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(sorted by presenter's last name)

THE ROLE OF PHOSPHATE AND CALCIUM-REGULATED PROTEIN, PCRP, IN RESISTANCE OF A HUMAN PATHOGEN, *PSEUDOMONAS AERUGINOSA*, TO POLYMYXIN B

Maha Achour, Tarosha B. Salpadoru, and Marianna A. Patrauchan, Oklahoma State University-Stillwater

Pseudomonas aeruginosa (Pa) is a Gram-negative human pathogen and a leading cause of acute and chronic infections. It is known to cause airway blockage in patients with Cystic Fibrosis (CF) – leading to high morbidity and mortality. This pathogen has been of particular interest due to its multi-drug resistance, including "last resort antibiotic", polymyxin-B (PMB). Studies have shown that elevated calcium (Ca2+) and lowered phosphate (Pi) alter bacterial susceptibility to antimicrobial treatment – implying their regulatory role in Pa resistance. Previously, we showed that elevated Ca2+ levels, detected in airways of CF patients, enhance PMB resistance through novel Ca2+-dependent mechanisms. We have also shown that the upregulation of putative phophonatase PA2803, is mediated by both Ca2+ and Pi -- designating it as PcrP (phosphate and calcium-regulated protein). Although studies of pcrP deletion mutant supported its role in Pa PMB resistance, PcrP function remains unclear. Via enzymatic studies, we found that PcrP has no phosphonatase activity, and therefore explored its potential protein-binding function. By using protein-pull down assays in the presence or absence of Ca2+ and Pi starvation conditions, we identified several putative binding partners of PcrP followed by bacterial two-hybrid system (B2HS) for validation. The Beta-Galactosidase activity of the co-transformed constructs was assayed both qualitatively and quantitatively to evaluate the strength of protein-protein interactions. B2HS supported the earlier observed dimerization of PcrP and validated the interaction of PcrP with hypothetical protein PA3518 and Acyl-carrier protein 3, Acp3. Based on sequence analysis, PA3518 may have a role in heavy metal (notably, Cu2+) sensitivity. Acp3's interaction with Catalase shows it may be involved with reactive oxygen species (ROS) regulation in cells. Collectively, we showed that PcrP reduces Ca2+-dependent ROS production in Pa. Thus, the interaction of PcrP with Acp3 may contribute to Pa resistance to ROS and therefore enhance its resistance to PMB.

UNLOCKING THE POWER OF BIOINFORMATICS: PRACTICAL APPLICATIONS FOR UNDERGRADUATE RESEARCHERS

Evonn Annor and Julianna Goelzer, Oral Roberts University

Outstanding Undergraduate Paper in Science Communication and Education

Bioinformatics has revolutionized biological research, providing a powerful toolkit for analyzing and interpreting vast amounts of biological data. This presentation introduces undergraduate researchers to the practical applications of bioinformatics tools through a series of mini case studies. The presentation demonstrates the use of Wash U Epigenome Browser to visualize the organization of the entire genome within a nucleus, providing insights into gene regulation and cellular processes. Next, it demonstrates how NCBI BLAST can be used to select a suitable model organism for a specific research question based on sequence conservation. Finally, it extracts the DNA sequence of an enhancer or promoter region using Wash U Epigenome Browser and NCBI BLAST, designing a guide RNA (gRNA) for CRISPR-Cas9 gene editing. These case studies highlight the versatility of bioinformatics tools in addressing diverse biological questions and designing experiments, empowering undergraduates to make significant contributions to biological research and innovation.

