

SCRC Abstracts 2023

Sorted by Last Name of Presenter

NCBI Blast: An Approachable Bioinformatics Tool for Genetic Analysis of Pan paniscus and Homo sapiens Genomes

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Bioinformatics considers the application of tools of computation and analysis to capture and interpret biological data. Projects like the Human Epigenome Project have created large quantities of sequencing data from various organisms. As a result, researchers created various tools to analyze raw sequencing data further. Although many tools are available, their overall organization may make them unapproachable. Considering this, the study aims to make bioinformatics tools more approachable and to demonstrate their efficiency in genetic analysis by introducing a commonly used tool called NCBI Blast. The study uses specified offsets between chromosome one of the Pan paniscus (including the Mhudiblu _PPA_v0 and panpan.1.1 genome) and the Homo sapiens Hg.38 genome to locate potential protein-coding genes within the two organisms. Preliminary findings suggest similar protein-coding genes in the Pan paniscus and Homo sapiens genomes, thus supporting previous claims. However, the study acknowledges the need for further analysis to validate these findings by expanding the analysis to include other chromosomes in the two genomes and investigating the significance of non-match locations. This study highlights the efficiency of bioinformatics tools in genetic analysis. By making these tools more approachable, researchers can potentially uncover new insights into the genetic makeup of organisms.

Survey of Parasite Component Community in Snails from Sunset Pond

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During the semester of Fall 2022, a survey was conducted in Sunset Pond, San Angelo, TX, to determine the parasite community of freshwater snails. The dominant snail species collected was *Physa acuta*, followed by *Gyraulus* sp. and *Helisoma anceps*. After collection, snails were isolated in plastic jars for 24h to allow shedding of cercaria and observation of patent infections. The shell length was measured, and the snails were observed under a microscope. Metacercariae and oligochaetes were then typed, and their abundance was recorded. Cercariae were removed from the jar and observed under a compound microscope to determine their cercariotype. To date, 290 snails have been sampled totaling 25 *H. anceps*, 95 *Gyraulus* sp., and 170 *P. acuta*. Cercariotyping revealed that three different cercariae were present. These included echinostome, and both brevifurcocercous and Longifurcocercous cercariae. Although 80.7% of the snails were infected with metacercaria, only 3.5% of the snails produced cercaria. Three different metacercariae infected the snails: echinostome, tetracotyle, and an unknown metacercaria. This study will be compared to research conducted in the Fall of 2021 and Spring of 2022. By comparing my data to theirs, I aim to determine changes in the parasite component community following the drought of 2022.

Examining the effect of PA28 γ levels on the expression of E2F3B and its transcriptional partners

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The *retinoblastoma tumor suppressor protein* (Rb) regulates cell cycle progression by controlling the G1 to S-phase transition. Through its inhibition of *adenoviral early region 2 binding factors* (E2F), Rb inhibits tumor growth. Particularly, the E2F3B isoform is a critical driver in cancers and attenuates the expression of genes that promote differentiation. Similarly, PA28 γ , a ubiquitin and ATP-independent proteasome activator that assists in protein degradation in the cytosol, is overexpressed in many tumors. As the expression of both PA28 γ and E2F3B are correlated with tumorigenic hallmarks, this project analyzes the ability of PA28 γ to regulate the Rb-E2F pathway and focuses on E2F3B activity. It is hypothesized that PA28 γ provides a pathway to induce E2F3 activity and thus cell proliferation. Cancerous mouse cell lines and wild-type and knockout mouse cells are used to analyze the consistency in expression of PA28 γ and E2F3. Preliminary MTS assays have shown greater growth rates of A9 and 4T1 as compared to MEFs, while RT-qPCR data confirms that E2F3 regulation is not occurring through gene expression. Western blotting amongst the cell lines additionally revealed the expression of E2F3B protein to growth rate. Rad18, a transcriptional target, was used as a precursor to study E2F3 activity via RT-qPCR.

The Effect of Fructose-1,6-Bisphosphatases in Autophagy Upregulation

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Coxiella burnetii is an intracellular pathogen that causes the zoonotic disease, Q fever. During infection, *C. burnetii* manipulates the host cell into forming an environment conducive to its replication by constructing a lysosome-derived vacuole where the pathogen resides and replicates, termed the *Coxiella*-containing vacuole (CCV). As *C. burnetii* expands the CCV, it fuses with autophagosomes resulting in the accumulation of microtubule-associated protein 1A/1B light chain 3 (LC3) in the CCV. Throughout its infection, *C. burnetii* will inject several effector proteins into host cytosol through its Dot/Icm type IVB secretion system (T4SS) that facilitates CCV biogenesis. Among those proteins, Cbu0513, a fructose-1,6-bisphosphatase, is released. A mutation in *cbu0513* led to the failure of CCV biogenesis with autophagosomes. The aim of our research is to understand if fructose-1,6-bisphosphatase enzymes induce autophagy or if it is intrinsic to a feature of Cbu0513. To solve this, we performed tests expressing the FBP found in *C. burnetii*, *Thermococcus kodakarensis*, and *Escherichia coli* and quantified the LC3 levels to determine the effect of the fructose-1,6-bisphosphatase. This experiment shows significant promise in understanding a role of *C. burnetii*'s effector proteins and their exploitation of autophagy for *C. burnetii*'s benefit and provide insight on how cells regulate autophagy.

Analysis of Expression of Pro-angiogenic Factors Following the Epigenetic Downregulation of Angiomotin

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Glioblastoma multiforme (GBM), an aggressive malignant brain cancer, arises in the glial cells of the central nervous system (CNS). Among the CNS gliomas, GBM is the most aggressive, with a recurrence rate of approximately 90% and most lethal, with a 5-year survival rate of 10%. The aggressive nature of GBM is attributed in part to the intrusiveness of angiogenesis, the formation of new vasculature from existing ones, in these tumors. Angiogenesis occurs during development, wound healing, and tumor growth, and is an auspicious area of research for cancer therapy. As new vessels rapidly form to support the growing tumor, vessel leakiness increases and the blood-brain barrier is compromised, causing interstitial fluid pressure to rise, increasing patient co-morbidity and interfering with drug delivery. Angiomotin serves as one of the chief drivers of angiogenesis by binding inhibitors of angiogenesis and promoting pro-angiogenic factors. In this study, we transfected glioblastoma cells with the epigenetic modifier CRISPR-dCas9 to methylate and inhibit expression at three different locations within the angiomotin promoter. These samples were then evaluated using RT-qPCR on their corresponding expression of pro-angiogenic factors. The results of this experiment shed light on the use of angiomotin as an effective target for cancer therapy.

Road fatalities of butterflies in Crockett County, Texas

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Roadkill is a suspected major source of mortality among all wildlife. The majority of studies document the mortality of vertebrates, but the impacts on invertebrate populations are largely under-documented. More specifically, there is concern that monarch butterflies are experiencing additional mortality due to vehicular collisions. To quantify the impact of vehicular impact on monarch mortality, we collected road killed specimens along Interstate 10 at four 100 meter transects in Crockett County, Texas during fall 2022. In addition to monarchs, we also collected other species of Lepidopteran. The collected specimen were then sorted and identified. Overall, 340 individuals were collected from 19 species or genera across four collection periods in October 2022. The 3 most abundant species documented were gulf fritillaries (*Agraulis vanillae*) (N=86), orange sulphurs (*Colias eurytheme*) (N=71), and monarchs (*Danaus plexippus*) (N=61). As fall progressed, Lepidopteran mortality increased and peaked in mid-October. Our results suggest vehicular traffic may be responsible for a large number of Lepidopteran mortalities.

