

2022 Annual Technical Meeting Abstracts (sorted by presenter's last name)

Hyacinthe Aboudja¹, Sheela Duggirala², Venkata Jaipal Reddy Batthula², Michael Howell², Richard S. Segall³, Peng-Hung Tsai², Daniel Berleant³. (¹Oklahoma City University, ²University of Arkansas at Little Rock, ³Arkansas State University)
10:30-10:45 in 331 Tandy

WOMEN IN SPACE: FROM HISTORICAL TREND TO FUTURE FORECASTS

In the history of space exploration, the gender balance has tended to favor men. However, the STEM (science, technology, engineering, and mathematics) fields have increasingly had women represented, a trend that is often encouraged nowadays as openness to gender diversity in technology has been realized to be beneficial to the overall level of expertise in the fields, to the economy, and to those wishing to be part of these fields. Exploration of outer space forms an interesting case study. Historical examples include a group of women named First Ladies Astronauts Trainees (FLAT), a group later called Mercury 13, and a group of seven women astronauts who visited the space shuttle Discovery before its launch in 1995. As early as 1961 humans had been flying into space; the first woman went into space from Earth in 1963. Here we explore the contribution of women as astronauts in terms of their percentages of astronauts and the trend of these percentages over time. Historical events and data that have prevented or encouraged their participation in this field of technology, and the overall trend of women's participation around the world is relevant to these trends. Up to now, there have been dozens of women who have flown into space, including cosmonauts, astronauts, payload specialists, and space station participants, starting with the first, Russian cosmonaut Valentina Tereshkova, who flew on Vostok 6 on June 16, 1963. Our study showed that women involved in space exploration throughout the world has increased over time and we analyze this trend of increase.

Nikkita Addy, Yonatan Gelaye, and Lindsey J. Long (Oklahoma Christian University)

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*EVOLUTIONARY CONSERVATION OF SIMA AND PTP61F IN *DROSOPHILA GRIMSHAWI*

This study focused on the evolutionary conservation of the two genes *sima* and *Ptp61F* in the species *Drosophila grimshawi*. *D. grimshawi* is a highly diverged species from *D. melanogaster* and oftentimes within a highly diverged species the conservation of genes decreases, therefore, we hypothesized that because *sima* has higher connectivity to other proteins within the Insulin/TOR signaling pathway it would be more conserved than *Ptp61F*. The genomic neighborhood of *sima* and *Ptp61F* in *D. grimshawi* was compared to the genomic neighborhood of *sima* and *Ptp61F* in *D. melanogaster*, then both genes were annotated in *D. grimshawi*. Any anomalies encountered while annotating were used to calculate a divergence score for each gene. Results indicated a similar divergence score of *sima* and *Ptp61F* in *D. grimshawi*, which led us to conclude that our hypothesis was not supported.

Matthew Ahlemeier, Colter Esparza, Pragma Sharma, and Horrick Sharma (Southwestern Oklahoma State University)

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*EVALUATION OF LDHA INHIBITORS THROUGH LACTATE ACCUMULATION ASSAYS IN PANCREATIC CANCER CELL LINES

Metabolic reprogramming is considered a new hallmark of cancer. Cancer cells undergo extensive metabolic rewiring and alter the metabolism of glucose, glutamine, and fatty acid to support their growth and proliferation. Cancer cells get addicted to glucose and convert the pyruvate to lactate. Lactate dehydrogenase-A (LDH-A) is the primary metabolic enzyme that converts pyruvate to lactate and is overexpressed in multiple tumors, including pancreatic cancer. Lactate accumulation in the tumor microenvironment is associated with increased tumor aggressiveness, metastasis, inhibition of the antitumor immune response, and resistance to therapy. Thus, targeting human lactate dehydrogenase is a promising approach for treating advanced carcinomas. Various groups have recently reported several LDHA inhibitors; however, their development is hampered due to a lack of cellular activity and metabolic stability. In the present study, we tested the ability of new LDHA inhibitors, synthesized by our collaborator, to inhibit lactate production in MIA PaCa-2 pancreatic cancer cells. Compounds inhibited lactate production as compared to untreated control. Future studies will involve studying the effect of these compounds on other metabolites, including intracellular pyruvate level.

Mubaraak Akinbola¹, Jacob Nakanashi¹, Nesreen Alsbou¹, and Imad Ali² (¹University of Central Oklahoma;²University of Oklahoma Health Sciences Center)

9:30-9:45 in E378 Forensic

*INCREASING THE NUMBER OF ANTENNAS AND SWEEPING DIFFERENT FREQUENCIES TO ENHANCE MICROWAVE IMAGING SYSTEM RESOLUTION

This research aims to enhance the resolution of images obtained using a microwave imaging system for different phantoms representing different parts of the human body. The Microwave Imaging System is considered more advantageous than other available imaging systems like x-rays, CT scans, and MRIs. CT scans are preferred for identifying specific cancers, such as lung,

and liver, but CT scans expose the patient to ionizing radiation which can cause damage to healthy tissues while MRI consumes more power and a huge equipment setup. The microwave imaging system used in the lab consists of a vector network analyzer, antennas for transmitting and receiving RF signals, SPDT and SP8T switches to allow for multiple antennas to be added to the system to increase the image resolution. Microwave Imaging equipment is not expensive compared to other Imaging techniques, making microwave imaging a cost-effective technique. The immediate objective of this research project is to get images of different objects with a different frequency range using vector network analyzer to sweep over different frequencies and different kinds of antennas to determine what range or antenna array configuration is best used to get clearer and better images for each scan. The system used is portable which makes it easily move to scan different objects at different locations compared to the currently available huge imaging modality. The system will be characterized and the data collected will be analyzed to find the relation between the different types of antennas, increased number of antennas, different frequency ranges used and the quality of images obtained.

Altherr (Joseph) Alcuitas, Rachel Uhlig, Jarret Smith, Ryan Agyemang, and Rickey Cothran (Southwestern Oklahoma State University)

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***FEMALE AMPHIPODS ADJUST BROOD SEX RATIOS BASED ON MATE CHOICE**

There are several determinants of sex ratios in nature all falling under two main categories genetic or environmental. The expectation from theory is that the sexes will be produced in a 1:1 ratio because investing in the rarer sex is expected to provide greater fitness returns. However, biased sex ratios are common in nature and can be the result of both genetic and environmental factors. We hypothesized that females bias the sex ratio of broods in favor of sons when allowed to choose their mate in the wild. We collected mating pairs of amphipods (*Hyalella* sp.) from two pools in the same natural spring system. Half of the females were separated and repaired with their original mate—i.e. they were allowed to choose their mate. The other half of the females were separated and assigned a new male at random. Each pair was placed in their own 50-ml jar and placed in an environmental chamber. We checked the pairs three times a week and recorded offspring sex ratios. We predicted females with a choice in their mate would pick higher quality males and in turn produce more male biased broods and females assigned a mate at random will produce more of an even brood sex ratio. Preliminary results show a non-statistically significant trend of females given a choice of a mate producing a higher proportion of sons in their broods than females mated at random. Such a strategy would allow females to maximize fitness by investing in sons only when high quality mates are present in a mating system characterized by strong sexual selection on males.

Victor Andreev¹, Joshua Puzey², Lizzy Davies², Carrie Olson-Manning³, Sydney Kreutzmann³, and Mark Fishbein¹ (¹Oklahoma State University; ²College Of William And Mary; ³Augustana University)

10:15-10:30 in 353 Tandy

****NOVEL MORPHOLOGICAL AND GENETIC EVIDENCE FOR INTROGRESSIVE HYBRIDIZATION BETWEEN TWO MILKWEED SPECIES**

Understanding patterns of variation in closely related species is essential for studying their evolution. One system that can help us better understand the evolution of plant species in prairie ecosystems includes two milkweeds, *Asclepias speciosa* and *A. syriaca*. The ranges of these species overlap on the Great Plains, and many individuals of intermediate morphology can be found in this area. Several researchers proposed hybridization as an explanation for the observed pattern of morphological variation. However, presence of a range of morphological intermediates does not necessarily imply hybridization. Alternative explanations would include preservation of ancestral polymorphism or the action of selective pressure imposed by environmental clines. Our goals were to characterize putative hybrids and validate the hybrid origin of intermediates using morphological and genetic approaches. In order to do that we analyzed a range-wide sample of about 600 individuals. Our morphological analyses were based on measurements of 15 floral and vegetative traits, and genetic analyses were based on 7480 genome-wide SNPs. The analyses revealed that there is no evidence of continuous morphological variation between *A. speciosa* and *A. syriaca* that is correlated with geographic distance. These species can be reliably distinguished on morphological and genetic levels, and putative hybrids are morphologically and genetically intermediate between them. There is also evidence of interspecific gene flow in sympatric populations of *A. speciosa* and *A. syriaca*. Individuals in the zone of sympatry demonstrate various degrees of admixture, and the pattern of shared genetic variation corresponds to that of advanced generation hybridization. We conclude that the individuals of intermediate morphology are indeed hybrids, since their existence cannot be explained by environmental clines or preservation of ancestral polymorphism. This research helps us to understand the spatial distribution of morphological and genetic variation in plant species on the Great Plains and the processes that shape this variation.

Josh Autaubo, Shaelyn Ward¹, Philo Waters¹, Elizabeth Garrett¹, Kelsi Batioja¹, Reece Anderson¹, Debra Furr-Holden², and Matt Vassar¹ (¹Oklahoma State University Center for Health Sciences; ²School of Global Public Health, New York University)

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****A SCOPING REVIEW OF HEALTH INEQUITIES IN ALCOHOL USE DISORDER**

Alcohol Use Disorder (AUD) poses a significant health burden, especially in medically underserved, as well as underrepresented racial and sexual minority populations. Ameliorating health inequities are vital to improving patient-centered care. Given the heightened focus on narrowing the health disparities gap, evaluating health inequities for patients with AUD has become of utmost importance. More research is needed to understand health inequities in AUD and the disproportionate impact on already marginalized populations. The objective of this scoping review is to chart the existing evidence on health inequities related to AUD and identify existing knowledge gaps to guide future equity-centered research. We performed a literature search using Ovid (Embase) and MEDLINE (PubMed) databases for articles on AUD that were published in the 5-year period spanning from 2017-2021 and written in English. This scoping review followed guidelines from the Joanna Briggs Institute as well as the PRISMA extension for scoping reviews. All studies were screened and extracted in a masked, duplicate manner. Frequencies of each health inequity examined were analyzed and main findings from each included study were summarized. Following screening, our sample consisted of 72 studies for data extraction and analysis. Alcohol Use Disorder was more likely in historically marginalized groups, among sexual minorities and more common in men, though there are rising rates in women. Our findings indicate that significant research gaps exist in education, rural under-resourced populations, and LGBTQ+ communities with Alcohol Use Disorder. Scoping review highlights the gaps in research on inequities in AUD, as well as the conflicting findings across studies. To bridge the current gaps, we recommend research on the following: 1) triage screening tools and the use of telemedicine for rural, under-resourced populations; 2) interventions to increase treatment engagement and retention for women; and 3) community-based participatory methodologies for the LGBTQ+ communities.

J. Tyler Babek, Jack Rea, Reece M. Anderson, Rigel Bacani, Jordan Staggs, and Matt Vassar (Oklahoma State University Center for Health Sciences)

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****THE CURRENT STATE OF HEALTH INEQUITIES IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE: A SCOPING REVIEW**

As of 2019, chronic obstructive pulmonary disease (COPD) was the third leading cause of death worldwide. An understanding of the health inequities surrounding treatment and prevention of COPD is required to address the barriers in order to improve care for underserved populations. This scoping review was conducted to identify the existing evidence of health inequity in COPD and identify the gaps in knowledge to help direct future research. We followed the guidelines from the Joanna Briggs Institute and PRISMA-ScR extension for this scoping review. In July 2022, a literature search using Ovid (Embase) and MEDLINE (PubMed) databases was conducted to identify articles on COPD, published between 2016-2021, written in English, and investigating at least one health inequity as defined by the NIH. All studies were screened for inclusion criteria and extracted in a masked, duplicate manner. Each health inequity was investigated, extracted, and summarized. Thirty articles were screened in full-text and 19 were found to meet inclusion criteria. The most commonly investigated COPD patient inequities were race/ethnicity, income status, education. Since the implementation of the NIH's sex and gender minority category in 2016, only one study within our sample examined the LGBTQ+ patients with COPD. The least commonly investigated inequities rural/under-resourced, sex/gender, LGBTQ+ affiliation. Occupational status was not investigated by any included studies in our sample. Our scoping review underlines the lack of research regarding inequities affecting COPD patients, especially in certain areas such as sex/gender and LGBTQ+. We recommend further research regarding LGBTQ+ spirometry findings, race/ethnicity associations with medication adherence, and more diverse race/ethnicity investigations.

Joshua Baer, Shania Do, Tiffany Jones, Abigail Kee, Karissa LeHew, Derek McGuire, Sarah Soliman, Sydney Spillane, Monica Vuong, Cari Marshall, and Ipe Paramel (Oklahoma State University Center for Health Sciences)

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****LEAN HEALTHCARE: EVALUATION OF BED THROUGHPUT AT OSU MEDICAL CENTER**

Several factors play a role in an organization's success to function on a daily basis. For example, one factor being the application of efficient protocols to produce effective and consistent results. There is a specific procedure, called LEAN, that has been increasingly employed throughout various types of corporate professions due to its favorable outcomes. Originally, LEAN practices were created to enhance workflow and manufacturing processes in the automobile industry. After other industries observed the success rates from applying these certain methods, LEAN has been progressively adapted by many businesses to achieve similar effects. By adopting the LEAN methodologies, corporations have been able to increase their productivity, value, and client satisfaction. An example of how versatile and beneficial the LEAN approach can be in other fields, besides manufacturing, can be portrayed within a healthcare setting. There have been multiple healthcare organizations that have applied LEAN strategies to their systems in order to amplify quality improvement, with an end goal to better patient care. In this poster, a model is presented on how to apply and replicate LEAN tactics in an effort to advance bed throughput within a hospital setting. In the summer of 2022, a team of medical students from Oklahoma State University College of Osteopathic Medicine (OSU-COM) applied LEAN tools and techniques to examine the delayed process of bed throughput from the Emergency Department to the hospital floors. In doing so, possible solutions were developed in hopes to improve workflow, culture, and most importantly, patient outcomes.

Eddy Bagaruka, Rajeswari Raguraman, Meghna Mehta, Anupama Munshi, and Rajagopal Ramesh (Oklahoma Christian University)

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***PHARMACOLOGIC INHIBITION OF HUR DISRUPTS CELL PROLIFERATION AND INDUCES CELL-CYCLE ARREST IN MEDULLOBLASTOMA**

Human antigen R (HuR) is an RNA binding protein that is overexpressed in a broad-spectrum of human cancers and is associated with poor prognosis, drug resistance and metastases. HuR post-transcriptionally regulates the stability of mRNAs that include several oncoproteins. Therefore, we hypothesized that targeted disruption of HuR will result in global downregulation of oncoproteins resulting in tumor cell death. To test our hypothesis, a small molecule inhibitor (CMLD2) targeted to HuR was tested for its antitumor activity against human medulloblastoma cells in vitro. Human medulloblastoma (Daoy and D283) cell lines were grown in an appropriate culture medium and used for cell viability, western blotting, and cell-cycle analysis. For all experiments, cells were seeded in six-well plates treated with two different concentrations (20 and 30 μ M) of CMLD2 and harvested at different time points (48 h, 72 h). An aliquot of the harvested cells was subjected to Trypan-Blue cell viability assay and the remaining cells were used to prepare total cell lysate for Western Blotting. In a separate experiment, CMLD2 treated cells were harvested and subjected to cell-cycle analysis. Cell viability studies showed CMLD2 treatment inhibited cell proliferation in both medulloblastoma cell lines in a dose- and time-dependent manner compared to DMSO-treated control cells. Western blot analysis showed CMLD2 treatment did not reduce HuR protein expression levels as CMLD2 does not inhibit but rather disrupts the interaction between HuR and its target mRNAs, an observation that concurs with our previous studies. In contrast, HuR-regulated anti-apoptotic protein Bcl2 was reduced in CMLD2-treated cells compared to control cells. P27 expression increased in CMLD2-treated D283 cells while the protein expression was reduced in CMLD2-treated Daoy cells. Cell cycle analysis showed CMLD2 treatment markedly induced G1 phase cell-cycle arrest in Daoy cells compared to DMSO-treated control cells.