EFFECTS OF IN OVO EXPOSURE TO POLYCYCLIC AROMATIC HYDROCARBONS (PAHS) ON HEPATIC TRANSCRIPTIONAL SHIFTS IN THE CHICK EMBRYO

Damon Corvelo, Yulianis Pagan, Hallum Ewbank, and Christopher G. Goodchild, University of Central Oklahoma

Outstanding Graduate Poster

Marine oil spills are known to cause immense damage to ecosystems, and this is known to affect avian populations as well. Most avian crude oil toxicity research has examined the physiological and behavioral changes that afflict the adult birds. However, nesting birds can expose their eggs to crude oil attached to the nesting material and their feathers. Eggshell oiling can result in polycyclic aromatic hydrocarbons (PAHs), toxic chemicals that occur naturally in crude oil, being transferred to the internal eggs contents, leading to embryonic exposure. Previous research in our lab has documented liver hypertrophy in chick embryos exposed to PAHs in ovo. Liver hypertrophy and concomitant shifts in hepatic gene expression of detoxification enzymes have been observed in adult birds exposed to crude oil. However, currently there is a lack of understanding of hepatic transcriptional shifts in chicken embryos exposed to PAHs. To test whether avian embryos can upregulate detoxification enzymes to metabolize PAHs in ovo, we exposed white leghorn chicken embryos to one of six PAHs (Fluoranthene, Anthracene, Pyrene, Benzo[a]pyrene, Chrysene, and Phenanthrene) on embryonic day 3. On embryonic day 18, we collected embryonic livers and examined mRNA expression of a suite of detoxification enzymes (IL6, GPx, GR, GST, SOD, Actin, and GAPDH) using qPCR. Preliminary analysis suggests that in ovo exposure to some PAHs alters hepatic expression of some detoxification enzymes.

CYTOTOXICITY OF 6-GINGEROL ON COLORECTAL CANCER CELL VIABILITY

Katherine Dempsey and Joel Gaikwad, Oral Roberts University

Outstanding Undergraduate Paper in Biomedical Sciences

Colorectal cancer is the third most common type of cancer and the second leading cause of cancer-related deaths in America. Common treatment options include invasive surgeries and chemotherapy but are often accompanied by complications of sepsis, bowel stress, and reduced immunity. Therefore, the search continues for natural therapeutic alternatives that differentiate between healthy and cancerous tissues. *Zingiber officinale*, commonly known as the ginger root, has been used for centuries in ancient Chinese and Indian Ayurvedic medicine due to its well-known anti-inflammatory and antioxidant properties. It was hypothesized that the main bioactive compound in ginger, 6-gingerol, may possess anticancer properties that would reduce the cell viability of colorectal cancer in a dose-dependent manner. Microscopic observations of HT-29 cells treated with gingerol were consistent with apoptotic morphology. Cell viability and caspase activity assays further supported the theory that gingerol induces apoptosis in cancer cells. In comparison, HEK293T cells displayed increased cell viability when treated with gingerol. Analysis of both qualitative and quantitative data suggest that gingerol is able to selectively target tumorigenic cells while promoting viability in noncancerous cells.

ANALYZING DIETARY DIVERSITY AND THE ECOLOGICAL SIGNIFICANCE OF THE GREEN SUNFISH (*LEPOMIS CYANELLUS*) IN AQUATIC ECOSYSTEMS OF THE GREAT PLAINS REGION

Jamie Eastep, Lindsey Bruckerhoff, and Keith Gido, Oklahoma State University-Stillwater

Outstanding Undergraduate Paper in Environmental Sciences

Green Sunfish (*Lepomis cyanellus*) are opportunistic predators, that readily consume a variety of invertebrates, with insects comprising a significant part of their diet. The consumption of insects by Green Sunfish has ecological implications, as they play a role in influencing insect populations in their habitats. Additionally, their ability to consume a variety of prey items contributes to their success as a species in a wide range of aquatic environments. Diet variability in fish is thought to be influenced by consumer body size due to gape limitations and indeterminate growth. However, prey availability and energetic benefits should also play a role, as suggested by optimal-foraging theory. In this study, our objective was to investigate the effects of body size of Green Sunfish on the number of unique prey items, variation in prey selection, and mean body size of prey. We hypothesized that as Green Sunfish increased in body size, there would be an increase in the number of unique prey items, variation in prey selection, and mean body size of prey. To test this hypothesis, we analyzed stomach contents from over 300 Green Sunfish in streams across the Kansas River Basin in the Flint Hills ecoregion of Kansas. Additionally, we conducted a mesocosm experiment to examine changes in diet variability with fish body size. This research is significant as green sunfish populations are growing due to habitat alterations and they likely serve as important meso-predators in streams.