Using DNA Barcoding to identify plant/endophyte relationships

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Aspirin (an anti-inflammatory drug that reduce the risk of heart attack), Morphine (a pain-relief medicine), and Taxols (a type of cancer chemotherapeutic agent) are all products of medicinal plants. The growth of these medicinal plants can be influenced by endophytic fungi. Endophytic fungi establish symbiotic relationships with plants without causing any adverse effects. They promote the physiological activities of the plant in several ways, primarily through the biosynthesis of secondary metabolites that increase plant resistance to biotic and abiotic stresses. Recent studies show that endophytic fungi, additionally, are capable of biosynthesizing these medically important secondary metabolites (i.e., phytochemicals) that were initially thought to be produced only by the host plant. These phytochemicals present in plants such as essential oils, phenols, terpenoids, carotenoids, xanthophyll and flavonoids are promising therapeutic agents because of their anti-inflammatory, antioxidant, and anti-cancer properties. As a result of such findings, endophytic fungi have become an intriguing potential alternative source of biologically active compounds for pharmaceutical use when these compounds are not commercially available. In our research lab, our aim is to identify possible plant/endophyte relationships through the use of DNA barcoding, and perhaps leading to the discovery of novel endophytes, genes, and metabolites.

Are the dauers formed by *unc-33;daf-7* double mutants actually dauers?

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C. elegans have a rather simple developmental life cycle that progresses from embryo through 4 larval stages to adulthood. However, *C. elegans* have the ability to halt this life cycle when they are exposed to environmental stressors by entering a “dauer diapause.” The dauer diapause stage is an alternative developmental stage that is activated by the inhibition of the DAF-7/TGF β signaling pathway. Previous results from our lab show that *unc-33* mutants aren't able to enter the dauer diapause, but the mechanism behind this is still unknown. To address this knowledge gap, we hypothesized that introducing a mutation on the *daf-7* gene in the *unc-33* mutant background would rescue dauer formation. To achieve this, we created *unc-33;daf-7* double mutants and quantified dauer formation by determining their resistance to 1% SDS. The results showed that double mutants formed dauers at wild-type levels. To confirm these animals are, in fact, dauers, we quantified lipid accumulation in their intestines. Dauers produced by *unc-33;daf-7* double mutants had higher lipid accumulation when compared to *unc-33* mutants, thus verifying the dauers produced by double mutants seem to be normal dauers. Together these results bring us closer to determining why *unc-33* mutants fail to form dauers under environmental stress conditions.

The effects of toluene exposure on the fecundity levels and developmental growth of *Drosophila melanogaster*

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Toluene is a substituted aromatic hydrocarbon that can be found in many household products, although there are low concentrations in these products, people who are exposed to this chemical could develop chemical and physical effects in the human body systems. Our team studies the long term effects of toluene on the fecundity and development stages of *D. melanogaster*. Humans and *D. melanogaster* share similar genes and similar biological processes, which makes them excellent test subjects to observe toluene exposure effects. In previous studies, we have calculated the LE₅₀ (50% of the population killed in 24 hours) for our female population to be 1000-12000 ppm of toluene concentration. We have crossed our female exposed population with an unexposed male population. After 5-day observations of larvae and egg count, our data indicates that the LE₅₀ for our male population may be higher than our female LE₅₀ toluene concentration. However, our data still indicates that there is a correlation between increased toluene concentration and decreased egg levels. Continuing our research, we will determine the LE₅₀ for our male population, examine the effects that long term exposure could have on the F2 generations, and conduct genetic testing to determine what genes are being affected.

The study of the effect of *Bacillus* expressing plant elicitor peptides on germination and growth parameters in soybean plants

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Soybean is the second most widely-grown crop in the US, but it suffers significant yield losses to plant-parasitic nematodes and other pathogens. In response to pathogens and stresses, plants produce plant elicitor peptides (Peps). Through artificially delivering doses of these Peps, it can provide extra protection against pathogens, but a need for delivering past the seed stage is necessary. A possible delivery method would be to use plant growth-promoting rhizobacteria (PGPR) such as *Bacillus subtilis*, which grows in close association with plant roots. The Goggin laboratory has developed a *B. subtilis* strain that expresses GmPEP3 for soybeans. With this delivery strategy, it is important to test for any beneficial or negative side-effects on plant growth. PGPRs typically promote root growth whereas some but not all studies report that Pep applications can inhibit root elongation. In this study, the objectives are to measure the effects of *B. subtilis* expressing GmPEP3 on plant growth and compare these effects to other treatments. To assess plant growth, the utilization of image-based phenotyping to measure root morphology, assessing germination rates, comparing above- and below-ground biomass, and other measures of plant vigor were examined. After data collection and evaluation, there were no negative effects observed.

Aryl Hydrocarbon Inhibition in Pancreatic Stellate Cells

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Pancreatic cancer is the fourth leading cause of cancer-related death. The tumor microenvironment makes cancer treatment challenging. Active pancreatic stellate cells (PSCs) cultivate a microenvironment that facilitates cancer progression through increased extra cellular matrix (ECM) production. The Aryl Hydrocarbon Receptor (AhR) is a nuclear ligand receptor that promotes immuno-suppressive cell phenotypes. The aim of the study was to evaluate the effect of AhR inhibition on PSC activation. PSCs were isolated from black male mice. PSCs were treated with 1 μ m of AhR inhibitor, BAY2416964, and incubated for twenty-four hours. PSCs were also isolated from AhR knockout (KO) mice. PSC activation markers were analyzed from the samples using real-time PCR. Genes downstream of AhR were also analyzed to confirm that AhR had been inhibited. An oil-red O stain was performed on AhR WT and KO PSCs.

Inhibition of AhR resulted in downregulation of AhR, CYP1B1 and AhRr, α SMA, Col1a, LIF, IL-6, IL-11, and FAP. Oil Red O staining indicated less lipid content in AhR KO cells versus the AhR WT cells. Our results suggest that AhR inhibition slows and or reverses PSC activation. Hence, PSC quiescence has a potential to be a cancer therapy.

ANTI-CANCER COMPOUNDS SECRETED BY *GANODERMA LUCIDUM*

Diego De La Torre* and William P. Ranahan PhD

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Cancer is a leading cause of death worldwide; while many therapies are available, there is no cure. One of the most common cancer treatments is chemotherapy. While chemotherapy is an effective way to kill cancer cells, it is also harmful to non-cancerous cells. Humans have used remedies found in nature to treat health conditions for millennia. The majority of drugs available today come directly from plants or are modifications to the naturally occurring compounds.

The goal of this project is to find a naturally occurring product that has selective cytotoxicity toward cancer cells. *Ganoderma lucidum*, the medical mushroom was cultured in vitro. Mushroom secretions were gathered and analyzed using a fast-protein liquid chromatography system (FPLC). A low molecular weight protein-containing polysaccharide was isolated. Viability data indicate that the isolated compound effectively reduces epithelial cancer cell viability while enhancing the viability of non-cancerous mammary epithelia. Future studies will focus on testing this compound against a range of cancer cell types.

