal fungal symbioses under current soil management practices that can increase drought tolerance for field grown hemp. We have data from two studies to begin to address mycorrhizal capacity of hemp in production fields. Root samples were collected from a project established at the TTU- Quaker farm in Spring 2022 in early summer just as the drought started, to assess arbuscular mycorrhizal fungal colonization levels of seven hemp varieties. We also have preliminary data from two hemp production farms in the Dumas area under center pivot irrigation from soil collected in September 2022. One farm was managed as a conventional tilled system and the other as a no-till and stubble managed system. For the Dumas study, ten composite soil samples were obtained across each field for assessing arbuscular mycorrhizal fungal inoculum potential in the green house using four varieties of hemp. The Quaker Farm results and results from the Dumas greenhouse study will be presented.

Does CRF in the optic tectum alter the behavioral response to live prey cues?

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KEYWORDS: CRF; Stress; *Xenopus laevis*; Endocrinology

Survival of prey animals depends on balancing feeding and fleeing behavior. To determine this behavior, prey animals rely on multisensory stimuli cues, which, in the frog *Xenopus laevis*, are processed in a brain region called the optic tectum. Although the mechanisms maintaining this balance are not fully understood, research suggests corticotropin releasing factor (CRF) in the optic tectum plays a role in inhibiting feeding behavior in *X. laevis*. We investigated whether the injection of CRF into the optic tectum of juvenile *X. laevis* alters the response to live prey cues, such as earthworms and crickets. Frogs were assigned to a treatment group (n = 15-18): one of 4 doses of CRF, saline, or left unmanipulated, and a stimulus condition (visual or lateral line). One hour after bilateral tectal injection, frogs were exposed to a stimulus condition, immediately followed by delivery of a multisensory, live prey stimulus (worm or cricket, respectively); feeding-related behaviors were recorded. We found that CRF subtly decreases, but does not abolish, responses to live worm prey cues. When treated with 0.001ug and 0.01ug doses of CRF, the juvenile *X. laevis* took longer to make contact with the worm and to put the worm in their mouth. This suggests that the frogs took longer to identify the worm as a prey cue. The data collection for the frog's response to the cricket is currently underway. However, we predict that when injected with the dose of 0.001ug and 0.01ug of CRF, then the frog will have an increased latency to contact the cricket and put the cricket in its mouth. Our data will aid in understanding the neuroendocrine mechanisms determining feeding/fleeing behavior. NSF Funded (Grant No.1656734).

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

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Microbial endophytes (fungi and bacteria that live within plant cells) are understood to play a significant role in the ecology of their plant hosts, but little is known of their response to climate change. Now, the diversity of microbes can be easily quantified with DNA sequencing, but there is little historical data with which to compare modern findings. Herbarium specimens provide an historical record of bacterial and fungal endophyte communities, allowing for study of how endophytic communities may have changed over time. In this study we analyzed 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. We extracted and sequenced DNA from herbarium specimens and analyzed data using standard microbiome data processing pipeline. We characterized endophyte species richness and phylogenetic relatedness across time points and plant host species. Our results provide proof of concept for characterizing endophyte diversity using herbarium specimens and contribute to building a better understanding of the change in composition of plant microbiomes, as a response to climate change.

Novel Behavioral Assays to Investigate Multisensory Responses in the Frog *Xenopus laevis*

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KEYWORDS: *Xenopus laevis*; behavior; multisensory; feeding; environmental stimuli

Prey animals must balance their behavior between finding food and avoiding predators in order to maximize their chances of survival. To do this, many animals gather sensory information from their environment and change their behavior accordingly. In the frog *Xenopus laevis*, a specialized region of the brain called the optic tectum receives and integrates a variety of sensory stimuli to determine feeding behavior in response to perceived threats in the environment. However, it is unknown whether a specific stimulus type, such as visual, vestibular, auditory, or lateral line, predominates in this decision-making process. In order to better understand the function of the optic tectum in *X. laevis*, we've developed behavioral assays that measure feeding behaviors in response to distinct sensory stimuli, namely visual and lateral line. Frogs were isolated and exposed to either a visual stimulus (iPad video of worms) or a lateral line stimulus (air puffs), then feeding specific behaviors were measured and analyzed. These assays significantly reduce irrelevant environmental stimuli while exposing the frogs to a deliberate, repeated, specific stimulus type in order to isolate the effects of discrete sensory information on feeding behavior. Our data show that the assays elicit consistent and specific feeding behaviors in frogs in response to specific stimuli. Ultimately, these novel behavioral assays present a systematic method of studying optic tectum function and its role in feeding and fleeing behavioral tradeoffs in *X. laevis*. NSF Funded (Grant No. 1656734)