Brooklin Bain, Kayton Kite¹, G. Caroline Schwab¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

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***EVOLUTIONARY CONSERVATION OF RICTOR**

The *Drosophila* species is one of the most important model systems used for biological sciences. Specifically, this study focused on the evolution of the insulin/TOR pathway within the species by using comparative genomics. The insulin/TOR pathway is a regulator of organism and cell growth, therefore playing a role in the lifespan and evolution of not only *Drosophila*, but in many animals. Within this study, comparative genomics was used to determine the conservation of a gene, rictor, within the pathways compared to different species of *Drosophila*. To compare, sequencing of the target gene in twelve species of the *Drosophila* genus was completed, along with computing divergence scores based on the gene neighborhoods and gene structure. Genomic neighborhoods of the target gene in each species were examined and compared to assigned divergence scores. Due to the many interactions rictor possessed, it was hypothesized that rictor would be well conserved throughout evolution and have a conserved genomic neighborhood. However, genomic neighborhoods indicated that rictor was not well conserved in species with high divergence. As species evolved, genomic neighborhoods became more diverged from that of *D. melanogaster*.

Troy Baird (University of Central Oklahoma)

9:15-9:30 in 351 Tandy

DOES STARTING FAST WIN THE FITNESS RACE? A DECADE OF BEHAVIORAL AND PARENTAGE STUDIES IN OKLAHOMA'S STATE REPTILE

Measurements of reproductive success over the entire lifespan of individuals are essential for examining the range of fitness variation acted on by selection. Such studies are especially interesting in populations where individuals adopt alternative reproductive tactics. Over a decade, we combined behavioral observations and genetic parentage data in collared lizards (*Crotaphytus collaris*) to determine the fitness consequences in males that established breeding territories during Year-1 versus males that delayed territory acquisition until Year-2. Nearly 80% of males delayed territorial defense and approximately 90% of these died before Year-2. A small subset (9.5%) of males sired 37.2% of all offspring, whereas nearly one-fourth of males failed to produce any offspring before dying. Selection gradient analyses revealed that both total breeding lifespan and longevity of territory ownership were under strong positive selection. Surprisingly, however, males that postponed territory acquisition until Year-2 still obtained average lifetime fitness similar to males that established territories during Year-1, indicating that both delayed and accelerated ontogenetic trajectories can be successful. The relative number of first-year males that accelerated or delayed territory acquisition was relatively stable throughout our decade-long study, suggesting that variable social ontogenies may have a genetic basis. Accelerated territory acquisition was more frequent in males that were larger at the beginning of Year-1 and hatched from first clutches, both traits likely influenced by heritable contributions from one or both parents. Our results demonstrate the power of combining genetic parentage analyses with detailed behavioral observations over the entire lifespan of individuals to address factors influencing fitness variation in populations characterized by alternative social ontogenies.

Jennifer Ballheim and Jami Gurley (OUHSC)

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***THE ROLE OF RETINAL ENDOTHELIAL CELL CAVEOLIN-1 IN SMOOTH MUSCLE CELL LOSS IN RETINA MICRO-VESSELS**

Loss of Smooth muscle cell (SMC) coverage in retina micro-vessels occurs with age and metabolic disease. At present, the mechanism behind the SMC loss is unclear. Previous data from our lab show that SMC loss in retina micro-vessels also occurs in mice with endothelial cell (EC) Caveolin-1 (Cav1) depletion. Here, we establish a method to silence the Cav1 gene in human retinal endothelial cells (HRECs) to explore the role of EC Cav1 in loss of SMC coverage in retina micro-vessels. HRECs were cultured and transduced with Adenovirus-5 (Ad5) Cav1- silencing shRNA. Increasing viral titers and incubation periods were performed to optimize the shRNA-mediated Cav1 transduction and CAV1 protein knockdown. Transduction was confirmed by the presence of a green fluorescent protein (GFP) reporter imaged via fluorescence microscopy 24 hours post viral transduction. The culture was incubated in viral-infected media for 48 hours before being replaced with new media. The cells were harvested 96 hours post viral transduction. Cav1 silencing was confirmed with Western blotting for CAV1 protein. The Western blot CAV1 protein was quantified via densitometry using LI-COR Image Studio Lite. Our preliminary data suggests that Cav1 protein is reduced by more than 80% with transduction by the Ad5 Cav1 silencing via shRNA compared to the un-transduced HREC samples. HREC Cav1 silencing was achieved with over 80% efficacy with shRNA viral transduction. Depletion of CAV1 in HRECs will allow exploration of retinal EC-CAV1's role in retinal microvascular SMC loss. Future studies include assessments of retinal EC-CAV1 expression on retinal EC metabolic functions.

Nicholas Baurer, Caitlin Wayland, Payden Farnsley, and Vijayakumar Somalinga (Southwestern Oklahoma State University)

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IDENTIFICATION AND PRELIMINARY CHARACTERIZATION OF AN α -CARBONIC ANHYDRASE HOMOLOG FROM THE "BRAIN-EATING AMOEBA", *NAEGLERIA FOWLERI

Naegleria fowleri is a thermophilic, free-living amoeba that inhabits aquatic ecosystems and water distribution systems. *N. fowleri* causes primary amoebic meningoencephalitis (PAM), a rare, fatal and rapidly destructive infection of the central nervous system. Current treatments consist of repurposed antimicrobial agents, which are not effective, leading to very high mortality rates. Therefore, identification of new and effective drug targets is imperative. Recent studies have shown that fatty acid utilization plays an important role in *N. fowleri* growth, and a central enzyme in fatty acid metabolism is a bicarbonate-requiring carboxylase. Carbonic anhydrases (CA's) are metalloenzymes that catalyze the reversible hydration of carbon dioxide into protons and bicarbonate, a ubiquitous reaction important for physiological functions. Bicarbonate produced by the catalytic activity of CA's are utilized by carboxylases for the synthesis of molecules essential for cellular activity. In addition, recent studies have shown that CA's may play a role in the virulence of bacterial pathogens. Surprisingly, CA's and their role in metabolism and virulence of eukaryotic pathogens remains largely uncharacterized. Using BLAST analysis, we recently identified a protein, FDP41_009806, from *N. fowleri*, with 25% identity to human α -CAII. Both conserved domains and multiple sequence alignments analyses showed the presence of metal-coordinating histidine residues and catalytically important glutamate and threonine residues conserved in many closely related α -CA's. In addition, homology modeling of FDP41_009806 revealed conserved structural elements such as the central β -sheet core that harbors the metal binding residues essential for CA catalytic activity. Although FDP41_009806 shows all the hallmarks of an α -CA, phylogenetic analysis indicated that this *N. fowleri* homolog may represent a new type of α -CA. The structural and conserved active site homology led us to hypothesize that FDP41_009806, hereafter NfCA1 α , is an uncharacterized α -CA in *N. fowleri*. The goal of this project is to characterize NfCA1 α using biochemical and structural methods.

Bethany Bings and Jessica Brumley (East Central University)

9:15-9:30 in E393 Forensic

***A STATISTICAL ANALYSIS OF COVID-19 CASE AND DEATH RATES AMONG TRIBAL NATIONS IN OKLAHOMA**

COVID-19, the infectious disease caused by the variant of coronavirus SARS-CoV-2, has had a significant impact in the United States. Recent research indicates that Native Americans are among the most severely affected groups. However, the data used in these studies are often aggregated and do not accurately reflect the situation in individual tribal nations or populations. This study utilized the Supreme Court case *McGirt v. Oklahoma* to analyze COVID-19 cases and deaths among areas in seven tribal nations in Oklahoma to determine how they have been affected by COVID-19 compared to the general population of Oklahoma, as well as what factors might have influenced these rates. Descriptive statistics and incidence and case-fatality rates were evaluated and correlated with population density, access to healthcare, and government funding allotments. Time series plots were created to illustrate the rates of new cases per day in each tribal nation. Finally, multiple linear regression models were created to predict COVID-19 deaths from cases, population, and tribal status of counties in Oklahoma. This analysis found that, in general, areas within tribal nations do not have significantly different COVID-19 case and death rates from Oklahoma. Higher population density correlates with higher case and death rates, while healthcare access and government funding have no correlation with incidence and case-fatality rates. Since these results contradict the findings of previous studies, they indicate both the need for more research among Native American populations and the importance of data analysis in research.

Jude Birkenholz and Mark Fishbein (Oklahoma State University - Stillwater Campus)

10:00-10:15 in 353 Tandy

****EVOLUTION OF NUCLEAR RIBOSOMAL DNA IN *ASCLEPIAS* (MILKWEEDS): PATTERNS OF INTRAGENOMIC POLYMORPHISMS AND COPY NUMBER VARIATION**

Nuclear Ribosomal DNA (nrDNA) has been a widely used genetic marker for estimating phylogenetic relationships. Recent studies have found unexpected levels of intragenomic polymorphisms and copy number variation which could suggest that nrDNA's use in phylogenetic studies might be error prone. The genus *Asclepias* was previously found to have significant intragenomic variation at the species level and potentially between individuals of the same species. To further assess patterns of sequence evolution, I assembled the 35S nrDNA cistron of 901 individuals representing 87 species of the genus *Asclepias* using Illumina 150bp paired-end reads. I used Geneious Prime for both mapping and variant calling. I estimated copy number by mapping my samples to 603, *Asclepias* specific, single-copy genes and then dividing each sample's nrDNA coverage by their average single-copy coverage. Preliminary results show widespread within-genome polymorphic variation between species. I found that closely related species tended to share similar levels of polymorphisms. Ribosomal copy numbers show even greater variation both within and between species. Taken together, these results highlight that nrDNA genes harbor greater variation than was previously thought. This further suggests that nrDNA's use as a phylogenetic marker needs to be reassessed as more is learned about its evolution.

Kwabena Boateng¹, Moses Omeneki¹, Imad Ali², and Nesreen Alsbou¹ (¹University of Central Oklahoma; ²University of Oklahoma Health Science Center)

9:15-9:30 in E378 Forensic

****DESIGN OF MICROWAVE IMAGING SYSTEM WITH MOVING ANTENNAS AND MULTI-LAYER SCANNING FOR APPLICATIONS INCLUDING BREAST CANCER DETECTION**

Breast cancer is the most prevalent type of cancer among women. It is projected there will be approximately 287,850 cases diagnosed in the United States making up 30% of all cancers in 2022. X-ray mammography and Magnetic Resonance Imaging (MRI) are methods adopted by clinicians to detect breast cancer in women. Nonetheless, the X-ray technique can ionize human tissue which can be very harmful if exposed long-term. Moreover, MRI is another technique that is non-invasive but very expensive. The disadvantages of conventional breast cancer techniques have prompted researchers to investigate alternative methods including microwave imaging. This research focuses on designing a portable microwave imaging system that has an array of equally spaced antennas arranged in linear or circular configuration. The array of antennas will be located on a 50x50cm platform that is supported by four actuators on the four corners that allow the platform of antennas to move vertically with high accuracy. The adjustable moving platform will have a 30 cm diameter circular imaging field of view in the center allowing for the scanning of different objects. The innovative microwave imaging system will scan the phantom objects under test by moving vertically in an adjustable and controllable increments producing a multi-layered scan using differential dielectric properties of the scanned object. The collected scans of a multi-layered breast tissue can be used to reconstruct and produce 2D images. The reconstructed images can be studied to determine the size and location of the tumors in the breast phantom and other phantom. The prospect of making microwave imaging systems commercially available in the medical market is still in the early stages and considered a work in progress despite all the challenges associated with the process. However, once it is achieved it would be significant because of its non-ionizing, non-invasive, and low cost.

Douglas Bryhan (East Central University)

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SCALE OF POTENTIAL RADIATION RELEASE EVENTS MODELED FROM HISTORICAL EVENTS

On 26 April 1986 reactor 4 at the Chernobyl Power Plant (CPP) experienced a violent power excursion that resulted in a fire and the release of significant amounts of radionuclides into the environment. Estimates vary, from 1850-2960 PBq (1 petabecquerel = 10¹⁵ fissions per second) from Soviet authorities to 166.5 Ebq (1 exabecquerel = 10¹⁸ fissions per second) by Lawrence Livermore National Laboratory. This latter number would represent one half of the reactor core leaking into the outside environment. Recently concerns have been raised about potential future releases from the Zaporizhzhya Nuclear Power Plant (ZNPP), as well as other facilities in that troubled region. Historical events will be used to project the potential human and ecological damage from a potential catastrophic compromise of containment. The specifics of reactor operation will not be considered, only the potential for environmental contamination based on fuel type and load, since any release would be the result of outside events.

Katie Burch and Dusti Sloan (Oklahoma State University Center for Health Sciences)

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****EXPLORATORY ANALYSIS OF ESTROGEN-MEDIATED GENE EXPRESSION IN CENTRAL INSULIN SIGNALING PATHWAYS**

As of 2020, 67% of Americans are overweight or obese. Especially concerning is the prevalence of obesity in post-menopausal women. Previous studies have shown that estrogen decreases food intake and body weight; however, the process by which

estrogen affects central metabolic pathways is not yet clear. To address this, we used a microarray to compare estrogen-mediated changes in gene expression within the insulin signaling pathway. This pathway contains brain areas known to be involved in the regulation of metabolism and food intake including: the arcuate nucleus of the hypothalamus (ARC), the paraventricular nucleus of the hypothalamus (PVN), and nucleus of the solitary tract (NTS). Adult female rats were bilaterally ovariectomized and treated with either oil or estrogen injections. After termination, RNA was collected from the brain regions of the ARC, PVN, and NTS. Isolated RNA was sent to Thermo Fisher Scientific for microarray analysis. Results were analyzed using Transcriptome Analysis Console software. In the brain areas examined, we found that estrogen influenced gene expression for multiple neurotransmitters, neuroreceptors, and intercellular signaling molecules involved in the insulin pathway. The changes found in body and uterine weights confirmed the effects of estrogen. The ARC, PVN, and NTS displayed a variety of genes regulated by estrogen, confirming that estrogen does mediate gene expression within the insulin signaling pathway. This displays a potential mechanism of how estrogen affects central pathways to decrease food intake and body weight.

Priscilla Chatman, Brittney Conn, Emma Maritz, Toby L. Nelson, and Karen L. Wozniak (Oklahoma State University - Stillwater Campus)

8:45-9:00 in 333 Tandy

ANTIFUNGAL ACTIVITY OF NOVEL COMPOUND EIPE-1 AGAINST THE FUNGAL PATHOGEN *CRYPTOCOCCUS NEOFORMANS

Cryptococcus neoformans is an opportunistic fungal pathogen that affects immunocompromised individuals. Antifungal drugs have been used to treat fungal infections for many decades; however, due to similarities between fungal and mammalian cells, these drugs are often toxic. In these last few decades, the fungi have also become resistant to the antifungal drugs. EIPE-1 was synthesized from vanillin, and was shown to have activity against methicillin resistant *S. aureus* (MRSA), and other gram-positive bacterial pathogens. We hypothesized that EIPE-1 could be used to kill fungal pathogens. For this study, we tested EIPE-1 against *C. neoformans* using a minimum inhibitory concentration (MIC) assay and an in vitro model of intracellular fungal growth using RAW macrophages. EIPE-1 has antifungal activity against *C. neoformans* in our MIC assay, with an MIC value of 1.749 µg/ml. In addition, following phagocytosis of *C. neoformans* by RAW macrophages, treatment with EIPE-1 had significant antifungal effects on *C. neoformans* compared to *C. neoformans* alone and compared to *C. neoformans* with RAW macrophages (without treatment). In further studies, we will perform RNA sequencing experiments and more comparison studies with other antifungal drugs.