Comparing arthropod communities across seasonal temperature variation

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Arthropods are a highly diverse group of organisms that perform essential ecosystem roles, including pollination and decomposition. However, arthropod lifecycles and distribution

are highly dependent on conditions like temperature and humidity, which vary seasonally and spatially. Any changes in phenology or distribution caused by climate change could have cascading effects on the ecosystem as a result of changes in populations or trophic mismatch. The goal of this project was to determine how species richness and diversity varies seasonally across three representative sites at Wild Basin Wilderness Preserve to determine how temperature and climate change may affect species distributions. Arthropod samples were collected from three sites across Wild Basin, a wilderness preserve in the Texas Hill Country. Invertebrate samples were collected using malaise and pitfall traps at a ridge, mid-slope, and riparian site across the preserve in both October and December to model temperature and humidity effects of seasonality on arthropod distribution. Temperature and humidity values were captured continuously at each site using iButtons. Preserved samples were identified to the family level. Data analysis is ongoing, but preliminary data indicate that arthropod abundance and richness are higher in warmer seasons, with most significant declines in Lepidoptera and Hymenoptera.

The effects of 6-gingerol on cell viability in HT-29 colorectal cancer cell line

Katherine Dempsey and Joel Gaikwad

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Colorectal cancer is the third most common cancer type and the second leading cause of cancer-related deaths in America. Current treatments like chemotherapy often result in long-term side effects like reduced immunity, or invasive surgery and colostomies are often accompanied by post-surgical complications like bleeding, infection, and bowel stress. Therefore, more natural therapeutical options are being explored. *Zingiber officinale*, commonly known as ginger, has been used for 7enturyes in ancient Chinese and Indian Ayurvedic medicine due to its well-known anti-inflammatory and antioxidant properties. It was hypothesized that the main active compound in ginger, 6-gingerol, may possess anticancer properties and would reduce the cell viability of colorectal cancer in a dose-dependent manner. An MTT cytotoxicity assay was performed on HT-29 cells treated in duplicates with 10, 20, 40, and 60 $\mu\text{g}/\text{mL}$ concentrations of gingerol diluted in DMSO. Microscopic observation of treated cells exhibited morphologies characteristic of apoptotic cells. The number of floating dead cells increased as the gingerol concentration increased, with the survival rate decreasing from 62% to 48.6% viability. Before fully accepting the hypothesis, future planned experiments include flow cytometry with propidium iodide staining and a Caspase-3 activity assay to analyze the induction of apoptosis.

Synthetic mechanical loading of Autophagy-deficient osteocytes in vitro

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In previous studies, macroautophagy was eliminated in the entire osteoblast lineage via conditional knockout of *Atg7* in mice utilizing the protein cre recombinase under the osterix 1 promoter. After the conditional knockout of *Atg7* a significant decrease of periosteal diameter was observed indicative of a reduced response to load. This decrease in bone turnover was due to decreased effector bone cell number. We hypothesize that the morphologically altered osteocyte

network leads to improper response to load and contributes to low bone mineral density in vivo. To test this, we will examine if mice lacking autophagy in the osteoblast lineage can respond to synthetic mechanical loading in a normal fashion. Piezo1 is a calcium sensing receptor in osteocytes that is involved in the influx of calcium ions for a proper response to load. This receptor can be allosterically activated by a small molecule named Yoda1. Stimulation of bone organ cultures in vitro with Yoda1 was performed. Afterward, Atg7-flox; Osx1-Cre cells that are treated with Yoda1 effectively simulating mechanical load, were analyzed for the expression of genes responsive to mechanical loading. It was discovered that Yoda1 induced load on macroautophagy deficient osteocytes in vitro increases expression of genes responsive to mechanical loading.

The Effects of Winter Storm Uri on Texas Birds

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Winter Storm Uri was a winter storm that occurred in February of 2021 across the United States and Northern Mexico which led to below freezing temperatures and persistent ice and snow for a weeklong period. It is believed that this storm had major effects on wildlife populations across the United States. Some of these populations were likely more resilient to the harsh conditions than others. This research aimed to investigate the effects of Winter Storm Uri on avian populations in Texas. In particular, aspects of diet and body size were explored to determine if any particular life history traits conferred advantages. This research utilized data from the North American Breeding Bird Survey for the period between 2000 and 2021 to estimate the impact of this winter storm on resident passerines. From this dataset, 16 bird species with differing traits were selected to investigate the relative abundance of each species in the state of Texas over the time period outlined. Linear models were created for each species using the bbsBayes package in R. These models were then analyzed to determine the rates of change for each species from 2019 to 2021 as a result of the Winter Storm.

Antimicrobial Effects of Essential Oils From Brewer's Spent Grain and Spent Hops

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The United States brewing industry produces approximately 23 billion liters of brewer's spent grain (BSG) and hops (BSH) per year. Currently, BSG and BSH are sent to landfills or used as inexpensive animal feed. However, both have high nutritional value and high essential oil content (EO), leading to many alternative uses. EO are aromatic compounds derived from plants with antiseptic, antibacterial, antiviral, and insecticidal properties. This experiment aimed to characterize the essential oil profile then determine toxicity and antimicrobial activity of essential oils extracted from BSG and BSH. Steam distillation was used to isolate roughly 8±2 mL of EO from BSG and BSH. Thin line chromatography (TLC) characterized the EO profile, showing the presence of limonene. A brine shrimp assay tested toxicity of the oils resulting in an LC50 of >100,000 mg/mL. *E. coli* Disk diffusion assays assessed antimicrobial activity. The

BSG and BSH EO prevented *E. coli* growth with inhibition zones from 18.3 ± 1.8 mm to 36.3 ± 1.4 mm, respectfully. EO extracted from BSG and BSH prevented growth of *E. coli* while being non-toxic. Further studies will assess antimicrobial assays against different bacteria and additional TLC plates with NMR analysis will further characterize the EO.

The effect of apiculture stressors on the immunological response of Italian honeybees

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Colony collapse disorder (CCD) has caused widespread death of honeybees, but the exact causes are not understood. Many scientists, however, agree that pathogenic threats most likely contribute to CCD. Due to the integral ecosystem role bees fulfill, it is important to understand how honeybees respond immunologically to different factors to better inform practices to combat CCD. Quantifying the immunological cost of two different beekeeping approaches allows us to better understand how beekeeping practices affect bees' susceptibility to CCD. Two colonies were maintained, one with an internal plastic foundation on their frames and one without. The frame foundation provides structural support for the creation of honeycomb. Beekeepers utilize frames with no foundation to harvest beeswax. However, beeswax is more energetically costly for colonies to produce, causing energetic stress, which affects the colony's ability to fight pathogens. We collected bees from each colony and extracted their hemolymph to quantify their basal immunological protein levels to determine if frames with no plastic foundation resulted in the colony being less able to combat pathogens. Preliminary data suggests that bees from colonies with a plastic foundation will have higher levels of intracellular immunological proteins and, thus, will be more capable of fighting immunological threats.