Bloodmeal Host Identification of Vector Mosquitoes from Harris County, TX

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Female mosquitoes can acquire bloodmeals from a variety of hosts. These hosts can serve as potential reservoirs of pathogens that cause human diseases. Blood-engorged females of the *Culex* and *Aedes* genera were collected in Harris County, Texas. Molecular techniques, combined with database searches, were used to determine the sources of individual bloodmeals. Hosts identified include humans, canines, and various avian species. Our results suggest a broad spectrum of host utilization by vector mosquitoes in Harris County. Feeding preferences for mosquitoes can be used to predict potential routes of pathogen transmission and can help inform vector management strategies in major urban centers in the United States.

mRNA Translational Changes upon Loss of MAGE-L2 in Prader Willi Syndrome Mouse Model

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KEYWORDS: Prader-Willi Syndrome; MAGE-L2; Translation

Introduction: We aim to determine whether melanoma antigen L2 (Magel2) contributes to translational regulation in the hypothalamus and pituitary of the Prader Willi syndrome (PWS) mouse model. Translational controls of gene expression occur on polysomes (polyribosomes) which are made of mRNAs, ribosomes, several proteins, and non-coding RNAs. Dysregulation of protein translation contributes to human diseases, however, how it contributes to PWS pathogenesis, is not known. PWS clinical symptoms include excessive weight gain and developmental delay, suggesting hypothalamic dysfunction. Although it is well established that a cluster of imprinted genes, including MAGEL2, on human chromosome 15, is responsible for the PWS pathogenesis, the underlying mechanism is not known.

Methodology: Polysome profiling determines changes in the translation of individual mRNAs based on sucrose density gradient fractionation. We first optimized the fractionation of the hypothalamus and pituitary tissues.

Results, conclusions, and future directions: We have optimized the conditions for pituitary and hypothalamus polysome analysis for the experiments on wild-type and knockout mice. Our data will provide the first insights into translational regulation in PWS with potential therapeutic implications for PWS children.

A Qualitative Examination of Student Perceptions of their Instructors' Beliefs

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Previous work has indicated that students can perceive and are sensitive to their instructors' beliefs about their students' ability and intelligence. For example, quantitative studies show that these perceptions can influence students' psychological vulnerability (Muenks et al., 2020) and grades (LaCosse et al., 2021). This project's objective is to examine how students form their perceptions of their instructors' beliefs by asking two research questions: 1) What messages from instructors do students perceive as communicating their instructors' implicit beliefs about students' ability and intelligence? and RQ2) What is the content of this communication? Three relevant lay theories of intelligence will be studied in the undergraduate STEM context: mindset (I.e., the malleability of intelligence), universality (I.e., Is everyone capable of succeeding, or only some?), and brilliance (I.e., Is innate talent required for success).

We recruited 24 diverse undergraduate STEM students for participation in cognitive interviews, in which students were asked to respond to and reflect on their responses to the 25-item ULTrA survey (Limeri et al., 2022). These transcripts were then coded to identify major themes of student responses. To answer RQ1, we detected four messages containing belief signals: goal orientation (How does the instructor define success?), distribution of student success (What fraction of students is capable of success?), attribution of student performance (Why do students successful or unsuccessful?), and affordances (What characteristics enable students' success?). To answer RQ2, we identified communication modalities of the aforementioned messages which we classified as statements, actions, course policies, and non-verbal behaviors.

This study may eventually help inform instructor-targeted interventions where instructors can be taught about how to send positive belief signals to their students, which can help optimize student persistence, retention, motivation, and performance by improving their psychological profiles. Even minor changes in instructor behavior may have the capacity to profoundly benefit students' classroom experiences.