Devon Chen, Cameron Wood¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 37

***THE EVOLUTIONARY STATUS OF SIMA AND PTP61F**

The insulin/TOR pathway is responsible for maintaining homeostasis by regulating cell growth, blood glucose levels, and protein synthesis. This study focused on the synteny and conservation that occurred between the genes *sima* and *Ptp61F* in the insulin pathway. Within a gene, more physical interactions that are connected will consequently hinder the evolutionary alterations that occur. It was hypothesized that *sima* will be more conserved than *Ptp61F* because *sima* contains a higher number of physical interactions. This was tested by locating the genes *sima* and *Ptp61F* in multiple species in *Drosophila* and comparing them to the reference species *Drosophila melanogaster*. Annotations of each gene were performed using web-based resources and using data from other students and researchers, the divergence scores of multiple species were calculated. The results indicated that the gene *sima* was less evolutionary diverged than *Ptp61F* due to a higher number of physical interactions.

Karidjatou Cisse¹, Imad Ali², and Nesreen Alsbou¹ (¹University of Central Oklahoma; ²University of Oklahoma Health Science Center)

10:45-11:00 in E378 Forensic

****MICROWAVE IMAGING USING MULTIPLE PASCO RECEIVERS**

Microwave imaging technology is based on measuring different dielectric properties of human tissues. The water content varies in different tissues, for example, tumors have more water content than regular healthy tissues. In this study, we used one Pasco microwave transmitter and five receivers. A Gunn diode is used to create microwave signal that is guided and transmitted to the imaging field. The receivers use a Schottky diode to receive the polarized microwave after being reflected or transmitted through the imaged object. Both the transmitting and receiving diode have the same polarization because they are mounted in the same plane. An adjustable platform with vertical and rotational motion capabilities is used to scan different phantom objects with variable intensities representing different parts of the human body were used such as foam, plastic, jell material, wood, and water. In this study the characteristics of the microwave signal and its dependence on the density of the objects in the imaging field were quantified. The data collected was reconstructed in two-dimensional images using MATLAB software.

Jerry Clark (East Central University)

Poster 9

QUANTUM TO CLASSICAL WALK TRANSITIONS TUNED BY SPONTANEOUS EMISSIONS

We have realized a quantum walk in momentum space with a rubidium spinor Bose-Einstein condensate using a periodic kicking potential as a walk operator and resonant microwave pulses as a coin toss operator. The generated quantum walks appear to be stable for up to ten steps before quickly transitioning to classical walks due to spontaneous emissions induced by laser beams of the walk operator. We investigate these quantum to classical walk transitions by introducing well-controlled spontaneous emissions with an external light source during quantum walks. These findings demonstrate a scheme to regulate the robustness of the quantum walks and can also be applied to other cold atom experiments involving spontaneous emissions.

Brady Combs, Phil Sites, Joshua Dickey, and Bryson Combs (University of Central Oklahoma)

9:00-9:15 in E378 Forensic

*IMPLEMENTATION OF A MINATARE ATOMIC CLOCK ONTO BUDDY SUPERCOMPUTER

We are living in a world with devices capable of accessing the internet with a click or touch of a button from anywhere. Many have experienced a long wait time or “Buffering”. This term can be described as the time it takes to receive enough data packets in the correct order to begin playing the video after requesting to stream. When networks are not communicating at the same speed, data can be lost or could be received out of order resulting in a corrupted file or an extremely long download time. Implementing an atomic clock on the Buddy Supercomputer will increase data transfer rate while decreasing the timing errors. The project requires an accurate timing source that will be received from a GPS (Global Positioning Satellite). When a network user connected to our network wants to transmit or receive a file, the atomic clock will send out the correct time to ensure the other side is transmitting or receiving at the same rate. The results of the improved clock will shorten the data transfer process, effectively increasing the speed of information to display on your device. To test our design, we will send packets of data before and after implementing the improved clock source from our supercomputer to a network across campus. By tracing the file, we can compare the time and accuracy of the data to determine our effectiveness across the network. Problems are to be expected and will play a critical role in the development of the long-term use of the atomic clock. The specific placement of the device, how the device is mounted, airflow, and cooling will all play a part in the final design phase of the project.

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Paul Crawford, Wyatt Thiel, and Lindsey Long (Oklahoma Christian University)

Poster 35

*THE DIFFERENCE IN EVOLUTIONARY CONSTRAINT BETWEEN SIMA AND PTP61F GENES IN *DROSOPHILA* SPECIES

The Insulin-like receptor pathway influences the maintenance of blood glucose levels and progresses growth and development in multiple species, especially in *Drosophila* fruit flies. All genes located within this pathway evolved at differing rates. In this study, the *sima* and *Ptp61F* genes were tested for their level of evolutionary constraint. Using the UCSC Genome Browser, the location of the genes was identified in both the target species and *D. melanogaster* (*D. mel*). Once the location was determined, a Tblastn was performed, which tested the protein sequence in *D. mel* to the target species. All isoforms of the gene in the target species were annotated. The results of the annotation were verified using the GEP Model Checker, and the dot homology plot was recorded alongside the percent identity of the protein sequence. The evolutionary divergence scores were calculated for all tested species of *Drosophila*. From the data, *sima* shows more constraint in its evolutionary progress than *Ptp61F*.

Charles Crittall and Daniel McInnes (East Central University)

Poster 7

MOLECULES OF NATURE: A SUMMER ACADEMY FOR RISING 8TH AND 9TH GRADERS

The Molecules of Nature Summer Academy is a residential summer camp sponsored by the Oklahoma State Regents for Higher Education. The camp serves twenty rising eighth and ninth graders from Oklahoma, and is held on the campus of East Central University. The primary goal of the Academy is to demonstrate to participants that they can thrive while living and learning in a campus environment.

Jonathan Crosse, Joseph Moberly, and Janaki K. Iyer (Northeastern State University)

8:30-8:45 in D107 Lecture Hall

*CHARACTERIZATION OF A UROPATHOGENIC STRAIN OF *KLEBSIELLA PNEUMONIAE*

Urinary tract infections (UTIs) are common bacterial infections that affect a wide variety of people including children. They account for 25% of the bacterial infections encountered by women and are associated with significant costs for treatment. Uropathogenic *Escherichia coli* (*E. coli*) is the most common etiologic agent followed by *Klebsiella pneumoniae* (*K. pneumoniae*). *E. coli*-mediated pathogenesis, in the context of UTIs, is widely studied but similar detailed information is not available on *K. pneumoniae*-mediated pathogenesis. UTIs caused by *K. pneumoniae* are harder to treat and cause more morbidity. There are also reports of increased antimicrobial resistance in different uropathogenic *K. pneumoniae* strains. In the current study, we have characterized a strain of *K. pneumoniae* (UCI-41) isolated from the urine of a patient diagnosed with a UTI. This strain is resistant to different bacteriostatic and bactericidal antibiotics and hence can serve as a good model to study pathogenesis mechanisms employed by antibiotic-resistant *K. pneumoniae* strains. Experiments involving ELISAs showed that *K. pneumoniae* UCI-41 induced the secretion of pro-inflammatory cytokines in a human epithelial bladder cancer cell line. This strain was able to internalize into bladder cells as determined by a gentamicin protection assay. This indicated that this strain was invasive and hence had the potential to cause recurrent UTIs. These findings support the use of *K. pneumoniae* UCI-41 as a model for future experiments that study invasive antibiotic-resistant uropathogenic bacteria and design novel strategies for treatment of infections caused by these strains.

Stephen Daniels¹, Macie Enman², and Vikas Dudeja² (¹Oral Roberts University; ²University of Alabama at Birmingham)

8:30-8:45 in 331 Tandy

*THE EFFECTS OF ARYL HYDROCARBON IMBIBITION ON PANCREATIC STELLATE CELLS

Pancreatic cancer is the fourth leading cause of cancer-related death. Pancreatic stellate cells (PSCs) are known to help create a suitable tumor microenvironment (TME) for pancreatic cancer. PSCs do this by increasing extracellular matrix production (ECM). The Aryl Hydrocarbon Receptor (AhR) is a nuclear ligand-receptor in the cell's cytoplasm. AhR promotes immunosuppressive cell phenotypes. AhR serum levels have also been reported higher in patients with pancreatic cancer. AhR is a possible target for pancreatic cancer treatment. In this study, we evaluate the effect AhR inhibition has on PSCs. PSCs were isolated from wild-type BLG mice pancreases and plated on plastic. AhR inhibitor, BAY2416964, was used in PSCs and cultured for twenty-four hours. Then RNA was extracted and turned into cDNA to analyze PSC activation markers with quantitative PCR. Genes downstream of AhR were also analyzed to confirm that AhR had been inhibited. An oil-red stain was also done to determine relative PSC activation levels. Pharmacological inhibition of AhR resulted in the downregulation of downstream markers of AhR, including CYP1B1 and AhRr in the PSCs. Furthermore, markers of PSC activation, such as aSMA, Col1a, LIF, IL-6, IL-11, and FAP, were downregulated in PSCs with AhR inhibition. Oil Red O staining indicated the reappearance of oil droplets in the activated PSCs after AhR inhibition, suggesting a reversal of the activated phenotype of the PSCs. The results suggest that AhR inhibition leads to some degree of quiescent characteristics in pancreatic stellate cells. PSC quiescence could lead to less fibroblast and extracellular matrix production. Less ECM production will help current cancer treatments to be more effective.

Noopur Dasgupta, Prakash Sah and Erika Lutter (Oklahoma State University - Stillwater Campus)

Poster 24

**H-89 PHARMACOLOGICAL INHIBITION OF HOST SIGNALING DURING *CHLAMYDIA TRACHOMATIS* INFECTION

Chlamydia trachomatis is an obligate intracellular pathogen and the most common leading cause of bacterial sexually transmitted disease in the United States. Every year 3 million cases of sexually transmitted bacterial infection cases are recorded in the United States. *C. trachomatis* can be treated by antibiotics, but post-clearance the pathogen leaves long term damage to the host that results in many complications such pelvic inflammatory disorder, ectopic pregnancy, and infertility, among others. Given its intracellular nature it is known to depend on the host for its replication and survival; however, the extent of host cell signaling modulation is not known. The long-term goal of this project is to determine PKA phosphorylation of both host and chlamydial substrates during infections PKA is an important host kinase regulating transcription, protein expression and cell survival. During *C. trachomatis* infection, we have previously shown that PKA contributes to extrusions production and increased phosphorylation of PKA substrates in late infection. We hypothesize that PKA is important for *C. trachomatis* growth and exit. To confirm the role of PKA, we tested a known PKA pharmacological inhibitor, H-89. We were interested in looking at how

different concentrations of this inhibitor affects the viability of the host cells and how it affects the inclusion development and infection forming units post-infection with *C. trachomatis*. PKA manipulation during infection is important but how changes in PKA activation benefits *C. trachomatis* is not clear. We anticipate that the results obtained with further study will help us understand to what degree is the host cell being manipulated during infection and also in developing effective future strategies for prevention and control of long-term sequelae like pelvic inflammatory disease and excessive scarring after *C. trachomatis* infection.

Leonard Cole Davis¹, Sam Krebsbach², and Dengjun Wang² (¹East Central University; ²Auburn University)

Poster 51

***UTILIZATION OF BIOCHAR FOR EFFICIENT PFAS REMOVAL FROM WATER**

Per and polyfluoroalkyl substances (PFAS) are a class of synthetic fluorochemicals which have been used in a wide variety of industrial and commercial products. PFAS are highly resistant to degradation, so PFAS are also called “forever chemicals”. The widespread use of these substances, their persistence in the environment, and potential toxicity to human health require us to develop an efficient, cost-effective means for their removal. This research aims to explore the potential of biochar (a carbonaceous substance formed from the pyrolysis of agricultural and forestry wastes) as a sorbent to remove PFAS from water. This research explores how certain characteristics of the biochar will impact their sorptive ability to remove PFAS. The characteristics investigated include surface charge, hydrophobicity, surface area and pore volume, and the functional groups on the biochar surface. Our sorption data showed that biochar produced at higher temperatures will be more effective in removing PFAS from water.

August Davison, Emma L Davison, and Lindsey J Long (Oklahoma Christian University)

Poster 45

DIVERGENCE OF SIMA IN *DROSOPHILA

Many protein-coding genes are conserved across species, in conserved genes the DNA sequences code for proteins that have similar amino acid sequences, and similar numbers of exons. So far, researchers have annotated the genome of the fruit fly, *Drosophila melanogaster*, however, the genomes of other *Drosophila* species are yet to be annotated, meaning that the protein-coding regions of their genome are yet to be determined. This study contributes to the Genomics Education Partnership project of annotating the genes of other *Drosophila* species. Examined the conservation of sima, a gene that codes for a transcription activator that is a part of the insulin/TOR pathway. This pathway conserved in humans and is important for regulating cellular growth and metabolism. Given the importance of this pathway, we hypothesized that sima would be relatively conserved across *Drosophila* species. The degree of conservation and divergence of sima by examining the genomic neighborhood, gene annotation, and divergence scoring. Results showed that sima was conserved in many of the annotated species, with higher divergence for species farther from *D. melanogaster*.

Diego De La Torre and William P Ranahan II (Oral Roberts University)

9:00-9:15 in 333 Tandy

ANTI-CANCER COMPOUNDS SECRETED BY *GANODERMA LUCIDUM

Cancer is currently one of the leading causes of death worldwide; while many therapies are available, there is no definitive cure. One of the most common cancer treatments is chemotherapy. While chemotherapy is an effective treatment to control and kill cancer cells, it is also harmful to non-cancerous cells. Before this modern treatment, humans used natural remedies found in nature for millennia to treat health conditions. The goal of this project is to find a naturally occurring product that has selective cytotoxicity towards MDA-MB-468 triple negative cancer cells. For this project, mushroom secretions were gathered and analyzed using a medium-pressure liquid chromatography system (FPLC) from *Ganoderma lucidum*. A low molecular weight protein-containing polysaccharide was isolated and tested. Viability data indicate that the isolated compound effectively reduces 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.

Joshua Dickey, Phil Sites, Brady Combs, and Bryson Combs (University of Central Oklahoma)

9:00-9:15 in E378 Forensic

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Emma Dilbeck, Vicente Rios, and Raina Miller (Southern Nazarene University)

Poster 68

***MOSQUITO COMMUNITIES AND WEST NILE VIRUS DETECTION IN CENTRAL OKLAHOMA**

Understanding mosquito communities is a crucial approach to mitigating public health risks. In this study, we characterized the mosquito community in the greater Oklahoma City area and used molecular assays to detect West Nile Virus (WNV) between May and June 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. We found a correlation between the phenology of mosquito genera with clusters of similarity amongst landscapes based on ANOSIM analysis (p=0.049) with suburban areas clustered together as well as rural areas. The mosquito phenology in the early mosquito season was mostly represented by the *Aedes* genera, with *Aedes vexans* being the most abundant specimens in our traps but subsequently surpassed by culicine mosquitoes, particularly, the *Culex pipiens/quadrinaculatus* complex. Female mosquitoes of the same species were pooled ($5 \leq n \leq 30$) and purified RNA used for WNV RT-qPCR screening; five out of the 248 pools were positive. Three of the positive pools were *Culex pipiens* with the other two pools composed of *Aedes vexans* and *Aedes albopictus*, respectively. Altogether, mosquito assemblage varied across locations; *Culex* complex peaked towards the end of the early season, coinciding with WNV detection, suggesting *Culex pipiens* major role as vectors of WNV in central Oklahoma. Knowledge of changes in mosquito communities and arboviral detection can inform vector-borne disease control.