Raspberry Pi-based Automated Phenotyping of *Arabidopsis thaliana* during early development

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Long non-coding RNAs (lncRNAs) are found in all eukaryotes, do not encode a protein, and are emerging transcriptional regulators. Research into lncRNAs is novel, thus the vast majority of them have not been thoroughly characterized. The Nelson lab recently identified the sequence and expression characteristics of thousands of lncRNAs in the plant family Brassicaceae, which includes *Arabidopsis thaliana* and *Brassica rapa*. Many lncRNA candidates of interest were identified due to their high levels of expression during seed germination and seedling development, and for their elevated levels of nucleotide conservation evolutionarily. Preliminary research investigated the biological role of several candidate lncRNAs by identifying *Arabidopsis thaliana* plants with a mutated lncRNA gene and observing the phenotypic effects the mutation has on seedling development. To determine the relationship

between these lncRNAs early growth and rosette development, we used high throughput phenotyping coupled with PlantCV based bulk image analysis. We identified four T-DNA insertion lines with significant effects on growth characteristics of young Arabidopsis seedlings. From this data, we concluded these candidate lncRNAs play a functional role in seed germination and early seedling/rosette development. Future experiments will determine the molecular basis of the role these candidate lncRNAs play during early seedling development.

Phylogenetic Analysis of West Nile Virus in Oklahoma

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Understanding mosquito communities is a crucial to mitigating mosquito-borne disease risks. In this study, we characterized the mosquito community in the Oklahoma City area between May-September 2022. We sampled at 19 locations with varying landscape characteristics across four counties in central Oklahoma using host-seeking and gravid traps to capture the community diversity. In total, 5,589 mosquitoes were caught comprising 27 species representing 7 genera with the majority of the specimens belonging to the *Culex* genus and *Culex pipiens* ($n = 3100$) as the dominant species collected. Female mosquitoes of the same species were pooled ($5 \leq n \leq 30$) and purified RNA will be used for West Nile virus (WNV) detection via RT-qPCR. Following, WNV positive RNA pool was used for cDNA library and an amplicon-based multiplex PCR approach to amplify the whole viral genome. Successfully amplified genomes will be sequenced using the Oxford Nanopore platform to generate whole WNV genomes. We assembled genomes in Geneious and perform phylogenetic analysis using maximum likelihood method. The goal of this study was to generate WNV whole genomes from wild-caught mosquitoes in Oklahoma and understand the phylogenetic associations of the WNV strains in Oklahoma in the context of the Midwest and continental USA.

C. elegans axonal anchoring complex plays a role in transporting cellular waste for degradation

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Autophagy is the process in which cellular components are degraded and recycled. The ternary complex, composed of the microtubule-associated proteins (MAPs) UNC-33, UNC-44, and UNC-119, contributes to neuronal development, transportation of autophagosomes, anchoring microtubule bundles to the cortex, and inhibiting microtubule sliding. Defects in the ternary complex may contribute to the development of neurodegenerative diseases. In our laboratory, we investigated the autophagy process in *C. elegans* mutants lacking the components of the ternary complex. We hypothesize that the lack of these functional proteins will result in defects in autophagy. To test this hypothesis, we monitored autophagy flux using western blots and autophagosome maturation via confocal microscopy. Autophagy was induced via

starvation and compared to basal autophagy results. Preliminary analysis of western blot results shows that ternary complex mutants undergoing starvation fail to induce autophagy flux. Results from confocal microscopy demonstrate that mutants lacking UNC-33, UNC-44, and UNC-119 have autophagosomal mislocalization in neurites. These results suggest that microtubule sliding, a phenomenon seen in MAP mutants, may affect autophagosome transport and cargo degradation. These findings support the role of the ternary complex in autophagy in neurons.

Preliminary survey of native bee species in Tulsa Co., Oklahoma

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Native bee populations have been decreasing. Native bees are important pollinators that are adapted to local climate and to native plant species. In Oklahoma, there is limited information on the native bee populations. For this study, we collected and identified bee specimens for a preliminary survey of native bee species in Tulsa Co., Oklahoma in conjunction with the state-wide survey being conducted by the Oklahoma Biological Survey. Also, a pollinator garden was observed and maintained for the purpose of identifying which plants best attract native bee pollinators.

M.A.R.S. on Mars: Microbial Analysis of Regolith-Grown Species

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With a societal push to discuss colonization of Mars, the Institute of Competition Sciences started a Plant Mars competition where simulated Mars regolith is sent to teams. The SWOSU to Mars team has been studying ecological diversity by studying the microbes within Mars and Earth soil and the diversity of plant species. Our team selected a variety of plants, making sure we had plants with above ground and below ground vegetation, along with a nitrogen fixing legume. Some pots contained many microbes while others contained few, as we were curious whether the number of microbes would affect growth. We measured height, pH, and leaf coloration. At the end of the experiment in spring 2022, we cultured microbes to assess differences in Mars and Earth conditions. At the end, Mars plants were non-existent while Earth plants were thriving. This season, we changed our soil composition and are testing new additives as well as different species of plants. The watering system also changed after research in the fall concluded that timed bottom watering was the most successful. We hope to successfully harvest crops from Mars soil. The knowledge can also carry over to agricultural techniques and food supply on Earth.

Foraging Behavior of Fruit Flies (*Drosophila melanogaster*) in a 3D Arena

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Fruit flies (*Drosophila melanogaster*), exhibit negative geotactic behavior, which has many advantages, including the ability to escape from predators. We tested the effect of negative geotactic behaviors on foraging. We presented the flies with a feeding cube (2.5 cm side length) to test their feeding preference in a 3D arena (10 x 10 x 10 cm) to determine their preference to feed from the top, sides, or bottom of a cube with 9 wells on each side filled with colored sucrose solution. Top, bottom, or sides had either red, yellow, or blue solution. The flies were deprived of food for 24 hours and tested in the dark for one hour. They were then frozen and the contents of their abdomens were evaluated for color. There was a preference for feeding on the top over the sides and/or the bottom of the cube. The flies also preferred the yellow solution, while avoiding the red solution regardless of position (top, bottom, sides). The decision about where to feed on the cube seems to be influenced by several variables, including resource quality, possible ability to escape or hide from predators, and difference of energetic cost caused by feeding against gravity.

Metagenomics Analysis of Viral Families Carried by *Aedes Aegypti* Mosquitos in the Greater Houston Area

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Mosquitos are vectors of many important viral diseases, but little is known about viral strains they carry. Historically, culturing techniques were used to study microbial diversity, but genomic analyses have demonstrated that culturing methods are biased and inadequate to understand true diversity. In our research, we use a metagenomic approach to characterize the viral populations carried by different species of mosquitos found in Houston. In this work, we sequence entire genetic material of mosquito samples and analyze it with computational tools. We collected mosquitos in Houston and separated them by species and sex using morphological characteristics. We confirm our separations by using DNA barcoding. Total DNA and RNA were extracted from each sample, and RNA samples are converted to cDNA to facilitate sequencing. Combined DNA/cDNA pools were sequenced using 454 sequencing technology. Then a modified BLAST workflow developed in-house by alumni David Brittain to analyze our sequences. Our first analysis involved samples of male and female *Aedes aegypti* mosquitos. A total of 91 different species of viruses were identified in male and female samples. These studies will help us better understand the viral collections carried by different mosquitos in Greater Houston.

Expanding the need to study endophytes and plants interactions

Natalie Le*

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Endophytic fungi are those that live within the living tissues of plants without causing any apparent harm to the host. These fungi may form mutualistic symbioses with plants, providing protection against pathogens or other stresses, while the plant provides the fungi with a nutrient-rich habitat. Fungi can promote plant growth and enhance their metabolic capabilities by producing hormones such as gibberellins and indoleacetic acid. Understanding the interactions between plants and endophytic fungi can potentially enhance our agricultural practices. DNA barcoding can be used to identify endophytic fungi in plants and aid in the study of mutualistic relationships between plants and fungi. Our research can contribute to the growing knowledge base of the important roles that endophytic fungi play in plant-microbe interactions, improving agricultural practices, developing new biotechnology, and conserving biodiversity.