Measuring the cultural assets that diverse students bring to Texas Tech University

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When students struggle academically, educational institutions often attribute those struggles to a deficit in cultural capital. Cultural capital refers to the experiences, knowledge, and skills valued by the privileged majority. Community Cultural Wealth (CCW) is an asset-based framework based in Critical Race Theory (CRT) that reframes the deficit perspective to focus on the cultural strengths that students possess. CCW consists of 6 forms of capital: aspirational, navigational, social, linguistic, familial, and resistant. Using a QuantCrit approach, we are developing the first complete quantitative measure of CCW to better understand the different forms of capital that minority students use to be successful in higher education. QuantCrit is a research method that takes a more equitable approach to data analysis by applying CRT principles to data collection and analysis. This presentation will focus on questions in the CCW measure related to navigational and resistant capital. Navigational capital refers to the knowledge and problem-solving skills used to maneuver through oppressive systems. Resistant capital refers to the knowledge and skills required to challenge oppressive systems and seek reformation. As part of the QuantCrit approach, we considered identity, wrote positionality statements and individually drafted questions to describe our lived experiences. We then collectively reviewed, revised, and consolidated individual questions to create a composite measure. We are currently conducting cognitive interviews to identify and revise any confusing questions that may exist in the measure. We hope to use this measure to start critical discussions about equity in education and challenge deficit perspectives.

Analyzing Microbiome Changes in Wild and Domesticated Bananas using Metatranscriptomics

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KEYWORDS: Domestication; Bananas; *Fusarium*; SAMSA2

Domestication generally reduces a plant's genetic diversity, increasing its vulnerability to pathogenic fungi and bacteria, but perhaps as importantly, domestication can also reduce the diversity of disease-protective plant microbiomes. Domesticated bananas are threatened by *Fusarium* wilt caused by the fungus *Fusarium oxysporum* f.sp. *cubense*, but we hypothesized that one potential strategy to control *Fusarium* wilt may be to transfer the more diverse microbiome from wild-type bananas to domesticated bananas. To test this idea, we extracted the microbiomes from 3 wild banana plants (*Musa balbisiana* or MB) using a modified enrichment protocol, and inoculated it into roots of domesticated *Fusarium*-susceptible banana plants (*Pisang awak* or PA). After one month, *Fusarium* pathogen (Foc Race 1, ATCC) grown in a potato dextrose agar (PDA) medium and incubated at $25\pm1°C$ for 4 days was introduced as a spore suspension (106 spore/ml) to PA plants with and without MB's microbiome. Plant disease symptoms were recorded. Results suggested MB-treated plants were healthier than untreated controls. Plants were harvested and microbiomes were isolated to study gene expression changes (RNAseq) with analysis in SAMSA2 which aggregates and annotates mRNA transcripts and taxa using DIAMOND. The goal will be to assess microbe and host gene expression changes to understand the underlying mechanisms contributing to enhanced disease protection in plants inoculated with wild-type microbiomes to ultimately develop new sustainable strategies for controlling disease.

Characterization of novel Pseudomonas spp. bacteriophages from environmental samples of fresh water public lakes.

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AFFILIATION(S): (1) Texas Tech University

Pseudomonas aeruginosa is a bacterium that opportunistically infects immunocompromised individuals, mostly through nosocomial transmission. However, it also infects a variety of hosts found in soil, biofilms, and bodies of water. Our purpose is to isolate environmental phage from environmental samples and characterize them. We hypothesize that phage from sites closely associated with human disturbance will have increased phage populations able to infect human-isolated *P. aeruginosa* strains. We collected environmental samples across various locations that vary by human disturbance. After centrifugation and filtration, we plated samples on *P. aeruginosa* lawns and then collected phage communities. We then isolated individual phages and triple plaque purified then. Their genome, size, and whether they are segmented were assessed using gel electrophoresis. Phage are classified by sequencing and are further characterized by measuring their growth rate on several pathovars of *P. aeruginosa*. In the future, we will assess if the phage are good candidates for phage therapy by testing their ability to disrupt biofilm formation.

Flammability and Fire Response in 20 Perennial C4 Grasses

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KEYWORDS: Fire ecology, grass flammability, grasslands, C4 grasses