Shania Do, Joshua Baer, Tiffany Jones, Abigail Kee, Karissa LeHew, Derek McGuire, Sarah Soliman, Sydney Spillane, Monica Vuong, Cari Marshall, and Ipe Paramel (Oklahoma State University Center for Health Sciences)

Poster 16

****LEAN HEALTHCARE: EVALUATION OF BED THROUGHPUT AT OSU MEDICAL CENTER**

Several factors play a role in an organization's success to function on a daily basis. For example, one factor being the application of efficient protocols to produce effective and consistent results. There is a specific procedure, called LEAN, that has been increasingly employed throughout various types of corporate professions due to its favorable outcomes. Originally, LEAN practices were created to enhance workflow and manufacturing processes in the automobile industry. After other industries observed the success rates from applying these certain methods, LEAN has been progressively adapted by many businesses to achieve similar effects. By adopting the LEAN methodologies, corporations have been able to increase their productivity, value, and client satisfaction. An example of how versatile and beneficial the LEAN approach can be in other fields, besides manufacturing, can be portrayed within a healthcare setting. There have been multiple healthcare organizations that have applied LEAN strategies to their systems in order to amplify quality improvement, with an end goal to better patient care. In this poster, a model is presented on how to apply and replicate LEAN tactics in an effort to advance bed throughput within a hospital setting. In the summer of 2022, a team of medical students from Oklahoma State University College of Osteopathic Medicine (OSU-COM) applied LEAN tools and techniques to examine the delayed process of bed throughput from the Emergency Department to the hospital floors. In doing so, possible solutions were developed in hopes to improve workflow, culture, and most importantly, patient outcomes.

Sudhir Doranga and Tyrrell Conway (Oklahoma State University - Stillwater Campus)

9:15-9:30 in D107 Lecture Hall

****OMPC AND BILE TOLERANCE ARE IMPORTANT FOR *E. COLI* COLONIZATION OF THE MOUSE INTESTINE**

Outer membranes of *Escherichia coli* contain channel-forming proteins which allow exchange of nutrients and waste products with the environment. Previous studies in our lab showed that the GI tract of streptomycin-treated mice fed with wild type *E. coli* MG1655 selects for envZ missense mutants which are better colonizers than the wild type (WT). The better colonizing envZ missense mutants also have altered outer membrane protein (OMPs) profiles compared to the WT. This suggests a possible role for OMPs in colonization of the mouse intestine. We offer the hypothesis that OMPs play a key role in colonization of mouse intestine by *E. coli* by facilitating bile tolerance. We showed that in competitive colonization experiments, ompA and ompC KO mutants are outcompeted by the WT. Interestingly, the ompF KO mutant colonized better than the WT in competitive colonization experiments and all three OMP mutants appear to compete with the WT in the same niche. Further experiments to understand why the ompF mutant has a competitive advantage indicated that the ompF mutant overproduces OmpC. However, both overexpression of OmpC and deletion of ompF are required to confer the colonization advantage. We also showed that ompC mutant is a poor competitor because it takes time to adapt in the intestine due to its bile sensitivity. Increasing the bile salt concentration in the mouse intestine by feeding bile in mouse chow renders the ompC mutant even worse in competition against

the wild type. We confirmed, through RNA seq analysis of *E. coli* RNA from mouse cecal mucus, that OmpC is important for *E. coli* in the intestine while OmpF is non-essential as ompF is highly downregulated. These experiments provide a better understanding of how OMPs affect the ability of *E. coli* to compete in the mammalian intestine.

Eden Dowell, Jordan Elkinton¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 32

***DIVERGENCE OF SPECIES IN THE INSULIN/TOR PATHWAY**

This research project focused on understanding the evolution of the Insulin/TOR pathway. New *Drosophila* species arise as pathways evolve. Elements of each pathway diverged at different rates due to constraints and interactions of various proteins. Using comparative genomic techniques and the DNA data from various species of *Drosophila*, the genes dock and rictor were analyzed to determine which was more diverged. More specifically, the divergence of dock and rictor were compared using web-based tools to annotate the genes of various *Drosophila* species. A meta-analysis of 8 different species of *Drosophila* analyzed the divergence scores and percent identities of dock and rictor proteins to the nucleotide sequences of *D. melanogaster*. Ultimately, it was determined that rictor was more diverged than dock.

Hayleigh Drake, Constance Green, and April Nesbit (East Central University)

Poster 22

TESTING ANTIBIOTIC PRODUCTION AGAINST *ENTEROCOCCUS FAECALIS

Enterococcus faecalis is a bacterial pathogen that causes infections in the human body. These infections include urinary tract infections, endocarditis, bacteremia, and wound infections. Just like many other infection-causing pathogens, *E. faecalis* has built resistance to multiple antibiotics overtime. To counter increased antibiotic-resistance, we are working to discover novel antibiotics produced by non-pathogenic bacteria isolated from soil samples. The purpose of my research project is to challenge possible antibiotic producing bacteria against *E. faecalis*. The bacteria we are observing are from four different samples that were previously isolated from soil. Previous studies have shown that these four isolates inhibited growth of a different pathogen, *Enterococcus faecium*, by creating a zone of inhibition around the soil isolates on nutrient agar plates. A zone of inhibition forms when a bacterium secretes antibiotics that inhibit or kill the pathogenic bacteria. In order to test for the formation of a zone of inhibition between the isolated bacteria samples and *E. faecalis*, I performed a modified Kirby-Bauer method that moved pieces of agar from the original plate with antibiotic-producing bacteria to a plate with the pathogen spread on it. Of the four samples, D4-2 produced a zone of inhibition during a preliminary analysis. We are following up on the preliminary results and hope to possibly isolate a novel antibiotic from D4-2 bacteria in the future.

Leah S. Dudley (East Central University)

10:30-10:45 in 353 Tandy

NATURE'S NOTEBOOK AND THE NATIONAL PHENOLOGY NETWORK, A CITIZEN SCIENCE PROJECT IN A GENERAL BOTANY COURSE

Phenology is the study of lifecycle events. For humans, we are often interested in when to plant and harvest; these are both based on plant phenology. The National Phenology Network is a citizen science group that gathers phenological data and shares it. The scientific community uses collected data to do things such as construct climate change models and evaluate these models with real data (the data that you help to record). I will discuss the use of Nature's Notebook, an online integrated animal and plant-monitoring program, which provides standardized protocols for phenological status monitoring and data management for over 1200 animal and plant species nationwide in a General Botany, semester-long undergraduate course. Students are asked to monitor trees on campus throughout the semester and then to visualize their data and their previous classmate's data, using a visualization tool. During the course of the presentation, I will briefly outline the process to become a certified observer, creating a site, and student resources to complete their observations. Resources demonstrated during the presentation will be made available to those interested.

Jordan Elkinton, Eden Dowell¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 32

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Colter Esparza, Matthew Ahlemeier, Pragma Sharma, and Horrick Sharma (Southwestern Oklahoma State University)

Poster 54

***EVALUATION OF LDHA INHIBITORS THROUGH LACTATE ACCUMULATION ASSAYS IN PANCREATIC CANCER CELL LINES**

Metabolic reprogramming is considered a new hallmark of cancer. Cancer cells undergo extensive metabolic rewiring and alter the metabolism of glucose, glutamine, and fatty acid to support their growth and proliferation. Cancer cells get addicted to glucose and convert the pyruvate to lactate. Lactate dehydrogenase-A (LDH-A) is the primary metabolic enzyme that converts pyruvate to lactate and is overexpressed in multiple tumors, including pancreatic cancer. Lactate accumulation in the tumor microenvironment is associated with increased tumor aggressiveness, metastasis, inhibition of the antitumor immune response, and resistance to therapy. Thus, targeting human lactate dehydrogenase is a promising approach for treating advanced carcinomas. Various groups have recently reported several LDHA inhibitors; however, their development is hampered due to a lack of cellular activity and metabolic stability. In the present study, we tested the ability of new LDHA inhibitors, synthesized by our collaborator, to inhibit lactate production in MIA PaCa-2 pancreatic cancer cells. Compounds inhibited lactate production as compared to untreated control. Future studies will involve studying the effect of these compounds on other metabolites, including intracellular pyruvate level.

Kade Ezell and Chase Lee (Oklahoma State University Center for Health Sciences)

Poster 56

HEALTH INEQUITIES IN ORTHOPAEDIC TRAUMA SURGERY IN THE UNITED STATES: A SCOPING REVIEW

Health inequities have been shown to have negative effects on patient care and the healthcare system. It is important for orthopaedic trauma surgeons and researchers to understand the extent to which patients are affected by these inequities. We conducted a scoping review as outlined by the Joanna Briggs Institute and the Preferred Reporting Items for Systematic reviews and Meta Analyses extension for Scoping Reviews (PRISMA-ScR) checklist. We searched PubMed and Ovid Embase for articles relating to orthopaedic trauma surgery and health inequities. After exclusion criteria were applied, our final sample consisted of 52 studies. The most frequently evaluated inequities were sex or gender (43 of 52 [82.7]), race/ethnicity (23 of 52 [44.2]), and income status (17 of 52 [32.7]). The least frequently evaluated inequities were LGBTQ+ identity (0 of 52 [0.0]) and occupational status (8 of 52 [15.4]). Other inequities evaluated included rural/under-resourced (11 of 52 [21.1]) and educational level (10 of 52 [19.2]). No trend was observed when examining inequities reported by year. Health inequities exist in orthopaedic trauma literature. Our study highlights multiple inequities in the field that need further investigation. Understanding current inequities and how to best mitigate them could improve patient care and outcomes in orthopaedic trauma surgery.

Victoria Fairchild, Carlos Cuza, and Sapna Das-Bradoo (Northeastern State University)

Poster 41

***INVESTIGATING POLYMERASE EPSILON'S ROLE IN REPLICATION INITIATION AND ELONGATION BY THE ANALYSIS OF POL 2 MUTANTS**

DNA Polymerase Epsilon (Pol ϵ) is essential for replication of a cell's genome. It plays an important role in the synthesis of the leading strand of DNA. Malfunctions of Pol ϵ are associated with cancers and other diseases. Replication of DNA is a very important process and thus prompts the investigation into the structure, function and associations of Pol ϵ . There is still more to understand about the structure of Pol ϵ , but it is known that it is made of four subunits each with their own unique roles. In yeast the subunits are referred to as Pol2, dpb2, dpb3, and dpb4. In our laboratory, we are interested in investigating if mutations in the essential C-terminus of Pol2 disrupt origin activation and the replication elongation process. For this purpose, we studied two Pol2 mutants, pol2-GE1425,1428AA, which disrupts interaction with Mcm10 and pol2-W1272A, which interferes with a stable Pol ϵ complex formation. DNA sequences bound to Pol2 were pulled down by Chromatin immunoprecipitation and purified. Then PCR was performed to test for the presence of early, late origins and non-origins to assess if there was a loss of functionality in replication within the mutant yeast cells. Our findings exhibit that pol2-GE1425,1428AA mutants show a delay in binding to early and late origins (late S phase) while the pol2-W1272A mutants exhibit an unstable association with both early and late origins. These results are in contrast to the wild-type Pol2 cells that associate with early and late origins in early S phase. Similarly, wild-type Pol2 proceeds with elongation, but the mutants showed significantly delayed progress. We plan to repeat our experiments with the mutants and perform quantitative PCR to further investigate this replication delay in the mutant cells.

Payden Farnsley, Caitlin Wayland, Nicholas Bauer, and Vijayakumar Somalinga (Southwestern Oklahoma State University)

Poster 20

IDENTIFICATION AND PRELIMINARY CHARACTERIZATION OF AN A-CARBONIC ANHYDRASE HOMOLOG FROM THE "BRAIN-EATING AMOEBA", *NAEGLERIA FOWLERI

Naegleria fowleri is a thermophilic, free-living amoeba that inhabits aquatic ecosystems and water distribution systems. *N. fowleri* causes primary amoebic meningoencephalitis (PAM), a rare, fatal and rapidly destructive infection of the central nervous system. Current treatments consist of repurposed antimicrobial agents, which are not effective, leading to very high mortality

rates. Therefore, identification of new and effective drug targets is imperative. Recent studies have shown that fatty acid utilization plays an important role in *N. fowleri* growth, and a central enzyme in fatty acid metabolism is a bicarbonate-requiring carboxylase. Carbonic anhydrases (CA's) are metalloenzymes that catalyze the reversible hydration of carbon dioxide into protons and bicarbonate, a ubiquitous reaction important for physiological functions. Bicarbonate produced by the catalytic activity of CA's are utilized by carboxylases for the synthesis of molecules essential for cellular activity. In addition, recent studies have shown that CA's may play a role in the virulence of bacterial pathogens. Surprisingly, CA's and their role in metabolism and virulence of eukaryotic pathogens remains largely uncharacterized. Using BLAST analysis, we recently identified a protein, FDP41_009806, from *N. fowleri*, with 25% identity to human α -CAII. Both conserved domains and multiple sequence alignments analyses showed the presence of metal-coordinating histidine residues and catalytically important glutamate and threonine residues conserved in many closely related α -CA's. In addition, homology modeling of FDP41_009806 revealed conserved structural elements such as the central β -sheet core that harbors the metal binding residues essential for CA catalytic activity. Although FDP41_009806 shows all the hallmarks of an α -CA, phylogenetic analysis indicated that this *N. fowleri* homolog may represent a new type of α -CA. The structural and conserved active site homology led us to hypothesize that FDP41_009806, hereafter NfCA1 α , is an uncharacterized α -CA in *N. fowleri*. The goal of this project is to characterize NfCA1 α using biochemical and structural methods.

Saher Fatima, Ramee G. Aranda, and Jeffrey A. Hadwiger (Oklahoma State University - Stillwater Campus)

10:15-10:30 in D107 Lecture Hall

**REGULATION AND FUNCTION OF THE ATYPICAL MAPK (ERK2) IN DICTYOSTELIUM

Mitogen-activated protein kinases (MAPKs) are found to be conserved throughout eukaryotes and are reported to be involved in multiple complex signaling pathways. They play roles in regulating many crucial cellular processes, including proliferation, stress response, apoptosis, and immune response, and they can contribute to diseases such as cancer. The upstream activator, specificity of the substrate, and regulation of an atypical subfamily of MAPKs, represented by MAPK15(ERK8) in mammals, remains unclear but substantial progress has been made by characterizing atypical MAPK function and regulation in the amoeba *Dictyostelium discoideum*, a model organism for studying cell movement and differentiation. The atypical MAPK homolog in *Dictyostelium*, Erk2 is essential for chemotaxis and regulation of the typical MAPK, Erk1. Erk2, like other atypical homologs, is not activated by a conventional MAPK kinase and others have proposed a mechanism of activation through autophosphorylation. Using a kinase-dead mutant of Erk2 we have observed the phosphorylation of the activation motif in response to the stimulation of cells with chemoattractants suggesting the existence of a nonconventional MAPK kinase that regulates atypical MAPKs in vivo. In order to examine the specificity and functionality of certain MAPK regions, we have constructed several MAPK chimeras by combining sections of Erk1 and Erk2. This MAPK chimeric analysis is expected to provide insights into the functional and regulatory specificity of atypical and typical MAPKs.