Annotation of Novel contig22 of *Drosophila kikkawai*

Megan Lewis*, Christian Siegle*, Cale Eaton*

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Gene annotation is the process of defining boundaries of relevant genes in newly sequenced and unlabeled genomes. Gene boundaries, exon start/stops, UTRs and ORFs start/stops, and promoters, are more subject to change across species genomes than sequences that affect coding sequences. Analysis of the boundaries conveys species specific changes or identifies processes important for a particular genus. Bioinformatical annotation compares the novel genome to a known annotated genome. Evolutionary changes at the coding extremities may elude bioinformatic software. Our project annotated three genes in contig22 of *Drosophila kikkawai*. Genscan and Geneid gene prediction tracks were used to search the unlabeled *D. kikkawai* sequence for genes and BLAST orthologs that match our model genome, *Drosophila melanogaster*. We examined our orthologs for changes across these species genomic boundaries using the Genomics Education Project (GEP) protocols (GEP Genome Browser, exon-by-exon, and splice site conservation rules). Analysis of contig22 of *Drosophila kikkawai* showed conservation of Ten-m, IleRS, and Hem genes with differences in exon boundaries and splice junctions. Analysis shows conservation differences of these boundaries with 23.1% in Ten-m, 40.0% in IleRS, and 62.5% conservation in Hem. The data was collated into report format for submission to GEP consortium aiding in genome evolution analysis.

Macrophage Inflammasome Trap *Shigella flexneri*

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Shigella spp. are major enteric pathogens, causing acute diarrhea and bacillary dysentery leading to severe mortality and morbidity worldwide. Yet, there is no licensed vaccine to prevent

shigellosis. *Shigella* virulence requires a T3SS and at least 30 secreted effectors that are often functionally redundant, yet required to invade host cells, maintain a replicative niche, minimize alarm signals, and promote colonization. Here we show that *S. flexneri* T3SS activity is detected in macrophages by caspase-1 inflammasomes, resulting in pyroptosis, a lytic form of programmed cell death. Macrophage pyroptosis is known to generate pore-induced traps (PITs), trapping, and neutralizing intracellular bacterial pathogens. However how PITs trap intracellular bacteria remains undetermined, here we propose to investigate the interaction between macrophages inflammasomes and *S. flexneri* to determine how pyroptotic macrophages from PITs trap intracellular bacteria.

The Armadillo as an Animal Model for Investigating Human Mineralization Pathologies (Preliminary Study)

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Armadillos mineralize their skin to form a shell during fetal and neonatal development. Therefore, they are a well-suited animal model to understand calcium homeostasis. Since calcium is likely required to maintain and grow armadillos' shells and bones, understanding calcium requirements in different armadillos' life stages is essential for formulating a diet for a captive breeding program. Armadillos were recruited from the wild, sedated with 2.5-3% isoflurane, and assessed pregnancy status by ultrasound. Shell, blood, urine, and fecal samples were also taken. Armadillos gradually transitioned to lab chow formula. Shell samples from one lactating female adult, six juveniles, and one independent wild-caught juvenile were assayed for total calcium (Calcium Assay Kit 701220). Serum ionic calcium from non-pregnant and non-lactating armadillos was measured. Six pregnant adults, two lactating adults, and six juvenile armadillo samples were assayed for vitamin D₃ (Cayman Elisa kit 501050). Preliminary data of total calcium suggests that supplemental dietary calcium and vitamin D₃ may affect mineralization of juveniles' shell. Serum ionic calcium and vitamin D₃ results suggests adult females maintain a similar level of serum calcium during pregnancy and lactation as when they are not. Circulating calcium and vitamin D₃ of juveniles appears to be sensitive to supplemental diet.

Exploring the Diversity of Soil Microbiota in Cadaver Decay Islands (CDI) located in Central Texas

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Decomposition is a highly variable process based on the local temperature, weather patterns, and more. As a cadaver progresses through decomposition the body begins to putrefy. Pressure from the buildup of gases forces cadaveric fluid from natural orifices, ruptures in the skin, and wounds. The cadaveric fluid creates a nutrient rich area underneath and around the cadaver called the cadaver decay island (CDI). Effects of the cadaver decay fluid on the soils underneath and around the body have gained interest as a method for determining the post-

mortem interval (PMI) of the cadaver. PMI is defined as the amount of time that has passed since death at the time of discovery. This study examines the effects of cadaveric fluid on bacterial diversity based on PMI, distance from the cadaver, and location of soil sample around the cadaver. Soil samples were analyzed via 16s rRNA sequencing. Results show bacterial diversity measured using alpha diversity measures may show biologically relevant trends but statistically insignificant results. Results contribute to the ongoing conversation regarding using the changes in the microbiome of the CDI to measure PMIs, while bringing awareness to the difficulty of replicability in studies of decomposition.

Developing a Functional Breeding Environment to Study Caudal Regression Syndrome in Early Embryonic *Danio rerio*

Karter Morris

Angelo State University

This project is based on previous research at Angelo State University by Miquela Farley, who noticed abnormal caudal development of *Danio rerio* embryos under exogenous cortisol administration. We seek to recreate these results to study the implications of cortisol's teratogenic effects in relation to Caudal Regression Syndrome (CRS). This first begins, however, with the proper setup for the model organism. Zebrafish are commonly used in scientific research, which is in part due to their high reproductive output. But proper care and breeding procedures are a requirement for successful experimentation. Optimal breeding conditions depend on a number of different metrics, including water/tank quality and maintenance, filtration methods, feeding techniques, and light cycles. Moreover, egg collections can prove to be challenging when necessary steps are overlooked. This poster outlines all the essential methodology associated with maintaining a successful zebrafish colony. The future objectives of this experiment will be studying the teratogenicity of various compounds, including retinoic acid, cortisol, and glucose, and their potential relationship with CRS. After the initial exposure, morphological and histological assessments will be conducted via proportionality measurements and Alizarin red/Alcian blue staining. Then, genetic analysis will be performed to estimate the expression levels for various genes of interest.

Exploring the Potential of Aqueous Dandelion Extract: A Comparative Study of Antimicrobial and Anticancer Properties

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Oklahoma City University

Certain plant-derived products have pharmaceutical uses due to their anti-inflammatory and anticancer effects, including Dandelion (*Taraxacum officinale* and *Taraxacum erythrospermum*). It has long been consumed safely as part of Middle Eastern and Ancient Chinese Medicine. Anticancer effects of aqueous DWE (Dandelion Whole Extract) have been vastly studied on HeLa cells and other cancer cell lines. As some anticancer compounds are also used as antibiotics, this study aimed to further investigate the antibacterial effects of different forms of dandelion extract.

The disk diffusion method was utilized to test Dandelion Aqueous Extract (DAE) on bacterial growth. Several Enterobacteriaceae were utilized: *Proteus*, *Enterobacter*, *Klebsiella*, *Escherichia*, *Serratia*, *Shigella*, and *Citrobacter*. All bacterial cultures were incubated at 37 °C for 24 hours, then colonies were isolated, suspended in tryptic soy broth (TSB), compared with 0.5 McFarland Standard, and cultured on Mueller-Hinton Agar (MHA). Sterilized paper disks were impregnated with DWE and applied to bacterial plates. After incubation, all plates were visualized for indication of DWE impact on bacterial growth.