BRIDGING DISCIPLINES ON MARS: SOUTHWESTERN OKLAHOMA STATE UNIVERSITY'S FIRST INTERCOLLEGIATE STUDY INTEGRATING BIOLOGY, COMPUTER SCIENCE, AND ARTIFICIAL INTELLIGENCE FOR MICROBIAL ANALYSIS AND PLANT GROWTH ON MARS

Payden Farnsley, Stevie Langstraat, Rachel Uhlig, Kade Flores, Lisa Boggs, and Sherry Westmoreland, Southwestern Oklahoma State University

With the increasing public demand for space exploration, astrobiology research is a growing scientific field, as colonies on extraterrestrial planets come closer to reality. For these colonies to be a success, efficient nutrient cycling in different environments must be studied. The NASA-affiliated Plant the Moon competition challenges research teams across multiple educational divisions to grow food in simulated Mars soil (regolith) – produced by the Exolith Lab at the University of Central Florida – within a given growth period. Multiple students at Southwestern Oklahoma State University have participated in this challenge and have studied the interactions between microbes, Mars regolith, mammal fecal matter, and the growth of plants that provide food production. With Mars regolith behaving differently than Earth soil, parameters involving the growth of crops have been tested on top of soil additives. In addition to documenting total plant yield, soil pH, seedling germination rates, and chlorophyll content have been assessed. These characteristics of plant growth have been tested in many crops including, but not limited to, lettuce, spinach, basil, and radishes. With the ever-growing field of computer science and artificial intelligence, a joint research project between two departments will perform parameter testing on soil additive concentrations and specific growth conditions, among other things. Using multiple parameter tests, we anticipate finding the best combination of growth conditions and concentrations for crop yield in extraterrestrial soils used in space exploration. Beyond these implications for food and waste management, the results we find may be beneficial to organic farmers and home gardeners.

INVESTIGATION OF L-LYXONIC ACID EFFECT ON CYTOCHROME BD-1 OXIDASE EXPRESSION

Eli Grasso and April Nesbit, East Central University

Escherichia coli is a widely utilized model organism in a vast number of biological investigations, yet the functions of roughly 1,264 of its genes have yet to be demonstrated. One such gene whose purpose has not been entirely established encodes for putative DNA-binding transcriptional regulator YfaX. The gene yfaX has been identified as being part of an operon responsible for the metabolism of L-lyxonate. This investigation sought to determine whether there is a link between YfaX putative transcription factor and expression of cydA promoter, which controls expression of cytochrome bd-1 oxidase that is involved in electron transport chain. The YfaX protein was of interest because previous labs have shown that it binds cydA promoter in vitro, and cydA expression decreases in the presence of L-lyxonic acid. Lyxonate may be a product of vitamin C degradation in human intestines. It is possible that a higher concentration of vitamin C may result in an increased concentration of lyxonate; this may disrupt overgrowth of *E. coli* in the intestines, preventing potential unforeseen health risks. The potential link was tested using an yfaX deletion mutant in a strain with cydA promoter fused to the reporter gene lacZ that allows measurements with β-galactosidase assays with growth in different sugars. Although cydA expression decreases in the presence of L-lyxonic acid, the deletion of yfaX did not have an effect. Moving forward, future investigation will utilize a fusion of lacZ to the yfaX promoter region for the purpose of determining if the yfaX gene responds to L-lyxonic acid as predicted by the role of other genes in that operon.