Grassland ecosystems are widespread across the world, covering more than 40% of the land's surface and sequestering approximately one third of the total terrestrial carbon store. Grasslands in warmer regions are dominated by species with the C4 photosynthetic pathway and C4 grasslands are often maintained by frequent fire. Perennial C4 grasses with buds protected at or below the soil surface are resilient to fire, especially when such fire occurs outside of the growing season. Fire can in fact indirectly aid such grasses because grasses provide fine fuels that can drive rapid fire spread and such fires can wound or kill woody plants that might otherwise overtop and shade grasses in the absence of fire. Grass species, however, are not uniform in their tolerance of fire and recent work suggests that they might also differ in their flammability. Understanding variation in flammability and how it correlates with fire response strategy can help aid fire management in these grasslands. Our study seeks to 1) determine what traits drive flammability differences across 20 C4 grasses and determine whether leaf or canopy traits better predict flammability; 2) test if flammability and post-fire regrowth are correlated across these species. We hypothesize that greater flammability will be associated with higher biomass, and greater canopy height ratio (relatively more mass carried above 10 cm height). Additionally, we hypothesize that more flammable species will have more rapid post fire regrowth. Our results will answer an open question regarding grass evolution: are flammability and fire tolerance evolutionarily correlated? This work will contribute to a better understanding of how fire has shaped evolution in fire-prone lineages and inform effective land management strategies in warm season grasslands. Preliminary data analysis indicates variation in ignition and volume consumed across species. Complete results to be presented.

Microscopic examination on Cyanobacteria and detrimental health effects caused by Cyanotoxin

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There has been a worldwide increase in harmful Cyanobacteria blooms that imposes public health on animals and humans. Cyanobacteria, or blue-green algae, is a Gram-negative prokaryotic microorganism that obtains energy through photosynthesis. It is the earliest form of life on the Earth that originated between 2.5 to 3.5 Billion years ago. Cyanobacteria can cause toxic poisoning that occurs in aquatic ecosystems such as lakes, rivers, ponds, etc. Nutrients like phosphorus and nitrogen are essential to the natural elements and to the growth of plants within the underwater environment. When runoff in urban and rural terrain flows into the lakes, ponds, and rivers, they create nutrient pollution and become fertilizer for the algae to bloom. There are about 40 genera of Cyanobacteria that are responsible for the toxin production but the two types that are common in the Texas region are Anabaena sp. and Microcystis sp. We collected samples from water bodies from different locations and observed them under a BX-40 Olympus microscope attached to a DP-74 Digital Camera equipped with CellSens software. The toxins produced by Cyanobacteria have proven to be deleterious to humans or animals, if ingested. The leading cause of toxicity from Cyanobacteria is the drinking of contaminated water due to the overpopulation of toxin-producing species of Cyanobacteria. The most common toxins that cause issues through contaminated water are microcystins, cylindrospermopsin, saxitoxins, and anatoxin-a. Anatoxin-a- and saxitoxins are classified as neurotoxins with saxitoxins being most prominent in shellfish poison, and microcystins and cylindrospermopsin are classified as liver toxins. However, there are many DWTPs, drinking water treatment plants, which are being used to counter water pollution. In addition, to the health risks caused by Cyanobacteria, they have a significant effect on environmental changes like atmospheric changes, the health of coastal environments, ozone changes, endocrine chemical disruption, and bioaccumulating toxicants-remains.

Developing a novel treatment for systemic lupus erythematosus

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One chronic autoimmune condition causing severe inflammation and pain throughout the body is systemic lupus erythematosus (SLE) is. The only approved FDA therapy for SLE carries the deadly black box warning. Worse, it treats downstream events in lupus instead of underlying causes. One factor causing SLE is deficiency of the endonuclease Dnase1L3. Dnase1L3 cleaves pro-inflammatory DNA released from dying cells. Without Dnase1L3, immune complexes build up in the body, causing the symptoms of lupus. Mice lacking Dnase1L3 develop lupus-like phenotypes, so they represent a model for testing Dnase1L3 replacement therapies. In order to distinguish Dnase1L3-/- mice from wild type mice, genotyping of these mice by PCR is needed. Here I optimized the genotyping protocol for Dnase1L3-/- mice. The mice provided by UC Davis were unable to be genotyped with the primers provided, hence new primers were designed and tested to be able to correctly identify which mice we expect to show a lupus-like phenotype. The original primers showed significant smearing in each DNA sample tested. Attempting to optimize the UC Davis PCR protocol, the reagents were validated, and then varying concentrations of DNA and primers were tested. The annealing temperature and number of amplification cycles were tested through a gradient, ultimately leading to inconclusive genotype results. New primers were then designed and tested, and the genotype of the Dnase1L3-/- mice were able to be obtained. Determining the mouse genotype will enable us to evaluate lupus-like phenotypes in these mice along with control mice, and breed mice for testing Dnase1L3 replacement therapy. Dnase1L3 replacement therapy represents a novel treatment for a devastating condition. Treating an underlying cause of the lupus - rather than treating the symptomatic onset - is expected to sustainably prevent symptoms from occurring.