Kyle Fitzgerald and Rohaan Muhammad (Oklahoma State University Center for Health Sciences)

Poster 52

**ASSESSMENT OF THE REPORTING OF HARMS IN SYSTEMATIC REVIEWS FOCUSED ON CAR-T CELL THERAPY: A CROSS-SECTIONAL STUDY

Our primary objective was to investigate complete reporting of harms in systematic reviews (SRs) on CAR-T therapy. Eligible SRs evaluating the effects of CAR-T therapy were identified by performing a search of major databases including MEDLINE (Pubmed and Ovid), EMBASE, Epistemonikos and Cochrane Databases for Systematic Reviews in May 2022. Investigators conducted screening and data extraction in a masked, duplicate fashion. AMSTAR-2 was used to assess the methodological quality of included SRs. Corrected covered area (CCA) was calculated for overlap of primary studies between SR dyads. Inclusion criteria was met for 45 SRs consisting of 929 primary studies. We found 13 SRs reported no harms, and reported less than 50% of harms items. AMSTAR-2 appraised 41 SRs as 'critically low' (41/45, 91.1%) and 4 SRs as 'low' (4/45, 8.9%). A significant association was found between completeness of harms reporting and whether harms were specified as an outcome. No other statistically significant associations were found. Three CCA dyads had a CCA > 50% and were compared to investigate shared or different harms reported. The assessment of harms reporting was found to be insufficient. Because of the importance of SRs in clinical therapy decision-making, it is essential to enhance reporting of harms in every aspect.

John F. Geiger and Severin Simonsen (Cameron University)

10:00-10:15 in E393 Forensic

THE EFFECT OF A VERBAL AND VISUOSPATIAL SECONDARY TASK ON THE COMPREHENSION OF PROCEDURAL TEXT

When reading procedural texts, individuals will usually form a mental model of the object described by the text. The present study examined the role that both verbal and visuospatial working memory play in text comprehension and mental model construction by employing a secondary task during reading. Seventeen participants read two narrative style and two list like procedural texts describing the construction of simple machines while performing a visuospatial tapping task, or a verbal secondary task. No main effects were significant, but the 2 x 2 interaction approached significance, $p = .23$. This interaction

demonstrated that tapping secondary task reduced the proportion of idea units recalled from the narrative style texts, relative to the other three conditions. It appears that verbal working memory is most needed when reading a narrative style procedural text.

Yonatan Gelaye, Nikkita Addy, and Lindsey J. Long (Oklahoma Christian University)

Poster 34

EVOLUTIONARY CONSERVATION OF SIMA AND PTP61F IN *D. GRIMSHAWI

This study focused on the evolutionary conservation of the two genes *sima* and *Ptp61F* in the species *D. grimshawi*. *D. grimshawi* is a highly diverged species from *D. melanogaster* and oftentimes within a highly diverged species the conservation of genes decreases, therefore, we hypothesized that because *sima* has higher connectivity to other proteins within the Insulin/TOR signaling pathway it would be more conserved than *Ptp61F*. The genomic neighborhood of *sima* and *Ptp61F* in *D. grimshawi* was compared to the genomic neighborhood of *sima* and *Ptp61F* in *D. melanogaster*, then both genes were annotated in *D. grimshawi*. Any anomalies encountered while annotating were used to calculate a divergence score for each gene. Results indicated a similar divergence score of *sima* and *Ptp61F* in *D. grimshawi*, which led us to conclude that our hypothesis was not supported.

Jessica Gray, Monica Vuong, Joe McCreary, and I-Hsiu Huang (Oklahoma State University Center for Health Sciences)

Poster 53

****CHARACTERIZATION OF BIOFILM FORMATION BY ENVIRONMENTAL *CLOSTRIDIODES DIFFICILE* ISOLATES**

Clostridioides difficile is a gram-positive, spore-forming bacteria capable of causing disease, referred to as *Clostridioides difficile* Infections (CDI), which may include symptoms such as severe diarrhea and colitis. Every year in the United States, about half a million of these CDI cases result in approximately \$6 billion in medical costs. *C. difficile* is difficult to eradicate due to its antibiotic resistance, virulent properties, and the fact that there is no available vaccine. CDIs are thought to be iatrogenic, but accumulating evidence suggests that environmental transmission may play an important role as well. Previously, we were able to isolate multiple *C. difficile* samples from fish markets, hospital wastewater, and wastewater treatment plants in southern Taiwan. Genotypic analysis revealed the presence of toxigenic *C. difficile* isolates closely related to ones prevalent among humans and animals infected by *C. difficile*. To gain a better understanding of the virulence capabilities of these environmental isolates, a series of studies including growth rates, spore production, and cytotoxicity were performed; however, the biofilm forming abilities were not well characterized. In this study, biofilm formation ability of these isolates was observed over a 72-hour period, then biofilm mass was measured using a crystal violet staining assay. By using a One-Way ANOVA, results were compared to the control lab strains 630 and R20291 to identify any significant differences. Further comparisons were made between isolates based on biofilm morphology. We observed a diverse range in biofilm formation abilities as well as biofilm morphology, but we did not detect any significant correlation between the robustness of the biofilms and the presence of toxin genes. Ongoing experiments focus on assessing the ability of these biofilms to resist antibiotics. In summary, our preliminary results contribute to the characterization of multiple environmental *C. difficile* isolates obtained from water and seafood samples in southern Taiwan.

Julia Green, Lydia Ostmo, and Sapna Das-Bradoo (Northeastern State University)

Poster 42

***FLUORESCENTLY TAGGING PROTEINS TO FUTURE STUDY POLYMERASE EPSILON COMPLEX**

DNA polymerase epsilon is an essential enzyme responsible for synthesis of the leading strand during DNA replication. It is composed of four subunits, POLE1, POLE2, POLE3, and POLE4. Two of the subunits (POLE1 and POLE2) are essential components. Deficiencies and mutations in DNA polymerase epsilon catalytic subunit (POLE1) cause severe developmental abnormalities and cancers. Our laboratory is interested in understanding if mutations in POLE1 affect the interaction between the different polymerase epsilon subunits and thus the functionality of the complex. To this end, we decided to fluorescently tag the individual subunits and study protein-protein interactions through co-immunoprecipitation. Using restriction enzyme digestion, ligation, transformation, and sequence analysis, we have confirmed the successful construction of both the GFP-tagged POLE3 vector and YFP-tagged POLE4 vector. Western blot results further confirmed the expression of GFP-tagged POLE3. Next, we will complete tagging the POLE2 subunit and then study the interactions among the epsilon subunits in normal and mutant cell lines.

Logan Guthrie¹, Abigale Rogers¹, Amy Prendergast², Zuorui Liu², Orr Comay³, Michal Zyztov³, Yoav Motro⁴, and Miriam Belmaker¹ (¹University of Tulsa; ²School of Geography, University of Melbourne; ³The Steinhardt Museum of Natural History, Tel Aviv, Israel; ⁴Ministry of Agriculture, Israel)

8:45-9:00 in 351 Tandy

****VOLE (*MICROTUS GUENTHERI*) STABLE CARBON ISOTOPES AS CLIMATE PROXIES FOR THE MIDDLE AND LATE PLEISTOCENE OF THE LEVANT AND CAUCASUS**

The Mediterranean Levant and Caucasus are situated in mid-latitudes. Therefore, climate oscillations during the Last Glacial Period (LGP, c. 115,000– 11,700 years ago) are not as pronounced as in northern latitudes such as Europe and North America. One of the main questions is whether the LGP was cold and dry or cold and humid. Stable carbon isotopes are often used to

distinguish between C3 vs. C4 plants. However, in mid-latitudes most vegetation is dominated by C3 plants. Hence, $\delta^{13}\text{C}$ varies according to precipitation. To develop a modern model of the Levant's paleoecology, stable carbon isotopes of modern social voles, *Microtus guentheri*, were sampled from sites across Israel and correlated with GIS-derived mean annual precipitation. For the fossil study, vole teeth were selected from two Israel sites and from one Georgian site. Rantis Cave, Israel, (160 - 120 Kya) is in the central region of Israel, Amud Cave (45 Kya) is in the North of Israel while Dzudzuana (ca. 40 Kya), is found in the Republic of Georgia. Results of the modern study indicate a positive correlation between $\delta^{13}\text{C}$ and mean annual rainfall with an average of -15.47 ± 1.277 (n=39). This confirms observations of previous studies that more enriched $\delta^{13}\text{C}$ are indicative of higher mean annual precipitation. Results indicate that the carbon values for all fossil sites were enriched compared to modern voles; Rantis (n=9, -9.8 ± 0.25), Amud (n=20, -7.96 ± 0.46), and Dzudzuana (n=19 -7.2 ± 0.82). This suggests that Middle and Late Pleistocene sites had an increase in mean annual precipitation compared to modern populations. These results support the hypothesis that glacial periods in the Levant were cold and humid rather than cold and dry and demonstrates how stable isotopes in voles can provide relevant palaeoecological information in mid-latitude regions such as the Levant and Caucasus.

Halla Hamdan, Elizabeth Pascual, Franklin R. Champlin, and Sue Katz Amburn (Oklahoma State University Center for Health Sciences)

Poster 27

****EFFECTS OF GRAM-NEGATIVE BACTERIAL OUTER MEMBRANE PERMEABILIZATION ON *SERRATIA MARCESCENS*' GENE EXPRESSION**

Our laboratory has focused on understanding the effects of outer membrane permeabilizer compound 48/80 on the intrinsic resistance of gram-negative bacteria to hydrophobic antibacterial agents such as the biocide triclosan. Previously obtained RNAseq data were analyzed to identify gene expression changes potentiated by compound 48/80 in the opportunistic pathogen *Serratia marcescens*. These data indicated greatly upregulated expression of three genes, each involved in repair of outer membrane damage by other antimicrobial agents. The objective of the present study was to clarify the bacterial response to compound 48/80 treatment using RT-qPCR to follow gene expression, with the ultimate goal of establishing a proposed mechanism of action for compound 48/80-induced outer membrane permeability. Previous work indicated that *S. marcescens* is one of the few species of bacteria intrinsically resistant to triclosan, and that compound 48/80 induces transient sensitization to triclosan. The RNAseq analyses revealed a 50-fold increase in expression of slyB, phoP, and phoQ subsequent to compound 48/80 administration and qPCR primers were created in order to further investigate their regulation. The Bacterial and Viral Bioinformatics Resource Center (BV-BRC) analysis tools confirmed the upregulation of the aforementioned genes and provided Fragments Per Kilobase Million Mapped Reads (FPKM) to enable selection of an appropriate qPCR housekeeping gene, yfiR. RNA has been prepared from expression time-courses in preparation for the RT-qPCR process, in which qPCR primers for slyB, phoQ, phoP and yfiR will be used to measure expression changes observed over time.

Christopher Hamm, Sydney Bush, Dax Butler, and Matthew T. Cabeen (Oklahoma State University - Stillwater Campus)
9:15-9:30 in 333 Tandy

****RSBR PARALOGS IN *BACILLUS SUBTILIS* STRESSOSOMES ARE CAPABLE OF DISTINGUISHING BETWEEN ENVIRONMENTAL STRESSORS WITH THEIR ΣB RESPONSES, AFFECTING THE FITNESS OF CELLS**

Bacteria have a variety of systems in place designed to sense stress to mount an appropriate response to assure their survival. *Bacillus subtilis* uses a large multiprotein complex known as the stressosome to sense environmental stressors, triggering the alternative sigma factor σB and activating the general stress response. While the ability of the stressosome to detect environmental stressors remains unknown, it is believed to be mediated by the RsbR paralogs within the stressosome itself. Previous work using bulk culture assays to study the activation of σB doesn't allow for visualization of single cell responses, and agarose pads only allow for a short time frame. Here we use a microfluidic approach to look at how cells containing a stressosome comprised of a single type of RsbR paralog can respond to stressors over an extended period of time under uniform conditions. We found that wild type cells activate σB with the same characteristic response pattern irrespective of the stressor used, varying only in the magnitude of the response. We also found that the individual RsbR paralogs, except for RsbRA which mimics the wild type, are able to modulate their response profiles to ethanol, salt, oxidative and acid stress. Our competition experiments suggest these single RsbR responses convey a fitness advantage in competition experiments. When strains were mixed 1:1 in 4% ethanol, that RsbRA-only was able to outcompete all other strains except for the wild-type stressosome. RsbRB has mixed results against Wt and RsbRC, while RsbRD lost to everything in ethanol. However, in 1 M NaCl competitions, RsbRA loses to everything, while RsbRD dominates all strains it is competed with. While it remains unknown how these individual RsbR response profiles affect the survival of cells, it is clear they are capable of playing a role in the transcriptional level of σB , affecting fitness.

Annabelle Hawkins, Olabode Victor Olayode, and Renan Bosque (Southwestern Oklahoma State University)

Poster 5

***DIAMOND PATTERN AND PREDATION RATES OF WESTERN DIAMOND BACK RATTLESNAKE**

Aposematic signaling in animals has been a sector of interest to biologists for many years. Aposematic signals are used by animals to dissuade predators from attacking and is often communicated in the form of bright colors or patterns. The Western

Diamondback Rattlesnake (*Crotalus atrox*) is an animal that has two modes of aposematic signaling. The first mode is the well documented auditory aposematic signal the rattling of the tail. The second mode is still poorly studied and consist of the use of the diamond patterns on its back in order to avoid predation. In this study we sought to investigate how the diamond pattern on the snake affects its predation. The Western Diamondback Rattlesnake was chosen for its definitive marking and regional accuracy. To investigate snake predation, replicas of snakes will be made from clay. The clay replicas will vary in the size of the diamonds relatively to the replica size in order to test the impact of diamond size and predation. The models will be placed in natural areas nears Weatherford, Oklahoma for a single month. During the experiment the models will be placed onto white backgrounds to remove the natural cryptic effect of the patterns. Replicas will be analyzed by the imprint left by predation attempts. For this experiment we hypothesize that the diamond indeed work as an aposematic signal and that larger diamonds will act as a stronger warning signal. We expect higher predation rates on replicas without diamond patterns and a higher predation attempts on snake replicas with smaller diamonds when compared to replicas to replicas with larger diamonds.

Christian Hemmerich and Garrett Jones (Oklahoma State University Center for Health Sciences)

Poster 62

****COMPLETENESS OF HARMS REPORTING IN SYSTEMATIC REVIEWS OF FUNCTIONAL ENDOSCOPIC SINUS SURGERY: A CROSS-SECTIONAL ANALYSIS**

To evaluate the completeness of harms reporting in systematic reviews (SRs) pertaining to functional endoscopic sinus surgery (FESS). Using a cross-sectional study design, we performed a comprehensive search using MEDLINE (PubMed and Ovid), EMBASE, Epistemonikos, and the Cochrane Database of Systematic Reviews databases for SRs regarding FESS on May 15th, 2022. In a masked, duplicate manner we extracted general study characteristics, harms items, and overall methodological quality for each SR in our sample. Corrected covered area (CCA) was calculated for SR dyads. For data analysis, using Stata 16.1 we performed a bivariate analysis between variables. Fifty-five SRs were included in our sample after excluding 375 studies that did not meet our inclusion criteria. Of the included SRs, 19 (19/55, 34.5%) did not report harms, 23 (23/55, 41.8%) demonstrated a method of harms data collection, and 25 (25/55, 45.5%) had a balanced discussion of harms and benefits of FESS. Fifty-two SRs were appraised as 'critically low' quality using AMSTAR-2. A significant association was found between completeness of harms reporting and whether harms were listed as a primary outcome. Two SR dyads had CCAs between 20% and 50% overlap and were compared for unique and shared harms. Our study demonstrates gaps in harms reporting regarding FESS in SRs. We recommend future studies implement guidelines such as the STROCCS guidelines or the harms extension of PRISMA guidelines to improve harms reporting. Accurate harms reporting may advance patient safety and promote a more objective risk-benefit analysis for physicians and patients.