The results showed no zone of inhibition, indicating bacterial resistance to DAE in this method. In the future, broth dilution antibiogram assays will be conducted utilizing additional bacterial species and different formulations of dandelion extracts.

A germination study of nSiO₂ on the assessment of different priming conditions for optimal plant-nanoparticle interaction

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Houston Christian University

Seed priming is a pre-soaking treatment that facilitates germination by positively impacting plant growth and ameliorating the effects of abiotic stresses. During seed priming, seeds undergo partial imbibition without causing radicle protrusion through the seed coat therefore, seeds can be re-dehydrated and stored for future use. Nanomaterial priming has been recently explored and reports showed enhanced effects compared to conventional agrochemical priming. However, a wide variety of priming conditions reported makes it difficult to replicate. This study aimed at evaluating priming conditions that ensure that seeds remain viable and enhance plant growth. Two sets of experiments were performed: 1) assessment of nanoparticle (NP) concentration, and 2) comparison of priming methods. Both cases used SiO₂ NPs (nSiO₂) and bulk-SiO₂ (bSiO₂) as the priming agents in cucumber seeds. Concentrations evaluated were 20, 40, and 60 mg·L⁻¹, priming by soaking for 8 hours. Tested methods included sonication for 30 min, stirring for 8 h (400rpm), and soaking with no agitation for 8 h (all methods at 40 mg·L⁻¹). Next, seeds were air-dried for 4 days, grown, and watered for 50 days until harvest. Agronomical parameters (biomass, chlorophyll, and leaf area) were measured. Samples were then oven dried and homogenized for elemental analysis.

Exploring the role of the human microbiome byproducts as a potential new therapeutic treatment for Primary Open-Angle Glaucoma

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Primary Open-Angle Glaucoma is one of the leading causes of irreversible blindness worldwide. With many therapeutics failing to target the site of pathogenesis at the trabecular meshwork (TM), new molecular targets are greatly needed. Many studies have linked ocular diseases to dysbiosis (most commonly known as microbial imbalance). Short-chain fatty acids (SCFA) are by-products of the fermentation of dietary fiber by anaerobic commensal bacteria

(also known as our gut microbiome). It is possible that glaucoma patients do not have the necessary microbes in their gut to protect them from ocular diseases. Our central hypothesis is that metabolites (acetate, butyrate, and propionate) from our microbiome could be used as a therapeutic agent to lower fibrosis in the TM. In this study, we show that mouse TM cells treated with TGF β 2 in the presence or absence of butyrate (a by-product of commensal bacteria) can lower the expression of extracellular matrix proteins. These important findings provide a novel role for butyrate and may pave the way for developing innovative molecular targets.

TESTING THE CYTOTOXICITY OF *HERICIUM ERINACEOUS* MUSHROOM SECRETIONS AGAINST U-87 MG GLIOBLASTOMAS

Natalia Ramirez* and William P. Ranahan PhD

Oral Roberts University

Glioblastoma is one of the most aggressive brain cancers known. Within the first five years, only 6.8 % of glioblastoma patients will survive with the average length of survival being 8 months. Current treatments of glioblastoma include surgical removal of the tumor followed by intensive radiation therapy and chemotherapy. The development of a natural remedy with reduced side effects would significantly benefit cancer patients. Better known as Lion's Mane, *Hericium erinaceus* mushroom has been traditionally used to enhance immune system function, treat gastric ulcers, and aid the body in controlling cancer cell growth. Studies on *H. erinaceus* have suggested that it may regenerate nervous tissue in the brain. Due to its advantageous nervous system functions, this study focuses on the cytotoxic effects of *H. erinaceus* against U-87 MG glioblastoma cells in vitro. Full spectrum secretions from the mycelia and fruiting body, as well as two separate fractions, were used in a cytotoxicity assay. Results from the assay suggest that secretions from *H. erinaceus* may be efficacious in causing U-87 MG cells to undergo apoptosis as compared to U-87 MG cells in autoclaved millipore water.

Open-Ended Sequence Alignment Queries between Bonobo and Human Genomes: A Preliminary Study

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Oral Roberts University

In 1984-1987 single-copy nuclear DNA from Bonobo (*Pan paniscus*) and Human (*Homo sapiens*) were compared. A 98.5% match between each led to the close relation between Bonobo and Human in the Hominidae family.¹⁻³ Since then, significant technological advances in sequencing technology have been made. We first revisited the previous inference through whole genome sequence comparison of nucleotides. Using a high-performance computing system we asked open-ended sequence alignment queries between the bonobo (GCF_013052645.1) and human genomes (GCF_000001405.40). Our preliminary query was an unbiased sequence alignment between both first chromosomes of each species for matches at two levels of granularity. First, an alignment with a minimum of 200 base pairs and the next a minimum of 32 base pairs. We found 29.1% overall similarity between the two chromosomes and two long

matches, with a point mutation separating each. We report the success of the sequence alignment FASTA data output, verified using NCBI BLAST. Preliminary results indicate that point mutations are very common between the two genomes. There are significant differences in their noncoding regions, which wasn't explored in the primary literature. These results may play a role in verifying the previous comparison and allow for new visualization tools, based upon future outputs.

Annotation of Two Genes Within Contig6 of *Drosophila kikkawai*

Kaylyn Rowsey* and Jillian Brassfield

East Central University

The goal of this project was to annotate an unknown genome, *Drosophila kikkawai*, against the known model genome from *Drosophila melanogaster*. This project seeks to investigate chromosomal similarities across evolutionary conserved species through the use of standardized and systematic genome annotation protocols to deduce gene function and structure. With *Drosophila melanogaster* as our baseline, we utilized the gene prediction track GeMoMa to identify our top ortholog potential matches. Two genes within contig6 of *Drosophila kikkawai* were identified as jim and CG14448 and were annotated throughout this project. The annotation process was completed by utilizing Genomics Education Project (GEP) UCSC Genome Browser Mirror at WUSTL, FlyBase, and Basic Local Alignment Search Tool (BLAST). After examining differences between the orthologs jim and CG14448 and comparing them to *Drosophila melanogaster*, conservation was proposed to exist between these two species. This observation was based on the positioning of the start/stop coordinates and splice junctions. CG14448 and jim displayed 36% homology in conservation of gene structure in ORF components. The percent of conserved gene structure represents no change in coordinates from the null (*Drosophila melanogaster*). Additional bioinformatic variables such as changes in the size of the coordinate shifts are not represented in the homology conserved.

The Effect of Energy Expenditure on Immunological Response Between Drones and Worker Honeybees

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Colony Collapse Disorder (CCD) occurs when worker honeybees leave a colony and disappear without reason. Among many hypotheses, it is believed CCD is induced when an accumulation of stress factors surpasses the threshold in which honey bees operate. This is detrimental to the species, and others, since the ecosystem relies on honey bees for pollination. It is believed that prevalence of CCD may be influenced by immunological threats. Honeybee colonies operate within a hierarchical system. Female bees are the workers responsible for scavenging, building honeycomb, and producing honey. Males bees, known as drones, essentially deplete the nutrients produced by worker bees until they mature, leave the colony, and reproduce. The only female bee with developed ovaries is the queen who is responsible for reproduction. This difference in roles accomplished by each class of bee requires a different

amount of energy. The goal of this project was to determine if energy expenditure between drones and workers affects immunological responses since workers are constantly exposed to a myriad of pathogens when they leave the hive, as opposed to the drones who mainly stay within the hive.