SPATIAL PHYLOGENETICS OF VASCULAR PLANTS IN THE SOUTH-CENTRAL US

Sierra Hubbard and Mark Fishbein, Oklahoma State University-Stillwater

Outstanding Graduate Paper

While traditional measures of biodiversity are typically based on the species present in an area, phylogeny-based measures are able to capture information about the evolutionary history represented in an assemblage of taxa. Investigations of diversity using a phylogenetic framework can reveal the distributions of evolutionary lineages and the relative ages of plant assemblages. The South-Central United States (made up of Oklahoma and Texas) is a floristically diverse region that contains ^{3}8,000 vascular plant species. This region is also climatically diverse, with strong abiotic gradients in temperature, precipitation, and elevation. The current understanding of spatial phylogenetics in this region comes from a few continental-scale studies utilizing herbarium data. However, the South-Central US has not yet been included in any regional-scale studies, which could potentially reveal finer-scale patterns not apparent across broader study regions. Additionally, much fewer data have been available from Oklahoma and Texas compared to many other regions of North America; this may have led to incomplete conclusions about the spatial phylogenetics of plants in this region. Recent and ongoing digitization and georeferencing efforts have addressed this data gap by mobilizing a wealth of herbarium records from Oklahoma and Texas. In this study, we aim to use these newly available herbarium data to characterize the spatial patterns of phylogenetic diversity (PD) and relative phylogenetic diversity (RPD) seen in the vascular flora of the South-Central US. This approach highlighted regions that contain young plant assemblages in the High Plains and Southwestern Tablelands and identified concentrations of old lineages in the Eastern Temperate Forest and Edwards Plateau. In addition, we tested for associations between PD, RPD, and climatic gradients in precipitation, temperature, and elevation. We found that bioclimatic variables related to precipitation were the best predictors of PD and RPD.

COMPARISON OF CONSERVATION AND DIVERGENCE IN GENE RL COMPARED TO GENE GIG

Jenna Knox, Katie McCullock, and Lindsey Long, Oklahoma Christian University

Outstanding Undergraduate Poster

The goal of this experiment is to understand how pathways evolve using the insulin/TOR pathway. *Drosophila* was used as the model organism to identify gene conservation among various species that have increasing divergence from *D. melanogaster*. The specific gene of interest for this project was rl. In a paper published by Alvarez Ponce, it is hypothesized that more connections results in slower evolution of a gene. To show this we compared divergence scores in species closely, intermediately, and loosely related to *D. melanogaster*. We hypothesized that rl will be less evolutionarily conserved when compared to gig.

MATCHING-BASED COALITION FORMATION FOR MULTI-ROBOT TASK ASSIGNMENT UNDER PARTIAL UNCERTAINTY

Brenden Latham and Vladimir Ufimtsev, East Central University

Ayan Dutta, University of North Florida

Outstanding Undergraduate Paper in Mathematics, Computer Science, & Statistics

In this research, we examine the multi-agent coalition formation problem for instantaneous task allocation (IA) where a group of agents needs to be allocated to a set of tasks so that the tasks can be finished optimally. We will present new results in coalition formation for multi-agent systems in the presence of large partial uncertainty. We pair ideas from the Interval Hungarian Algorithm with a One-To-Many Bipartite Matching algorithm to achieve a scalable, parallel solution for allocation under partial cost uncertainty.

DESIGNING AN ORAL MUCOSAL VACCINE FOR ENHANCED PROTECTION AGAINST *CLOSTRIDIOIDES DIFFICILE*

Joseph H. McCreary and and I-Hsiu Huang, Oklahoma State University-Center for Health Sciences

Saeed Manouchehri and Josh Ramsey, Oklahoma State University-Stillwater

Yi-Wen Liu and Yu-Shan Lin, National Cheng Kung University-Taiwan

Clostridioides difficile is a gram +, spore forming, toxin producing anaerobe that is found throughout the environment. *C. difficile* is the leading agent of hospital acquired infections. Symptoms of *C. difficile* infection (CDI) can range from diarrhea to pseudomembranous colitis and if left untreated can lead to death. *C. difficile* is currently only treated with the antibiotics Metronidazole, Vancomycin, and Fidaxomicin. These antibiotics are non-specific to *C. difficile* and have the side effect of killing the normal microbiota of the gut. This microbiota helps to keep the gut resistant to CDI, and its destruction can lead to relapses of disease. Ongoing work in our lab is looking at preventing CDI using a nanoparticle based oral vaccine. In a mouse model of CDI, we previously demonstrated that using the receptor-binding domain of *C. difficile* toxin B (TcdB) as the antigen was effective in producing robust antigen specific IgA and IgG antibodies. These robust antibody responses to the *C. difficile* toxin were enough to prevent disease, however, it was not able to reduce bacterial burden leaving the potential for asymptomatic spread and relapses of disease. To fight this problem, we are working on two solutions. The first being a nanoparticle polymer that specifically is designed to be M cell targeting and pH activated. Second, we are also evaluating the immunogenicity using fusion proteins combining rTcdB with *C. difficile* surface proteins in a mouse model. We hypothesize that a two-target approach may decrease the bacterial load and lead to complete protection against *C. difficile* infections. Preliminary results looking at four formulations of this polymer all including rTcdB indicate a trend in IgG responses. More tests are needed to further validate these trends.