Christina Hendrickson¹, Melville Vaughan², and Nikki Seagraves² (¹Oklahoma City University; ²University of Central Oklahoma)

9:30-9:45 in 331 Tandy

DANDELION EXTRACT ALTERS EXPRESSION OF GENES REGULATING ATP AND NUCLEOTIDE BINDING IN CERVICAL CANCER CELLS

Cancer continues to be a major public health burden and one of the leading causes of death. Despite many forms of expensive existing cancer therapies, there continues to be a high mortality rate among cancer patients. Therefore, we based our research on plant derived products due to their anti-cancer effects that can help to produce an efficient and inexpensive pharmaceutical that is widely accessible. One such product is dandelion (*Taraxacum officinale*). It was hypothesized that anti-cancer properties of dandelion extract acts by disrupting key cellular processes in tumor cells which can result in growth inhibition, decreased invasiveness, and increased apoptosis of tumor cells. We performed our experiments by preparing dandelion whole extract (DWE), filtering, freeze-drying, and resuspending them in sterile PBS. Then cultured HeLa cells and Human Cervical Epithelial Cells (HCEC), under standard in vitro conditions, were treated with DWE concentrations between 0 to 8 mg/ml for 96 hours. The quantitative polymerase chain reaction (qPCR) was performed to further investigate the anti-cancer mechanism of DWE. The results showed that DWE inhibited proliferation and migration and promoted cell death in HeLa cells while leaving HCEC cells unaffected. The qPCR showed the analysis of 8 most significantly differential expressed genes ($p < 0.05$) resulted in enrichment of three annotation clusters. The top annotation cluster included genes associated with UP keywords ATP-Binding, Nucleotide-binding, Kinase, and Transferase as well as GO Terms ATP binding (Enrichment score=1.68). The next annotation cluster included genes associated with GO Term focal adhesion (Enrichment score=1.28). These data can provide a foundation to further investigate the mechanism of DWE toxicity in HeLa cells which can pave the way for future research in finding new anticancer pharmaceuticals.

Hollis C. Holcomb¹, Prakash Sah¹, Madison Tryzbiak¹, Jennifer H. Shaw², and Erika I. Lutter¹ (¹Oklahoma State University - Stillwater; ²Philadelphia College of Osteopathic Medicine, University of South Georgia)

Poster 25

****CHLAMYDIA TRACHOMATIS AND THE CHARACTERIZATION OF ITS INCLUSION MEMBRANE PROTEIN CT226**

Chlamydia trachomatis remains a significant human pathogen. Chlamydia's biphasic lifecycle has its replicative stage inside of a parasitophorous vacuole termed an "inclusion". Chlamydia secretes inclusion membrane proteins (Incs) into the membrane of the

inclusion to interact with host cell components. This study focuses on the Inc CT226 which has been shown to have multiple interacting partners including LRRFIP1, LRRFIP2, FLII, and TMOD3. TMOD3 is known to bind to and modify the actin cytoskeleton of the host cell while LRRFIP1, LRRFIP2 and FLII are negative regulators of the inflammasome. We hypothesize that Inc CT226 modulates the immune response during *Chlamydia trachomatis* infection. A comparison of L2 (wildtype) and L2ΔCT226 infection in HeLa cells was performed to examine recruitment of LRRFIP1, LRRFIP2, FLII and TMOD3 to the inclusion by immunofluorescent microscopy. L2 and L2ΔCT226 mutant was further used to compare infectivity and inflammation in the reproductive tract of mice using a murine cervicovaginal infection model. A comparison of L2 (wildtype) and L2ΔCT226 infection in HeLa cells by immunofluorescent microscopy showed a loss of recruitment of FLII by L2ΔCT226 to the chlamydial inclusion and altered/more diffuse recruitment of LRRFIP1 and TMOD3 surrounding the inclusion. Recruitment of LRRFIP2 was identical between L2 and L2ΔCT226. In the murine cervicovaginal model IFUs were higher in the L2ΔCT226 mutant than in the L2 wild type for the duration of infection. The deletion of CT226 influences both recruitment of its interacting proteins as well as an increased level of shed bacteria as observed in the cervicovaginal infection model. This study confirms and an important role for CT226 in Chlamydial infection.

Ellie Howell and Adam K. Ryburn (Oklahoma City University)

10:00-10:15 in 331 Tandy

*A SUSTAINABILITY ASSESSMENT OF OKLAHOMA CITY UNIVERSITY

Over the summer of 2022, a comprehensive sustainability assessment for Oklahoma City University (OCU) was completed. The need for this project presented itself as a response to a growing concern from the campus community about OCU's environmental sustainability, and a lack of transparency from the administration and facilities departments. Utilizing a self-assessment program from the American Association for Sustainability in Higher Education's (AASHE) called STARS (Sustainability Tracking Assessment and Rating System), each section of sustainability at the university was clearly evaluated and the results were compared with that of peer and benchmark institutions who have also enrolled in the STARS program. The main sections of the report detailed Academics, Engagement, Operations, Administration, and Leadership in relation to sustainability in higher education. The main areas for improvement discovered throughout this summer-long survey were primarily in Operations, given that there is currently not a complete recycling program, nor does any designated tracking of emissions, energy, or water usage take place at the university. A more positive part of the results came from the dining services subsection of Operations, in which it was found that our dining services provider actively makes strides to locally source produce and reduce food waste through consistent inventory and documentation. This report establishes a framework for other campuses to follow in order to evaluate and track sustainability in their institutions and suggests possible initiatives to implement in response to areas lacking in sustainability.

Cait Hudgens, Natalie Shreffler, Sydney Oliver, and Daniel Rocha (Southern Nazarene University)

10:30-10:45 in 351 Tandy

*FACTORS THAT AFFECT AMAZONIAN TERRESTRIAL MAMMAL DISTRIBUTIONS

Tropical forests are among the most biologically diverse areas on the planet. The Amazon Rainforest represents about 50% of the remaining tropical forests and hosts over three million different species. Of these species, mammals play vital roles in ecosystems across the globe such as predators, prey, seed dispersers, ecological engineers, and therefore are of conservation importance. The decline in mammal populations, particular large bodied ones, is a pressing issue globally, including in the Amazon forest. The first step to mitigate and prevent mammal declines, is to understand factors that affect mammal distributions. In this study, we used data from 182 camera trap sites from four different protected areas (Samuel Ecological Station, Amana Nature Reserve, Corumbiara State Park, and Guaporé Biological Reserve) of three Amazonian terrestrial mammal species (paca *Cuniculus paca*, white-collared peccary *Pecari tajacu*, and mountain lion *Puma concolor*). We used camera trap data in combination with remote sensing satellite data and hierarchical occupancy modeling to identify environmental and anthropogenic factors that influence species distribution in the Brazilian Amazon. Our results suggest that puma was positively affected by elevation. Paca was negatively affected by elevation and human footprint index. White-collared peccary negatively affected by forest fragmentation. Net primary productivity had a positive effect on the three species studied. Our results support that species occurrence is related to habitat quality and that the increasing human presence in the Amazon will likely negatively affect species distributions, which might require active conservation management.

Alyssa S. Hunt and Lyndee B. Jimboy (University of Central Oklahoma)

Poster 13

*ARE YOU A NEGATIVE NANCY? EXAMINING UNHEALTHY COLLEGE COPING STRATEGIES DURING COVID

This study examined the various ways in which college students coped during the Covid-19 pandemic. Students had to adapt quickly to different learning strategies during the pandemic, which may have produced unhealthy coping habits. Participants were college students attending the University of Central Oklahoma. They completed an online survey that contained demographic questions, three published scales (BDI, BIS/BAS, PSS), two modified sales (Stress Coping Resources Inventory, DAST-10), and researcher generated questions regarding covid related stress. The pandemic exacerbated the level of stress and uncertainty already felt by college students. Preliminary results suggests that the majority of students reported increased levels of depression

and stress, which they self-medicated with drugs, alcohol, and social media use. Approximately 14% of students had thoughts of self-harm. At this time, results from the BIS/BAS scale are inconclusive. It appears that students engaged in unhealthy coping strategies to mitigate the stress associated with the pandemic.

Saraya Hunt (Southwestern Oklahoma State University)

10:00-10:15 in 351 Tandy

***CREATING SUSTAINABLE HARVEST MODELS BY TRACKING CHANGES IN A *CYCLANTHERA NAUDINIANA* POPULATION**

SWOSU students have been tracking changes in the population of *Cyclanthera naudiniana* (Cucurbitaceae, Neesom 2014), an annual vine, since 2010. The native species was chosen as a case study for creating models of sustainable harvest, [effects of management changes, and invasion]. These models rely on information about population size and fluctuations in the absence of harvest or intervention, yet these baseline parameters are lacking for most species. Practically, cyclanthera, is a good choice of model as there is a population in an accessible natural area near the SWOSU campus and the plant flowers and fruits during the school year. Scientifically, cyclanthera is an interesting choice because the plant, congeneric with edible and medicinal species, has unusual dispersal through forcible ejection, and exhibits dramatic changes in population size. Through the 13 years of the study, the study population has ranged from 2 to 2,748 individuals and within season survivorship curves have varied. We present information about changes in population size and reproductive output over the long-term study, hypotheses about the changes, and future steps in creating better models.

McClain Irby, Amanda Nichols, Will Clothier, and Kevin Plumlee (Oklahoma Christian University)

8:30-8:45 in E393 Forensic

***SYNTHESIS AND POWER GENERATION CHARACTERIZATION OF PEROVSKITE SOLAR CELLS**

Perovskite solar cells are a type of solar cell that uses perovskite as one of the layers due to its semiconductor capabilities. The cell materials are layered to allow electron and hole transport. Patwardhan, et al showed that perovskite solar cells can be constructed using a deposition method by undergraduate students as a way to introduce solar energy and this unfamiliar type of solar cell. While perovskite solar cells that have different halides and divalent cations have been constructed, they have not been made using a simple deposition method. Two other halides were used instead of iodide (bromide and chloride ions), and different mixtures of the halides were used to fabricate the solar cells. Electrical power output of the cells was collected and compared to the commercial and literature values.

Lyndee B. Jimboy and Alyssa S. Hunt (University of Central Oklahoma)

Poster 13

***ARE YOU A NEGATIVE NANCY? EXAMINING UNHEALTHY COLLEGE COPING STRATEGIES DURING COVID**

This study examined the various ways in which college students coped during the Covid-19 pandemic. Students had to adapt quickly to different learning strategies during the pandemic, which may have produced unhealthy coping habits. Participants were college students attending the University of Central Oklahoma. They completed an online survey that contained demographic questions, three published scales (BDI, BIS/BAS, PSS), two modified sales (Stress Coping Resources Inventory, DAST-10), and researcher generated questions regarding covid related stress. The pandemic exacerbated the level of stress and uncertainty already felt by college students. Preliminary results suggests that the majority of students reported increased levels of depression and stress, which they self-medicated with drugs, alcohol, and social media use. Approximately 14% of students had thoughts of self-harm. At this time, results from the BIS/BAS scale are inconclusive. It appears that students engaged in unhealthy coping strategies to mitigate the stress associated with the pandemic.

Adrienne L. Jones, Jordan Clayborn, Elizabeth Pribil, Andrew Foote, Dagan Montgomery, Noha H. Youssef, and Mostafa S. Elshahed (Oklahoma State University - Stillwater Campus)

10:30-10:45 in D107 Lecture Hall

****TEMPORAL PROGRESSION OF FUNGAL AND BACTERIAL POPULATION IN DAIRY CALVES FROM BIRTH TO MATURITY**

Anaerobic gut fungi (AGF) are important constituents of the alimentary tract of Bovidae, but little is currently known regarding the progression of AGF communities in cows from birth till maturity. We followed the AGF community in eight dairy cows from birth (day 1) till maturity (12 months). We documented changes in diversity and community structure and correlated the community dynamics to salient events in the cows' anatomical development and feeding regimens. Surprisingly, the microbial communities in newly birthed calves were drastically different from their mothers. Calves' communities between day 1 and 2 months were more diverse than their mothers at the genus and species levels. The community was also dominated by genera mostly associated with hindgut fermenters (e.g. *Khoyollomyces*). A drastic shift in community structure was observed at 3-4 months, with a measurable decrease in alpha diversity and a shift towards communities typically encountered in cows (e.g. *Pecoramyces*, *Necollimastix* and *Orpinomyces*). As well, a remarkably high level of similarity in diversity estimates and microbial community structures between all eight subjects was observed within the first two months; with weaning and growth

associated with higher level of beta diversity. We demonstrate that the AGF community structure in newly birthed dairy calves is highly diverse, distinct from their mothers, and more closely resembles hindgut rather than adult cows AGF communities. The results emphasize the importance of age, and age-related anatomical development, and nutritional transitions as a factor in shaping AGF communities. Specifically, we propose that the progression of AGF community is highly dependent on the anatomical development and operational functionality of the rumen, which occur later (2-3 months post birth), as well as on the nutritional transition to plant substrates associated with weaning.

Garrett Jones and Christian Hemmerich (Oklahoma State University Center for Health Sciences)

Poster 62

****COMPLETENESS OF HARMS REPORTING IN SYSTEMATIC REVIEWS OF FUNCTIONAL ENDOSCOPIC SINUS SURGERY: A CROSS-SECTIONAL ANALYSIS**

To evaluate the completeness of harms reporting in systematic reviews (SRs) pertaining to functional endoscopic sinus surgery (FESS). Using a cross-sectional study design, we performed a comprehensive search using MEDLINE (PubMed and Ovid), EMBASE, Epistemonikos, and the Cochrane Database of Systematic Reviews databases for SRs regarding FESS on May 15th, 2022. In a masked, duplicate manner we extracted general study characteristics, harms items, and overall methodological quality for each SR in our sample. Corrected covered area (CCA) was calculated for SR dyads. For data analysis, using Stata 16.1 we performed a bivariate analysis between variables. Fifty-five SRs were included in our sample after excluding 375 studies that did not meet our inclusion criteria. Of the included SRs, 19 (19/55, 34.5%) did not report harms, 23 (23/55, 41.8%) demonstrated a method of harms data collection, and 25 (25/55, 45.5%) had a balanced discussion of harms and benefits of FESS. Fifty-two SRs were appraised as 'critically low' quality using AMSTAR-2. A significant association was found between completeness of harms reporting and whether harms were listed as a primary outcome. Two SR dyads had CCAs between 20% and 50% overlap and were compared for unique and shared harms. Our study demonstrates gaps in harms reporting regarding FESS in SRs. We recommend future studies implement guidelines such as the STROCCS guidelines or the harms extension of PRISMA guidelines to improve harms reporting. Accurate harms reporting may advance patient safety and promote a more objective risk-benefit analysis for physicians and patients.

Tiffany Jones, Joshua Baer, Shania Do, Abigail Kee, Karissa LeHew, Derek McGuire, Sarah Soliman, Sydney Spillane, Monica Vuong, Cari Marshall, and Ipe Paramel (Oklahoma State University Center for Health Sciences)

Poster 16

****LEAN HEALTHCARE: EVALUATION OF BED THROUGHPUT AT OSU MEDICAL CENTER**

Several factors play a role in an organization's success to function on a daily basis. For example, one factor being the application of efficient protocols to produce effective and consistent results. There is a specific procedure, called LEAN, that has been increasingly employed throughout various types of corporate professions due to its favorable outcomes. Originally, LEAN practices were created to enhance workflow and manufacturing processes in the automobile industry. After other industries observed the success rates from applying these certain methods, LEAN has been progressively adapted by many businesses to achieve similar effects. By adopting the LEAN methodologies, corporations have been able to increase their productivity, value, and client satisfaction. An example of how versatile and beneficial the LEAN approach can be in other fields, besides manufacturing, can be portrayed within a healthcare setting. There have been multiple healthcare organizations that have applied LEAN strategies to their systems in order to amplify quality improvement, with an end goal to better patient care. In this poster, a model is presented on how to apply and replicate LEAN tactics in an effort to advance bed throughput within a hospital setting. In the summer of 2022, a team of medical students from Oklahoma State University College of Osteopathic Medicine (OSU-COM) applied LEAN tools and techniques to examine the delayed process of bed throughput from the Emergency Department to the hospital floors. In doing so, possible solutions were developed in hopes to improve workflow, culture, and most importantly, patient outcomes.