Human sweat compound nonanoic acid causes lower attraction in mosquitoes

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Mosquitoes use odor cues to detect and track bloodmeal hosts using olfactory receptors encoded in their genomes. One family of receptors, the Ionotropic Receptors, has been implicated in detecting volatile acids in host odor emanations. Specifically, Ir75e responds to nonanoic acid, a component of human sweat. We used uniport olfactometry to test *Aedes aegypti* responses to nonanoic acid within a host-seeking context. We found that mosquitoes were less attracted to a blend of nonanoic acid and carbon dioxide (18.7%) than to carbon dioxide alone (28.1%). This raises questions about the ecological relevance of nonanoic acid for *Aedes aegypti*. Using CRISPR/Cas9, we are developing knock-in mosquitoes to explore further the roles of IRs in carboxylic acid behavioral responses.

Reusable bioinspired protein-based materials for rare earth elements extraction

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KEYWORDS: Rare Earth Elements; Lan Modulin; Maltose-binding protein

Rare earth elements (REE) consist of the lanthanide and actinide series on the periodic table. They are necessary components of high-tech consumer products, defense technologies and clean energy technologies, making them precious metals. Their low natural availability in ores makes the extraction methods of them a critical process. The discovery and characterization of Lanmodulin (LanM), a lanthanide-binding protein, has shown it to be highly selective of this group over common metals like Ca^{2+} and Mg^{2+} by up to 108 fold. Additionally, recent studies have proven the potential to improve current liquid-liquid extraction methods of lanthanides, which have been recognized as being time consuming, costly, and negatively impactful to the environment due to the harsh chemicals needed to run multiple cycles of these extractions. Studies have also shown that LanM has limited reusability in REE extractions when it is covalently immobilized to a substrate during column chromatography, exposing limitations to this method. Our group is working to alleviate the limited use of LanM during liquid-liquid extraction by creating a reusable LanM-based REE extraction resin. In this project, we will include a maltose binding protein (MBP) affinity tag to the LanM sequence due to the tag's known function of reversibly binding with amylose resins in the presence of maltose. This will allow the extraction process to be repeated multiple times by eluting degraded LanM and reloading it with fresh LanM. MBP will be attached to the C-terminus or N-terminus of LanM to first identify changes in efficiency of LanM in REE extraction. Next, our MBP-tagged LanM will be tested on its capacity to bind and elute from the resin. This could potentially remove the need to run size exclusion chromatography of LanM elutions with our reversible tag, reducing the days of preparation and having instead back-to-back REE extractions.

The Role of Tectal CRF in Lateral Line Related Feeding Behaviors

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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 frog *Xenopus laevis*, the optic tectum is responsible for consolidating visual and lateral line information and 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.

Responses to invasion by garlic mustard plants on native plant-mycorrhizal population

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KEYWORDS: Arbuscular Mycorrhiza; Garlic mustard, Invasive species

Biological invasion is a serious environmental issue that requires the development of effective prevention and management strategies to mitigate their impacts. Invasive species compete with native plants for water, nutrients and other resources and often outcompete them by releasing allelochemicals that can target several life processes of native organisms. Garlic mustard (*Alliaria petiolata*), an invasive herb found across North America, produces allyl isothiocyanate (AITC), which is toxic to Arbuscular Mycorrhizal (AM) fungi in its introduced range. AITC reduces growth, the abundance of AM fungal hyphae in soil, and soil respiration and root colonization, and is considered an allelochemical. When AM fungi are inhibited by invasive species, plants generally assimilate less carbon. Reorganization of the plant-AM fungal mutualism due to invasion can decrease AM fungal abundance inside roots and soils, shift AM fungal composition and species richness, and reshuffle plant-AM fungal interactions. The plant-AM fungal mutualism facilitates carbon flow to the fungus and nutrient flow to the plant. In that case, we expect to observe an increase in carbon allocation to less beneficial AM fungi which might lead to a decrease in nutrient transport to the native plants. On the plant level, increases in the carbon cost of nutrient acquisition may result in growth reductions or even loss of biomass. To explore plant physiological responses to *Alliaria* invasion, we plan on measuring leaf-level gas exchange, foliar chemistry, whole-plant metrics and conducting light-saturated net photosynthesis (A) by intercellular CO_2 (Ci) curves (A/Ci) simultaneously with fluorometry using a LiCor LI-6800. We will also measure foliar carbon, nitrogen, phosphorus, $\delta 13C$, and $\delta 15N$ molecules that will allow us to track nutrient uptake by leaves and compute leaf stoichiometry, photosynthesis, and nutrient use efficiency to understand the trade-off between water and nutrient use efficiency.