CO-EXPOSURE TO TWO POLYCYCLIC AROMATIC HYDROCARBONS (PAHS) ALTERS GROSS ORGAN MASS AND METABOLIC RATE OF CHICK EMBRYOS

Yulianis Pagan, Hallum Ewbank, and Christopher Goodchild, University of Central Oklahoma

Outstanding Undergraduate Paper in Applied Ecology & Conservation

Polycyclic aromatic hydrocarbons (PAHs) are naturally occurring toxic chemicals found in crude oil and are known to transfer from the external eggshell surface to egg contents. Previously, we conducted an egg-injection study with White Leghorn chicken (*Gallus gallus*) eggs and identified two PAHs, chrysene (Chr) and phenanthrene (Phe), that increased embryonic heart mass and decreased embryonic heart rate. In this study, we investigated whether co-exposure to Chr and Phe resulted in additive or synergistic effects on chick embryo development. On embryonic day (ED) 3, chicken embryos were exposed to Chr (800 ng / g of egg mass), Phe (800 ng / g egg mass), and Chr and Phe in combination (∑ PAH 1600 ng /g ng egg mass) via egg-injection. We then collected embryonic organ mass, heart rate, metabolic rate, and cardiac and hepatic mRNA expression of detoxification enzymes on ED 18. We observed a decrease in ED 18 heart rate across all treatments. We also saw an increase in ED 18 liver mass in eggs exposed to Chr and Phe simultaneously, and shifts in metabolic rate and mRNA expression of cardiac detoxification enzymes. Collectively, these data suggest in ovo exposure to PAHs may lead to congenital heart defects, which may have long-term implications for hatching success and hatchling survival.

OBJECTIVE COMPARATIVE GENOME SEQUENCE ALIGNMENT OF THE HOMININI SPECIES USING A HIGH-PERFORMANCE COMPUTING ALGORITHM TO REVEAL PHYLOGENETIC INSIGHTS

Christof Rosler, Derick DuFriend, Evonn Annor, Rita Njoroge, William P. Ranahan II, Matthew H. Goelzer, Stephen Wheat, and Julianna A. Goelzer, Oral Roberts University

Outstanding Undergraduate Paper in Biological Sciences - Zoology

The branching of the Hominidae family has long engrossed the minds of zoologists as the taxa includes *Homo sapiens*. Phylogenetic trees have been constructed using morphology, proteins, and genes yet often the genetic segments used neglect regulatory, non-coding genes. With a greater understanding of the importance of these genes due to advances in biochemical research, we reanalyzed the historical percent similarities, 96-98.4%, between the sister genus taxa *Pan* and *Homo* via direct base pair comparison across their whole genome. We used ORU's GeneCompare program on Titan, the high-performance computing system to examine whole genomes. The program can take two FASTA files and find exact matches of a minimum length between the two files, the experimental granularity. Each chromosome was individually tested in this manner, a base and against a target, until the whole genome was compared. The matches are recorded as genomic coordinates and can provide insightful data such as the total percent similarity between each specie's chromosomes. We found more enriched percent similarity relationships between *Pan paniscus*, *Pan troglodytes*, and *Homo sapiens* as specific chromosomes expressed a lower and upper range of 59.66-93.1%, and a total mean of 81.8% (excluding Y-chromosome). Using bioinformatics as a tool to expand the scope of zoology new insight into the phylogenetic relationships between the Hominini species was found.