Abigail Kee, Joshua Baer, Shania Do, Tiffany Jones, Karissa LeHew, Derek McGuire, Sarah Soliman, Sydney Spillane, Monica Vuong, Cari Marshall, and Ipe Paramel (Oklahoma State University Center for Health Sciences)

Poster 16

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Kathleen Kelley, Guangmau Xie, Qiang Lin, and Miriam Belmaker (University of Tulsa)

8:30-8:45 in 351 Tandy

****COULD ARCHAIC *HOMO SAPIENS* SURVIVE IN THE TROPICS OF SOUTHEAST ASIA? IDENTIFYING SMALL MAMMAL REMAINS FROM YAHUAI CAVE IN GUANGXI, CHINA AT 120 KYA TO DETERMINE THE PALEOECOLOGY**

It has been hypothesized that the lack of protein sources and technological skills prevented archaic *Homo sapiens* from penetrating the rainforest to forage for food prior to 40,000 years ago (kya). Accordingly, early modern humans dispersing from Africa to Asia ca. 120 kya would have preferred savanna over tropical environments. As a case study, we present an analysis of small mammal remains (Chiroptera, Rodentia, Eulipotyphla, Primates) from Yahuai Cave, Guangxi, China. The area in Yahuai cave focused on for this research excavated 53 stratigraphic layers, dated by OSL to 124.2 ± 16 kya. Early modern human remains were found nearby at several contemporaneous sites, such as Tongtianyuan and Mulan cave indicating the region was inhabited by ca. 120 - 100 kya. Species found include a wide range of murids such as *Niviventer andersoni* (Anderson's white-bellied rat), *Mus pahari* (Gairdner's shrewmouse) and other murid specimens identified only to the genus level, such as *Leopoldamys*, *Rattus* and additional species of *Niviventer*. Other species include several squirrel species such as *Hylopetes alboniger* (Particolored flying squirrel), and *Belomys personii* (hairy-footed flying squirrel). Ecological analogy as well as community structure methods are utilized in the paleoecological analysis. This analysis indicates a warm, humid, dense forested environment, probably more humid than the contemporaneous Indochinese peninsula. A diachronic comparison shows no appreciable differences in species composition across strata. This suggests the ecology of the area was similar in the lower strata, ca. 120 kya, to that in the upper levels, ca. 40 kya. This confirms the ability of early modern humans to utilize this novel ecosystem earlier than previously assumed.

Chad B. King (University of Central Oklahoma)

Poster 17

INTEGRATING EDUCATION AND RESEARCH: USING SCALE TO UNDERSTAND FIRE EFFECTS

Historically, fire was an important disturbance that shaped the grasslands of North America. In the absence of fire, woody encroachment is continually changing grassland structure that has ramifications on biodiversity and agriculture. In an effort to enhance research, extension, and education about the value of pyric herbivory in the Great Plains, The Prairie Project has developed a program that collaborates with K-12 and higher education professionals in developing educational units that focus on the role of fire and grazing. This presentation highlights the educational unit that I developed to engage students in investigating fire effects at the University of Central Oklahoma's Selman Living Laboratory (SLL). Specifically, this unit challenged students to assess fire effects at different spatial and temporal scales. The unit was written for a 4000/5000 level Plant Ecology course. Two wildfires (2016, 2017) affected a portion of the SLL. Students first completed a pre-survey about their agreement with statements regarding fire and grazing practices. Students were introduced to the concept of pyric herbivory through two lectures. To investigate the fire effects at a large spatial scale, students assess fire effects at SLL using the Rangeland Analysis Platform (rangelands.app/rap/). Following this activity, students investigated a 3-year data set on species composition and plant cover at SLL. The third component of the unit was a field trip to the SLL in order to assess how topographic variability affected fire behavior. Students completed a lab report that synthesized fire effects by accounting for measurements at different spatial and temporal scales. A post-survey was completed by students to assess how their opinions changed regarding fire and grazing. Survey results indicated students increased their agreement regarding statements about rangelands, fire benefits, and ecosystem services. This unit is being implemented again in Plant Ecology during Fall 2022.

Kohl D. Kirby, Jacob O. Williams, and Jacob T. LaMar (Oklahoma Christian University)

Poster 31

***CONSERVATION OF DOCK AND RICTOR IN *DROSOPHILA* SPECIES**

This study examined the evolutionary conservation of the dock and rictor genes in various *Drosophila* species. Based on the conservation trends seen in the insulin/TOR pathway of *Drosophila*, it was hypothesized that the more connections a gene had the more conserved it would be. In this case, rictor was expected to be more conserved than dock. To compare the conservation of dock and rictor, each of the genes were first annotated in *Drosophila melanogaster*. The genes were then annotated in other *Drosophila* species. The sequence of amino acids that encoded each protein were compared in the different species, and then an evolutionary divergence score was calculated using a special formula. The results did not support the original hypothesis, and dock showed to be more conserved than rictor. However, this outcome could be due to a flaw in the divergence scoring system.

Kayton Kite¹, Brooklin Bain¹, G. Caroline Schwab¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 33

***EVOLUTIONARY CONSERVATION OF RICTOR**

The *Drosophila* species is one of the most important model systems used for biological sciences. Specifically, this study focused on the evolution of the insulin/TOR pathway within the species by using comparative genomics. The insulin/TOR pathway is a regulator of organism and cell growth, therefore playing a role in the lifespan and evolution of not only *Drosophila*, but in many animals. Within this study, comparative genomics was used to determine the conservation of a gene, rictor, within the pathways compared to different species of *Drosophila*. To compare, sequencing of the target gene in twelve species of the *Drosophila* genus was completed, along with computing divergence scores based on the gene neighborhoods and gene structure. Genomic neighborhoods of the target gene in each species were examined and compared to assigned divergence scores. Due to the many interactions rictor possessed, it was hypothesized that rictor would be well conserved throughout evolution and have a conserved genomic neighborhood. However, genomic neighborhoods indicated that rictor was not well conserved in species with high divergence. As species evolved, genomic neighborhoods became more diverged from that of *D. melanogaster*.

Kara F. Kneuper¹, Isabel L. Estrada², and Karen A. Lewis² (¹Oklahoma Christian University; ²Texas State University)

Poster 46

***INVESTIGATING THE ROLE OF THE INTRINSICALLY-DISORDERED N-TERMINAL REGION OF ZEBRAFISH LARP6 IN MODULATION OF RNA BINDING ACTIVITY**

Collagen is an essential structural protein in animals, and the dysregulation of the production of collagen may result in diseases such as Ehlers-Danlos syndrome or fibrosis. LaRP6 is a protein that functions in the production of type I collagen by localizing collagen mRNA to the rough endoplasmic reticulum where collagen synthesis occurs, although the mechanism of RNA binding discrimination is not well understood. This project aimed to investigate the mechanism by which LaRP6 binds to RNA by creating truncations of the amino-terminal region, which is thought to interact with the core RNA-binding domain known as the La module. Electrophoretic Mobility Shift Assays (EMSAs) were used to investigate the modulation of the affinity of truncated LaRP6 for RNA ligands, and our results indicate that the N-terminal region is a major contributor to RNA binding specificity.

David M. Kunkel and Dr. Mark Fishbein (Oklahoma State University - Stillwater Campus)

9:45-10:00 in 353 Tandy

****NICHE DIFFERENTIATION WITHIN THE “ASPERULA CLADE” OF *ASCLEPIAS* (APOCYNACEAE)**

The ecological niche describes the conditions under which a species can persist. Assessing niche differences between closely related species is important for understanding how these species diverged. To examine niche differences among closely related species, I utilized the “asperula clade” which contains 6 species of *Asclepias*, *A. viridis*, *A. asperula*, *A. labriformis*, *A. welshii*, *A. involucrata*, and *A. macrosperma*. These milkweeds are located in west and southwest North America, with the exception of *A. viridis*. I hypothesized that these species differentiate along both climatic and edaphic gradients, primarily precipitation and soil texture. Here, I utilized 19 bioclimatic variables, elevation, % clay content, % silt content, % sand content, coarse fragments, nitrogen content, pH, and cation exchange capacity to characterize the climatic and edaphic niches of this clade. I used principal component analysis (PCA), linear discriminant function analysis (LDA), and ecological niche modeling to characterize the niches of these six species, and determine differences in niche characters between them. In the LDA analysis, most differentiation occurs through the annual mean temperature, mean temperature of warmest quarter, and the mean temp of coldest quarter, with substrate contributing little to this differentiation. However, in the ecological niche models we observe that substrate is consistently among the important predictor variables for these species. The degree of niche overlap (Warren’s I) was also calculated by comparing niche model outputs between pairs of species. We see the highest degree of niche overlap among sister species, with the exception of pairings with *A. macrosperma* and *A. involucrata*. These niche overlap values for each species comparison were then compared with phylogenetic distances between species via a Mantel test to look for correlation between phylogeny and niche. The results suggest that there is no correlation between these distances, which may be suggesting that niche is labile along the tree.

Jacob T. LaMar, Jacob Williams, and Kohl Kirby (Oklahoma Christian University)

Poster 31

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Kyla Langstraat, Rachel Uhlig, Payden Farnsley, and Saraya Hunt (Southwestern Oklahoma State University)

8:45-9:00 in 353 Tandy

***MICROBIAL ANALYSIS OF REGOLITH-GROWN SPECIES ON MARS**

With NASA having goals of humans back on the moon by 2030, a team of researchers from Southwestern Oklahoma State University participated in the Plant Mars Challenge hosted by the Institute of Competition Sciences to study how crops grow in non-Earth soils. We tested interactions between plant species and microbial diversity and how this affects crop yield. Five different crops were grown over a nine-week period and the biomass was measured at the end. Since mycorrhizal associations are known to increase surface area of root structures and are hypothesized to favor plant growth by increasing nutrient acquisition and limiting pathogenic microbes, we hypothesized that microbial diversity increases plant growth. To test this hypothesis, sixteen bottom-wicking pots were used for Mars-regolith versus Earth soil, high versus low microbial diversity, and three plants versus another three, with two trials of each treatment. We predicted that pots containing a higher microbial diversity would have more plant biomass. Germination occurred, but little to no growth was detected in Mars-regolith after nine weeks. Microbial activity was detected by fluorescein diacetate analysis and microbial load was determined by serial dilution plating using three medias. In the end, Earth soil was found to have significantly more microbial activity, suggesting that there was a higher rate of metabolism of microbes within the soil. We found that there were no significant differences between the microbial load in both soils regardless of microbial diversity differences. Due to the Mars-regolith pots becoming visibly waterlogged towards the end, future directions may include evaluating the presence or absence of water-retaining microbes. Some team members returned for future research and are currently troubleshooting problems that occurred in the previous semester. This presentation will focus on findings from the previous team, what is currently being done for the project, and future directions following this semester.

Brenden Latham (East Central University)

9:30-9:45 in E393 Forensic

***COALITION FORMATION UNDER UNCERTAINTY**

The complexity of a vast number of real-world tasks provides a great challenge for robotics. With the limited capabilities of robots currently available on the market, it is almost impossible for a single robot to complete a complex task. Thus, multiple robots would need to form themselves into coalitions for the completion of such tasks. In this research, we examine the multi-robot coalition formation problem for instantaneous task allocation (IA) where a group of robots needs to be allocated to a set of tasks so that the tasks can be finished optimally. We aim to produce new results in coalition formation for multi-agent systems in the presence of uncertainty. We propose a new way of pairing existing algorithms and methods of implementation to quantify the stability of optimal agent allocations when uncertainty is present in the relation between agents and tasks.

Brittney-Hien Le, Erik Odom, Alicia Ito Ford, Austin Jorski, Hannah Wendelbo, Taylor C. Rogers, Jantzen J. Faulkner, Amanda Foster, Joshua Gordon, Michelle Farabough, and Matt Vassar (Oklahoma State University Center for Health Sciences)

Poster 14

****CONSISTENCY OF NEW RESEARCH WITH A 2006 SLEEP MEDICINE PRACTICE PARAMETER FOR YOUNG CHILDREN**

Clinical practice guidelines are systematic reviews and synthesis of the scientific literature for specific diagnoses and treatment modalities. They provide important guidance to practitioners and patients. However, if a practice guideline is not updated regularly, then readers may not be aware of changes and newer developments in best practices. We identified a practice guideline that had not been updated since 2006, the American Academy of Sleep Medicine's Practice Parameters for Behavioral Treatment of Bedtime Problems and Night Wakings in Infants and Young Children. To determine whether the clinical trials and published research since 2006 remain consistent or conflict, we completed a systematic review. We constructed research questions based on the guideline recommendations using the Participants, Intervention, Comparator, Outcome (PICO) format, developed search strings based on these questions, and searched ClinicalTrials.gov, the World Health Organization's International Clinical Trials Registry Platform, and PubMed. Studies were screened for eligibility and exclusion criteria based on completion date and relevance. Retained studies were evaluated based on study type and design, stage of completion, and which recommendation they addressed. After the screening process, 36 studies were retained for review. Of these, 28 were completed with published results, including 19 randomized controlled trials, 8 non-randomized intervention studies, and 1 case report. The majority of studies addressed more than 1 recommendation of interest and supported the use of behavioral interventions. Research over the past 15 years continues to support the general effectiveness of behavioral techniques. However, published research and registered clinical studies have not aligned with research gaps that were identified in the 2006 guidelines. To further advance knowledge for clinical care of infants and young children with bedtime and night-waking problems, future research should target the previously identified research gaps as opposed to continuing to replicate well-established practices.

Chase Lee¹, Jack Rea¹, Micah Kee¹, Brayden Rucker¹, Holly Flores¹, Corbin Walters², Taryn Haney², Alicia Tomlin², & Matt Vassar^{1,3} (¹Oklahoma State University Center for Health Sciences; ²School of Global Public Health, New York University)

Poster 55

****HARMS REPORTING ASSESSMENT REGARDING SYSTEMATIC REVIEWS FOCUSING ON DIRECT ORAL FACTOR XA INHIBITORS: A CROSS-SECTIONAL STUDY**

Our primary objective is to evaluate the quality and completeness of harms reporting in systematic reviews (SRs) regarding factor Xa inhibitors through a cross-sectional analysis. We searched MEDLINE (PubMed and OVID), EMBASE, Epistemonikos, and Cochrane Database Systematic Reviews for SRs comprised of randomized control trials (RCTs) designed to evaluate direct oral factor Xa inhibitors. We performed screening and data extraction for harms among eligible SRs in a masked, duplicate fashion using a pilot-tested Google Form. This form, based on the published work of Qureshi and colleagues, quantified the reporting of harms among SRs. AMSTAR-2 was used to evaluate the methodological quality of the included SRs. Corrected covered area (CCA) was calculated for overlap of primary studies between SR dyads. Approximately 70 SRs comprising 242 unique primary studies met inclusion criteria and were included in the present study for analysis. Of these 70 SRs, 69 (69/70, 98.6%) reported harms as a primary outcome. Further, 23 SRs (23/70, 32.9%) completed 50% or less of harms items. Seven (7/70, 10%) SRs reported the total number of patient treatment discontinuations. Less than half of SRs (38/70, 54.3%) established severity scales to evaluate harms. CCA data showed 12 studies containing 50% or higher CCA values and many contained less than 50% overlap for harms. No statistically significant associations were found. We found the overall reporting of harms to be incomplete. Because SRs are often viewed for clinical practice, improvements must be made to better report harms.