Calcium Regulation in Armadillos

Emily Spillers*

University of the Ozarks

While using armadillos to better understand calcium regulation and how to better their diet for pregnancy and lactation, their quality of life should be monitored as well. The husbandry care that has to be given on the daily is a tedious and time intensive task. Although the husbandry care is very vital towards our research, the main goal is to understand how a lactating female armadillo allocates sufficient minerals to her offspring without incurring debilitating skeletal bone loss and to understand how the neonate regulates its orderly skin mineralization. Data to support our research has been analyzed and we have made progress towards our objectives collecting preliminary data on serum parathyroid hormone and total vitamin D3, and on calcium in serum, urine, feces and shell samples. To be able to gather all of the necessary data, the animals have to survive and be fed with quality nutrients and have sufficient calcium intake. From this study, the key takeaways should be if calcium is mobilized from the mothers shell during lactation and how calcium homeostasis is regulated during the stages of pregnancy, lactation, and neonatal growth.

How Mammal Presence Shapes the Soil, Plant, and Invertebrate Ecology of the Blackland Prairie

Davis Stellman* and Dr. Jessica Heally

Austin College

Mammals play a powerful and often overlooked role in maintaining prairie ecosystems. Previous research suggests that the presence of mammals in prairie systems alter the vegetation, affect invertebrate communities, and alter carbon to nitrogen ratios (C:N) in the soil. Understanding these ecological factors gives a better picture of how to focus restoration efforts in the Blackland Prairie, an endangered ecosystem in North Texas. This study aims to evaluate changes in subsections of a prairie restoration property from which mammals have been excluded for 10 years. We examined soil cores taken from three areas of the restoration property: 1) Small mammal exclosure plots (small and large mammals excluded), 2) Small mammal access plots (large mammals excluded), and 3) Control (unrestricted access). Soil cores were examined for differences in total C:N ratios between the plot types. This is carried out to observe possible relationships between small mammal presence, the presence of large ungulates and small mammals, and the absence of both mammal types on C:N ratios. Additionally, we investigated if the presence or absence of large ungulates and/or small mammals affect invertebrate community structure, and plant diversity and coverage within the prairie. We compared our findings to data from 10 years prior.

DNA Barcoding of *Peromyscus* From the Davis Mountains in Texas

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Angelo State University

Mice in the genus *Peromyscus* can be hard to distinguish without taking detailed measurements of the animals. Two species documented from the Davis Mountains of Texas, *P. boylii* and *P. nasutus*, can inhabit similar environments with overlapping elevations. *Peromyscus boylii* has been recorded as low as 1295 m but is more common above 1700 m. *Peromyscus nasutus* has been documented ranging from 1585 m to over 2300 m. There is slight color variation within the two species. *P. nasutus* has white around its ankles while *P. boylii* does not. Due to the habitat overlap and similar appearance of these mice, the possibility of misidentification is an issue. The status of *P. nasutus* in the Davis Mountains has been questioned in recent decades and there was concern that it had been extirpated from the area. By doing DNA barcoding we were able to identify samples collected around 2250 m in the Davis Mountains in 2021 and 2022. Once sequenced, we compared our samples to known *P. nasutus* and *P. boylii* from Genbank to positively identify eight of each species from the Davis Mountains.

Full Spectrum CBD Oil-Induced Changes in Gene Expression in Tumorigenic Mammary Epithelial Cells

Danielle Taylor*

Oral Roberts University

Breast cancer is the most common type of cancer in women, with millions diagnosed each year. Cancer is characterized by uncontrolled cell growth resulting in tumors. In breast cancer, these tumors can affect either the ducts or the lobules of the breasts. Traditional methods of fighting cancer include chemotherapy, radiation, mastectomy, and other therapies. Another form of treatment being studied is the use of cannabidiol (CBD). CBD is a cannabinoid from the cannabis plant hemp. In humans, there is a whole endocannabinoid system containing genes that encode for cannabinoid receptors (CBRs). Studies have found that certain signaling pathways including cell growth and apoptosis are connected to the endocannabinoid signaling. In this study, several genes were tested to see how CBD oil would affect regulation in breast cancer cells. The genes tested were GAPDH, SUMO1, NOTCH1, PCNA, PPARG, EGFR, and PTEN. When comparing the samples treated with CBD to the control, genes PTEN and SUMO1 had the greatest changes in regulation. In breast cancer cells treated with CBD oil, PTEN was significantly downregulated, whereas SUMO1 was significantly upregulated. Further studies would include Western blotting to confirm the proteins of the genes either increased or decreased.

The Comparative Genomics of the RBCL gene of *Cannabis sativa* and other Medicinal Plants

Triztan Thompson and Dr. Julianna Goelzer

Oral Roberts University

The chloroplast is one of the major organelles inside plants; even though we have been studying them for many years, they are still poorly understood. Plants with varying abilities like healing properties, poison production, and aromatic fragrances have the chloroplast as a major organelle. Sequencing the chloroplast could help scientists understand how much the organelle contributes to the plant's unique properties. One plant, *Cannabis sativa* is known for properties that aid in anxiety relief, pain relief, stabilization of mood disorders, and phytoremediation. Yet, due to controversy in politics and recreational usage, the *Cannabis sativa* plant has been known more for its psychedelic effects. One area that would improve the overall medicinal qualities would be unlocking optimal growth through the plant's chemical factory in the chloroplast. The *rbcL* gene, located in the chloroplast, directly correlates to carbon fixation and biomass. This study seeks to compare the chloroplast's *rbcL* gene genome between medicinal plants. The experiment will focus on using nucleotide BLAST on the NCBI website using the *rbcL* genome sequences of different medicinal plants. Ultimately, the BLASTs of the *rbcL* gene will be assessed by their similarity and help researchers understand what could make these medicinal plants more efficient.

Female Amphipods Adjust Brood Sex Ratios Based on Mate Choice

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Theory predicts even sex ratios because parents always benefit from producing the rarer sex. However, deviations in nature may occur to maximize reproductive success. On an individual brood basis, females may allocate resources to the offspring sex that returns the most fitness. We hypothesized that choosy females bias sex ratio of broods in favor of sons. Amphipods (*Hyaella sp.*) were used as it's possible to identify chosen mates because they physically pair for a short period before copulation. We collected mating pairs and a background sample of amphipods from a freshwater spring. Half of the females were separated and re-paired with their original mate—i.e. they chose their mate. The other half of the females were separated and assigned a new male randomly from the background sample. Each pair was placed in a jar inside of an environmental chamber. We checked the pairs three times weekly and recorded offspring sex ratios. As predicted, choosy females produced a higher proportion of sons in their broods than females mated at random. This strategy allows females to maximum fitness by investing in sons only when high quality mates are present in a mating system characterized by strong sexual selection on males.