THE DISTRIBUTION OF INVASIVE HONEYSUCKLE IN EASTERN OKLAHOMA

Sarah Short, Oklahoma State University-Stillwater

Outstanding Undergraduate Paper in Biological Sciences - Botany

The introduction and spread of invasive plant species has been an increasingly concerning environmental issue in recent decades due to the harmful impacts their presence has on the ecosystems they've been introduced to. Due to many factors, non-native species may have survival or reproductive advantages over native plant species in their introduced habitats, which can lead to direct and indirect negative impacts on these ecosystems and their biodiversity. These effects are often logistically difficult and expensive to manage, and they often lead to larger long-term issues down the line. *Lonicera maackii* and *L. japonica* are invasive honeysuckle species that have formed naturalized populations in Oklahoma, where they outcompete, inhibit, and reduce the growth of native species, thus posing a threat to local biodiversity. Both species reproduce quickly, grow aggressively, lack competitors and herbivores, and survive in a wider range of environmental conditions for longer periods than most native plant species. Using data collected from field surveys and herbarium records, my study aims to provide new information to the existing knowledge of the distribution of both honeysuckle species throughout eastern Oklahoma. Parks and public recreation areas of all 47 counties of eastern Oklahoma were surveyed. Between herbarium data and observation records from the field surveys, this research observed *L. maackii* in fewer counties than expected and *L. japonica* in nearly all counties surveyed. Data analysis shows a strong correlation between the presence of *L. maackii* and the population size of a town.

EVOLUTIONARY CONSERVATION OF GIG AND SLMB IN *DROSOPHILA*

Heather Sparks, Jackson Taubel, Lindsey J. Long, Oklahoma Christian University

Laura Reed, Genomics Education Program-University of Alabama

Outstanding Undergraduate Paper in Biochemistry & Molecular Biology

The insulin pathway functions to uptake glucose molecules into fat or muscle cells. This pathway is vital for several biological processes, such as cell metabolism, growth, proliferation, and differentiation. In this study, the insulin pathway was studied in *Drosophila*. Gig and slmb are two genes in the insulin pathway. The genetic interactions of these genes were analyzed, leading to a hypothesis. It was predicted that gig and slmb have similar evolutionary conservations in the insulin pathway of *Drosophila*. Using bioinformatic data, genes of *D. melanogaster* were compared to genes of other species. Genetic comparisons were performed using gene annotation data, nucleotide and protein sequences, as well as percent identities and similarities. This information was combined in order to calculate divergence scores. Results from data analysis showed that gig is less conserved and diverged faster than slmb.

EVALUATING CYTOKINE RESPONSES IN BLADDER CELLS INFECTED WITH UROPATHOGENIC *ESCHERICHIA COLI* AND *KLEBSIELLA PNEUMONIAE*

Tia Tafla and Janaki K Iyer, Northeastern State University

Outstanding Undergraduate Paper in Microbiology

Urinary tract infections (UTIs) are prevalent infections that are caused by different types of bacteria including *Escherichia coli* (*E. coli*) and *Klebsiella pneumoniae* (*K. pneumoniae*). When the bladder cells become infected, they respond by producing pro-inflammatory cytokines and chemokines. To gain a deeper understanding of the host's response to different uropathogens, we conducted an Enzyme-Linked ImmunoSpot (ELISpot) assay. This approach allowed us to assess the expression of multiple pro-inflammatory cytokines in a sample. We hypothesized that infections with various uropathogens would lead to varying levels of pro-inflammatory cytokine expression due to differences among uropathogens. To test this hypothesis, we infected human 5637 bladder cells with uropathogenic *E. coli* and *K. pneumoniae* strains for 24 hours and evaluated cytokine protein expression. The ELISpot results revealed that uropathogenic *E. coli* caused the secretion of IL-1ra, IL-6, IL-1a, and IL-1b compared to uninfected cells. However, the response of IL-6 and IL-1b was reduced in bladder cells infected with *K. pneumoniae* strains, thereby supporting our hypothesis. To differentiate between cytokine production and secretion, we decided to perform intracellular cytokine staining followed by flow cytometry. Brefeldin A (BFA) is commonly used in these experiments to prevent cytokine secretion. We conducted an MTT cell viability assay to evaluate any cytotoxic effects of BFA. Our results showed no statistically significant differences among the various BFA concentrations tested. Ongoing experiments will help us establish optimal conditions for detecting cytokine production by flow cytometry. These findings will enhance our insights into how uropathogens modulate innate immune responses in bladder cells during the infection process, contributing to the development of more effective UTI treatments.