Impact of HIV and SARS-CoV-2 on Immune Responses in the Human Airway

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The COVID-19 pandemic provides an opportunity for the collision of SARS-CoV-2 with chronic infections such as Human Immunodeficiency Virus (HIV). We previously studied the impact of HIV on COVID and showed prior HIV+ status did not increase inflammatory cytokines associated with COVID-19. However, SARS-CoV-2-mediated airway immune responses in the presence of HIV strains is unknown. HIV interacts with CCR5 (HIV-R5 strain) or CXCR4 (HIV-X4 strain) coreceptors and triggers different degrees of inflammation that may damage the lungs. Our previous studies demonstrated different biological effects of R5 or X4 viruses on pulmonary vascular cells. Herein, we investigated the impact of HIV on airway (epithelial) cells, the portal of entry for SARS-CoV-2. We hypothesized that the R5 and X4 virus will trigger different immune responses in epithelial cells exposed to SARS-CoV-2 spike protein. We cultured human bronchial epithelial cells (HBECs) on air-liquid interface (ALI). We challenged HBECs with recombinant HIV R5 or X4 at the basolateral side for 48 hours. We added recombinant SARS-CoV-2 spike protein (S1) at 50ng/mL on the apical side for 4 hours followed by analyses of innate/adaptive immune response gene expression. Exposure to HIV-X4 upregulated CD14 and downregulated SLC11A1, FOXP3, TLR4, and IL13 while HIV-X4+S1 downregulated FOXP3. Exposure to HIV-R5 upregulated CCR4, CSF2, MPO, IL1A, TLR2 and downregulated IRAK1 while HIV-R5+S1 upregulated IRAK1 and IL1B. Reactome analysis suggested that HIV-X4 affected signaling pathways associated with cell death, and HIV-X4 and HIV-X4+S1 downregulated the activation of Toll Like Receptors. HIV-R5 affected signaling pathways associated with IL10, as well as differentiation of myeloid cells. HIV-R5+S1 affected CLEC7A/inflammasome pathway and IL1 and IL10 signaling. Our preliminary observations let us conclude that pulmonary epithelial cells exposed to HIV-R5 or X4 combined with S1 triggered different immune signaling pathways. Further studies are needed to determine the impact of HIV/coronavirus co-infections in the vasculature.

Are Superbugs Around You? Watch Out...

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A superbug is a bacterium that is resistant to more than 2 antibiotics. In our findings, we determined most bacteria around us were resistant to more than 2 antibiotics. Antibiotics are used to treat bacterial infections in the body. In a previous study, samples were collected from Texas Tech Students in 2020 from the front and back of the mask, headphones, and cell phones. *Streptococcus epidermidis* and *Streptococcus aureus* were identified (among others) as bacteria leading to maskne (acne caused by frequent mask-wearing). In this study, we answer the question of which bacteria around us can be identified as a superbug and test the efficiency of the most commonly used antibiotics against them. We grew the bacteria on TSA plates and challenged them with eight antibiotics: neomycin, vancomycin, ampicillin, lincomycin, doxycycline, bacitracin, and cefotaxime. The susceptibility of bacteria was determined by measuring the zone of inhibition of the antibiotic disc. Based on our results, novobiocin and bacitracin (targeting DNA synthesis and cell wall synthesis respectively) were the least effective while doxycycline (targeting protein synthesis) was the most effective. Few of the samples were resistant to 1 antibiotic, most to more than 3, and few to at least 5. Most of the *S.aureus* were resistant to novobiocin, bacitracin, and cefotaxime. One isolated colony of *Micrococcus luteus* was highly resistant to antibiotics (5/8) along with *Streptococcus capitis* (5/8), the first found on the back of the mask and the latter found on the front. These findings indicate superbug bacterium can be found easily floating around us in the air or as a part of our microbiome. These bacteria could be considered carriers of resistant genes, and when they die, other bacteria such as *S. aureus* can pick up these genes and acquire extra resistance.