Exploring the Metabolic Plasticity of Pancreatic Cancer

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Pancreatic cancer is the second leading cause of cancer deaths in the United States, with a survival rate of 5%. Although reprogrammed metabolism is a general characteristic of cancer, different cancers show distinct metabolic addictions. The present study aims to identify specific nutrients that fuel and sustain pancreatic cancer cell growth. Using the pancreatic cancer cell line as a model, we are studying cancer cells' metabolic energy needs using nutritional starvation approaches and pharmacological inhibitors. We carried out the ATP rate assay to explore the bioenergetic status of pancreatic cancer cells. Our preliminary data indicate that pancreatic cancer cells do not depend solely on glycolysis for energy needs. Real-Time ATP Rate assay demonstrated glycolytically suppressed cells upregulated mitochondrial function and exhibited metabolic flexibility to obtain the ATP necessary for survival. Using RT-PCR and western blot analysis, we are currently studying metabolic gene expression associated with Glycolysis, glutaminolysis, and OXPHOS in Mia-Paca2 cells under nutritional stress conditions. These studies will provide insights into cancer cell vulnerability for designing therapies against pancreatic cancer.

The Identification and Characterization of Tango6 in Early Zebrafish Development

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The Undiagnosed Disease Network (UDN) is a collection of clinicians and researchers that diagnose individuals with rare or previously uncharacterized diseases. A UDN participant with mutations in TANGO6 presented with heart and brain abnormalities. The International Mouse Phenotyping Consortium (IMPC) knocked out Tango6, resulting in embryonic lethality, suggesting that it is required for development. However, the function and expression patterns of Tango6 is largely unknown. In order to understand the role that Tango6 plays in development, we utilized embryonic zebrafish to analyze the quantitative and spatial expression of Tango6. It is moderately expressed between 24 and 120 hours post fertilization (hpf). In situ hybridization demonstrated that Tango6 is present in the brain beginning at 24 hpf and expressed in the developing gastrointestinal system around 120 hpf. Preliminary data of mosaically edited Tango6 knockouts generated using CRISPR have found an accumulation of blood in the gut by 120 hpf, suggesting defects in gut morphogenesis or function. In total, these data suggest that Tango6 is involved in brain and gut development, and further analysis of knockouts and spatial expression patterns is underway to determine the precise role of Tango6 in development and disease.

Effects of *Trametes versicolor* Secretions on Lung Cancer Cells

Jue Wang* and Dr. William P. Ranahan

Oral Roberts University

Lung cancer is one of the most aggressive cancers and is one of the major causes of death in the world. Common treatments such as surgery and chemotherapy can lead to severe side effects and complications. Given the prevalence of this cancer type and the lack of treatments without side effects, alternative treatments must be explored. Medical mushrooms have been used for thousands of years in many Asian countries as medicine. Mushroom extracts are currently used as standard adjuvant therapies in Japan and China. One medical mushroom, *Trametes versicolor*, also known as *Coriolus versicolor* or turkey tail, is in phase III clinical trials in the United States for use as an adjuvant therapy in breast cancer. While mushroom extracts have been shown to be safe and effective at providing general immune support, their anti-cancer effects are poorly understood. Secretions captured from *T. versicolor* mycelia were tested for effects on cancerous and non-cancerous cell line viability. *T. versicolor* secretions significantly decreased cancer cell viability while having no significant impact on non-tumorigenic cells. Preliminary analysis suggests that *T. versicolor* secretes several biologically active peptides containing polysaccharides. Future work will center around the identification and characterization of these compounds.

In-Silico Analysis and Over-expression of an α -Carbonic Anhydrase Homolog from the “Brain-Eating Amoeba”, *Naegleria fowleri*

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Naegleria fowleri is a free-living amoeba and the etiological agent of primary amoebic meningoencephalitis in humans. Treatment consists of repurposed antimicrobials, which are ineffective, leading to high mortality rates. Therefore, identification of new drug targets is important. Studies have indicated that fatty acid utilization is vital for *N. fowleri* growth, and a central enzyme in this process is a bicarbonate requiring carboxylases. Carbonic anhydrases (CA) catalyze the reversible hydration of CO₂ into bicarbonate, which is then utilized by carboxylases for fatty acid metabolism. Using BLAST analysis, we identified a protein, FDP41_009806 from *N. fowleri* that has a 25% identity with a human α -CAII. Multiple sequence alignment showed the presence of metal coordinating histidine residues and other catalytic residues conserved in other α -CA's. Phylogenetic analysis showed the protein to be distinct despite the conserved regions. The sequence and structural homology led us to hypothesize that FDP41_009806, hereafter NfCA1 α , is an uncharacterized α -CA in *N. fowleri*. To characterize NfCA1 α , protein overexpression was performed using the full-length NfCA1 α and truncated NfCA1 α . Although over-expression was successful, none of the constructs produced soluble protein. Currently, we are in the process of fine-tuning over-expression conditions to obtain soluble NfCA1 α for biochemical and structural analysis.

The Influence of Age on Experience-Induced Behavioral Changes

Lindsey Wells*, Andrew Fuller II, Molly Wingard, & Mark J. Garcia

Southwestern Oklahoma State University

Animals will modify their behavior based on prior experiences. These “experience effects” can be obtained in a variety of contexts including courtship, aggression, and foraging. For example, individuals become more cautious and risk-avoidant after being exposed to a predation experience. Despite a multitude of studies focusing on experience-induced behavioral changes in adults, the effects of experience on juvenile behavior remain unknown. The aim of this study is to investigate the effects of age on experience-induced behavioral changes. We selected the Mangrove Rivulus (*Kryptolebias marmoratus*) fish as our study system. Adult rivulus are known to alter their aggressive and explorative behaviors following a fighting experience. We measured boldness and risk-taking behaviors in juveniles (2 months of age) and adults (6 months of age) before and after a predation experience. Boldness and risk-taking were measured as an individual’s willingness to leave the safety of a shelter and explore an open field, respectively. The predation experience was elicited by vigorously chasing individuals for 10 seconds within the open field. According to our results, both adult and juvenile rivulus show increases in boldness and risk-taking following simulated predation experiences, whereas early-life experience does not influence adult behavioral responsiveness to simulated predator attacks.

Seasonal Patterns in Reproductive Output in a Self-Fertilizing, Hermaphroditic Fish

Molly Wingard*, Lindsey Wells, Andrew Fuller II, & Mark J. Garcia

Southwestern Oklahoma State University

Animals adjust their reproductive output dependent on their physiological state (e.g., energy stores) and environmental conditions (e.g., temperature), which underlies seasonal variation in reproduction. Timing of reproduction often coincides with environmental conditions that can favor offspring survival. The Mangrove Rivulus (*Kryptolebias marmoratus*) is a self-fertilizing, simultaneous hermaphrodite capable of producing year-round, but evidence suggests reproductive output follows seasonal patterns.

Our study’s aim is to examine how cold-exposure during development affects developmental timing and life-history traits and elucidate possible mechanisms underlying seasonal variation in rivulus reproduction. We incubated eggs under temperature conditions that varied in either magnitude (15-20C for 17d) or duration (18C for 5-17d). Control groups were reared at 26C until hatching. Hatchlings were then measured every two months (up to six months of age) for growth and maturation rates. Data collection is ongoing, but initial results indicate cold exposure increases developmental time from ~17d (control) to ~30d (treated). Further, treated juveniles were significantly smaller (~0.05-0.06g) relative to control juveniles (~0.09-0.1g) at two months of age. Treated individuals reached sexual maturity ~30 days later than control groups (~117d). Results of our study may provide insights into whether offspring quality and survivorship drive seasonal variation in rivulus reproduction.