PROBIOTIC EFFECTS OF *LACTOCOCCUS LACTIS* AND *LEUCONOSTOC MESENTEROIDES* ON MORPHOLOGY, FECUNDITY, AND LONGEVITY IN *CAENORHABDITIS ELEGANS*

Brenda Tinoco-Bravo, Mylissa A. Stover, Crystal A. Shults, Sydney Marouk, Ratnakar Deole and Jacob R. Manjarrez, Oklahoma State University-Center for Health Sciences

Probiotic supplementation has been widely studied showing that it can sustain significant therapeutic benefits to overall health, which depends on the overall composition of the microbiome. In this study, we investigated the supplementation of potential probiotic lactic acid bacteria *Lactococcus lactis* and *Leuconostoc mesenteroides* in the gut of *Caenorhabditis elegans* and observed their effects in survival, size and morphology, and fecundity. Survival assays were used to analyze median and total lifespan, where analysis was performed until death. Fecundity assays were performed with the number of progenies counted daily. Body morphometrics were analyzed where length, width, area, and speed were recorded. Intestinal permeability was also evaluated using a dye-leakage assay (Smurf). Survival analysis using CeMbio, a *C. elegans* natural microbiome, demonstrated a decrease in survival when supplemented with *L. lactis* and *L. mesenteroides*. When *L. lactis* and *L. mesenteroides* was used as a sole food source or were supplemented to the standard *E. coli*, OP50, diet it showed an increase in survival. In terms of morphometrics, OP50-fed *C. elegans* supplemented with *L. mesenteroides* were smaller and slower when compared to *L. lactis*-supplemented OP50, which were larger and faster. Fecundity showed that OP50 supplementation with *L. mesenteroides* or *L. lactis* produced higher amounts of progeny than the *L. mesenteroides* or *L. lactis* monocultures. Intestinal permeability was shown to be higher in both *L. lactis* and *L. mesenteroides*, which also show to have an increase in longevity when compared to OP50. These results highlight the potential and beneficial applications for these lactic acid bacteria as a therapeutic probiotic. Our study indicates that both *L. lactis* and *L. mesenteroides* when supplemented with OP50 has a positive influence on the overall health and longevity of *C. elegans*.

TERRESTRIAL MAMMALS OF THE OKC METRO AREA

Zachary Woods and Daniel Gomes da Rocha, Southern Nazarene University

Urbanization is growing world-wide, and particularly in North America. As urbanization grows, so does our dependence on remaining urban green areas (e.g., parks, reserves, green belts) to preserve biodiversity and ecosystem services. The objective of this study is to understand how effective these green areas are in preserving species diversity. Additionally, we aim to identify environmental and anthropogenic variables that are influential to species diversity. We focused on the medium and large terrestrial mammal community in the highly urbanized Oklahoma City Metro area. Here we report preliminary data on 12 camera trap sites (active for ^{3}75 days during Summer 2022), in combination with site covariates (NDVI, road intensity, elevation, and number of domestic records) collected at and around the camera locations. We used Poisson Generalized Linear models (GLM) to test the effect of site covariates on mammal species richness. We also plotted species cumulative curves to assess the survey completeness. In total we detected 11 wild and 3 domestic medium and large terrestrial mammal species. We detected the majority of mammals species expected to occur in this region (with the exception of larger predators). Sites varied greatly in species richness (4-10) and composition. All site variables had a statistically non-significant effect (p-values>0.05) on species richness. This result is not unexpected considering the small sample size, but revealed some promising covariates to be tested as new data is added to the database (data from the Summer 2023 survey is being processed). Our species inventory serves as a baseline for future wildlife monitoring programs in the OKC metro area.