Chase Lee, Kade Ezell, Bryan Dunford, Danya Nees, Samuel Jacobsen, Jordan Staggs, Jake Checketts, and Matt Vassar (Oklahoma State University Center for Health Sciences)

Poster 56

****HEALTH INEQUITIES IN ORTHOPAEDIC TRAUMA SURGERY IN THE UNITED STATES: A SCOPING REVIEW**

Health inequities have been shown to have negative effects on patient care and the healthcare system. It is important for orthopaedic trauma surgeons and researchers to understand the extent to which patients are affected by these inequities. We conducted a scoping review as outlined by the Joanna Briggs Institute and the Preferred Reporting Items for Systematic reviews and Meta Analyses extension for Scoping Reviews (PRISMA-ScR) checklist. We searched PubMed and Ovid Embase for articles relating to orthopaedic trauma surgery and health inequities. After exclusion criteria were applied, our final sample consisted of 52 studies. The most frequently evaluated inequities were sex or gender (43 of 52 [82.7]), race/ethnicity (23 of 52 [44.2]), and income status (17 of 52 [32.7]). The least frequently evaluated inequities were LGBTQ+ identity (0 of 52 [0.0]) and occupational status (8 of 52 [15.4]). Other inequities evaluated included rural/under-resourced (11 of 52 [21.1]) and educational level (10 of 52 [19.2]). No trend was observed when examining inequities reported by year. Health inequities exist in orthopaedic trauma literature. Our study highlights multiple inequities in the field that need further investigation. Understanding current inequities and how to best mitigate them could improve patient care and outcomes in orthopaedic trauma surgery.

Karissa LeHew, Senait Assefa, Steven Rivera, Alejandro Torres, Dolores Vazquez Sanroman, and Gerwald Koehler (Oklahoma State University Center for Health Sciences)

Poster 28

****OPIOID EFFECTS ON INFLAMMATORY AND REGENERATIVE MARKER EXPRESSION IN RAT INTESTINE**

Opioids can have profound effects on the human gastrointestinal system, such as opioid-induced constipation. Conversely, the mammalian intestine is an organ that experiences constant regeneration, which is maintained by intestinal stem cells located in intestinal crypts. However, the exact impact of opioids on intestinal proliferation and regeneration is poorly characterized. This study focused on the effects of opioids on the epithelial regeneration of rat intestines. Specifically, it was examined how oxycodone administration altered inflammatory and regenerative marker genes expression levels. Moreover, in order to address whether oxycodone intoxication and withdrawal led to differential expression, treatment and control cohorts each were split into two groups, one receiving an acute naloxone injection to precipitate withdrawal and the other a saline injection as vehicle control. The mRNA expression levels of the stem cell/regenerative marker *Lgr5* and the inflammatory marker *IL-6* were analyzed by quantitative reverse transcription PCR. Additionally, we have begun protein-based analyses. We found increased expression levels of *IL-6* in the small intestine of oxycodone-treated rats. In contrast, oxycodone administration led to upregulation of *Lgr5* in the colon, which appeared to be reduced during naloxone-initiated withdrawal. Our preliminary results show that oxycodone may affect inflammatory and regenerative gene expression in rat intestine. Future analyses will include additional marker genes as well as protein expression detection methods. Furthermore, correlations with opioid-induced gut microbiota changes will be explored.

Sadie Lincoln, Senait Assefa, Gerwald Koehler, and Alicia Ford (Oklahoma State University Center for Health Sciences)

Poster 29

****SALIVA MICROBIOTA CHANGES DURING STANDARD RESIDENTIAL SUBSTANCE ABUSE TREATMENT**

The human oral cavity is home to a diverse community of microorganisms, the oral microbiota, with its members existing in complex relationships with one another and their human host. Bacterial species predominate the oral microbiota. Evaluation of a saliva sample is a simple way to examine the overall microbial composition of an oral microbiota. Opioid analgesics are a commonly prescribed class of pharmaceuticals that are used worldwide for pain control. In addition to their potential for misuse and overdose, opioid analgesics can have negative systemic effects. Opioid compounds can bind to immune cells and modulate immune function with both suppressive and/or stimulatory effects, including affecting the composition and diversity of host microbiomes. In this study, we are investigating whether the composition of the oral microbiome changes in an individual who has undergone opioid detoxification. Saliva samples were collected from study participants who have undergone the process of detoxification from opioid misuse and are now in treatment. The samples were used for microbiota profiling by 16S ribosomal RNA amplicon sequencing. We found that the composition of the oral microbiota changed over time in individuals who had undergone opioid detoxification. When comparing second samples to first samples, alpha diversity changes were discovered. The four most dominant genera in our samples were *Veillonella*, *Streptococcus*, *Prevotella* 7, and *Actinomyces*. Differential abundance analyses revealed bacterial groups correlating with host metadata. The ongoing study will aid in the evaluation of saliva microbiome biomarkers relevant for assessment of host health and recovery.

Laci Liter, Nisha Susan Thomas, and Elizabeth Wellberg (Oklahoma City University)

Poster 60

***EFFECTS OF ER-SIGNALING ON ADIPOCYTE PROGENITOR EXPANSION: POTENTIAL ROLE FOR WISP2**

Dysfunctional adipose tissue (AT) occurs when progenitors fail to expand and form new adipocytes during a positive energy balance. In this context, mature adipocytes become hypertrophic and ectopic lipid deposition can increase the risk for type 2 diabetes. Disrupted estrogen receptor alpha (ER α) signaling has been shown to contribute to AT dysfunction. We found elevated expression of Wnt1-inducible signaling protein (WISP2/CCN5) in APCs from obese mice after estradiol (E2) treatment. WISP2 regulates APC proliferation in mice and is induced by estrogen in human breast cancer cells. Analysis of human AT revealed a correlation between WISP2 and serum insulin levels. We hypothesized that WISP2 influences APC renewal and differentiation in response to ER α and potentially insulin signaling in AT. We aimed to investigate the connections between WISP2 and the progenitor phenotype plus WISP2 regulation by ER α in an in vitro model of adipogenesis. Mouse APCs (mAPCs) were cultured for all experiments. Adipocyte differentiation was visualized with Oil Red O-staining at days 0, 2, 4, 6, 8, 10, and 15. Expression of ER α and WISP2 after treatment with TAM, fulvestrant (ICI), insulin, and/or E2 in mAPCs was analyzed by PCR and Western blotting. The effect of WISP2 and E2 on mAPC progenitor proportions was measured by flow cytometry analysis of CD24 and Sca1. ORO-staining confirmed mAPC adipocyte differentiation over time. WISP2 expression increased after insulin-, E2-, and insulin+E2 treatments and decreased in treatments containing ICI. All treatments decreased ESR1 expression except ICI+E2+insulin. Western-blotting confirmed gene expression analyses. Consistent with previous work, E2 and insulin induced WISP2 expression in mAPCs. Further classifying associated signaling cascades will aid in investigating AT expansion and the pathology of adipocyte progenitors in obesity and diabetes.

Jake Lovinggood (Oklahoma Christian University)

Poster 47

THE CONSERVATION OF SIMA AND PTP61F IN *DROSOPHILA

Within the *Drosophila* species, the Insulin-like Receptor Signaling (ILRS) Pathway is controlled by a variety of genes that either inhibit or excite the ILRS pathway. Changes within pathways can potentially be dangerous to an organism and cause issues such as cancer. By investigating the insulin TOR pathway across many *Drosophila* species, we can investigate the selective pressures of evolution at different points within that pathway to understand how pathways are regulated. In previous studies, genes that are more connected physically have been found to show slower rates of evolution as a species diverges over time. In our research we annotated the genes *sima* and *Ptp61F* in a variety of *Drosophila* species.

Trevor Magee and Jay Modi (Oklahoma State University Center for Health Sciences)

Poster 58

****AN ANALYSIS OF HARMS REPORTING IN SYSTEMATIC REVIEWS REGARDING KETOROLAC FOR MANAGEMENT OF PERIOPERATIVE PAIN**

Due to the frequent perioperative use of ketorolac tromethamine and its ability to minimize postoperative opioid requirements, it is important to continually reassess harms associated with its use. Our primary objective was to investigate the extent of harms reporting in systematic reviews (SRs) on ketorolac for perioperative pain. In May 2022, we conducted a search of major databases, MEDLINE (Pubmed and Ovid), Embase, Epistemonikos, and the Cochrane Database of Systematic Reviews to identify eligible SRs on ketorolac for perioperative pain. Screening and data extraction was performed in masked, duplicate fashion. AMSTAR-2 was used to appraise the methodological quality of included SRs. Corrected covered area (CCA) was

calculated to determine overlap of primary studies between SR dyads. A total of 28 SRs evaluating 630 primary studies met inclusion criteria. Seven SRs (7/28, 25%) reported no harms and 17 SRs (17/28, 60.7%) reported $\leq 50\%$ of harms items. A significant association was found between completeness of harms reporting and whether harms were specified as a primary outcome (P 50% but neither reported harms). The extent of harms reporting in SRs was inadequate. Given the importance that SRs have on guiding perioperative decision-making, it is essential to improve the completeness of harms reporting.

Dulandika Malalage, Tarosha Salpadoru, and Marianna Patrauchan (Oklahoma State University - Stillwater Campus)
9:00-9:15 in D107 Lecture Hall

***PSEUDOMONAS AERUGINOSA DISPLAYS ENHANCED SURFACE MOTILITY TOWARDS METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS IN RESPONSE TO CALCIUM**

Pseudomonas aeruginosa is the leading cause of life-threatening lung infections in Cystic Fibrosis (CF) patients. *P. aeruginosa* is a challenging pathogen due to its ability to quickly adapt to the host environment and become resistant to multiple antibiotics. This rapid adaptation to the CF lung environment is in part facilitated by virulence factor production and includes its ability to interact with other pathogens. A second predominant pathogen of CF lung, *Staphylococcus aureus*, is detected simultaneously with *P. aeruginosa* in up to 50% of CF patients. The interactions between these pathogens co-existing during CF infections can shape their impact on the host and exacerbate the disease. Therefore, understanding their interactions at the molecular level will be helpful in developing novel effective treatments. We have previously established that elevated calcium levels found in the airways of CF patients play a significant role in enhancing the virulence and antibiotic resistance of *P. aeruginosa* thereby increasing its pathogenicity. Here we show that these calcium levels also increase the surface motility of *P. aeruginosa* towards Methicillin-resistant *Staphylococcus aureus* when grown in SCFM medium which mimics the CF lung environment. To determine the responsible mechanism, a panel of mutant strains lacking genes encoding several key components of calcium regulatory network in *P. aeruginosa* were tested. Among them, the Calcium-responsive response regulator CarR, a part of the calcium-regulated two-component regulatory system CarSR, was detected to play role in *P. aeruginosa* movement towards *S. aureus*. Further studies will corroborate the role of this two-component system as a novel factor controlling the interactions between the two pathogens and may help develop effective therapeutics to combat their lethal infections.

Randall Maples (East Central University)

Poster 10

ATR-FTIR DETECTION OF CHLORINATED HYDROCARBONS IN GROUNDWATER

Chlorinated hydrocarbons including aliphatic and aromatic compounds (CHCs) are toxic contaminants commonly found in groundwater samples and efficient detection and monitoring of these contaminants is an important part of the evaluation of water quality. Analysis is often complicated due to the presence of many compounds as well as interfering molecules. In this preliminary study, with an overall end-goal of the development of a novel, time and cost-efficient procedure for the determination of complex mixtures of CHCs in groundwater employing digital signal processing techniques, a method was developed for the determination of various CHCs in aquifer groundwater using Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy (ATR-FTIR).

Lena Marcikic¹, Madison Stephens¹, Asiah Powers¹, G. Caroline Schwab¹, Tyler Godsey¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 36

***THE EVOLUTIONARY CONSERVATION OF DOCK AS COMPARED TO RICTOR IN THE INSULIN-LIKE RECEPTOR PATHWAY**

The Insulin/TOR Signaling Pathway evolves in *Drosophila* as the species become further diverged from *Drosophila melanogaster*. In this study, a comparative genomics approach was used in order to determine the levels of conservation of two genes, rictor and dock, of the insulin pathway. A variety of genes from the *Drosophila* genus were annotated based on elements like genomic neighborhood and gene structure. Each gene annotated also had isoforms which varied in amino acid sequences and number of exons. We used this information to determine the organisms' evolutionary relationship to *D. melanogaster*. The scores were then compared using a bar graph which demonstrated divergence levels. The results demonstrated dramatically higher divergence scores of rictor than dock which was earlier on the pathway than rictor. Results indicated that dock was more conserved than rictor. Future research could be done to determine if other genes that are also early in the pathway are more conserved than those later in the pathway.

Laurel Marsh and Adam K. Ryburn (Oklahoma City University)

9:00-9:15 in 353 Tandy

***A FLORISTIC INVENTORY OF THE CENTRAL OKLAHOMA CAMP AND CONFERENCE CENTER, LOGAN COUNTY, OKLAHOMA**

We conducted a plant survey of the Central Oklahoma Camp and Conference Center in Logan County, Oklahoma, during the growing seasons of 2021 to 2022. Specimens were collected for 174 species in 140 genera and 58 families. The largest families

represented were the Asteraceae (33 species), Fabaceae (23 species), and Poaceae (22 species). No rare species currently being tracked by the Oklahoma Natural Heritage Inventory were encountered. No endangered species currently being tracked by the Oklahoma Natural Heritage Inventory were encountered.

Jamian R. Maxwell, Leah S. Dudley, and Timothy M. McGinnis (East Central University)

Poster 1

***MICROBIAL EFFECTS OF NATIVE *OENOTHERA* SPECIES EXTRACTS**

Plants of the genus *Oenothera* have been used in the practice of medical botany. Oklahoma is home to several native plants belonging to this genus. Finding plants that can be used medicinally is essential to growing the pharmacopeia, and is also less costly and has a wider availability than most modern pharmaceuticals. Finding medicinal value in native plants can benefit not only the people but the plant as well. Finding medicinal compounds in native plants can help lead to conservation efforts made to protect the resource and its habitat. Here, we test the antibacterial and antifungal properties of three species; *O. glaucifolia*, *O. macrocarpa*, and *O. serrulata*. Plant collections were conducted at the Pontotoc Ridge Conservancy and the Oka' Yanahli Preserve. Plant organs were separated and then ground down and put into a solution of either ethanol or methanol to extract chemical compounds. Using the extracts made, inhibition disc assays were conducted against bacterial and fungal species. The results were compared to a positive and negative control to view the efficacy of these plants. We expect that discs containing *Oenothera* extract will show a significant inhibition against both bacteria and fungi. We also expect that extracts made from organs such as the roots and seeds will perform the greatest due to the relatively high amount of secondary compounds they are expected to possess. The results will be important in showing the possible applications of medicinal botany in modern medicine. It will also illustrate the importance of Oklahoma's natural resources and the potential need for further conservation efforts.

Taylor Maze¹, Bryan Yockers², and Chad King¹ (¹University of Central Oklahoma; ²Jenks High School)

Poster 3

***PRELIMINARY RESULTS OF POST OAK TREE AGES AT TURKEY MOUNTAIN URBAN WILDERNESS AREA IN TULSA COUNTY, OKLAHOMA**

From western Texas and Oklahoma to New Jersey and south to Florida, post oak (*Quercus stellata* Wangenh.) is a long-lived tree species that gives a strong tree-ring record. This record can give an insight into historical climate conditions that can help scientists understand the effects of global climate change. In 2022, a potential ancient post oak forest was investigated at Turkey Mountain Urban Wilderness Area in Tulsa County, Oklahoma. We began research at Turkey Mountain Urban Wilderness Area to assess overstory post oak ages. We collected increment cores (n=27) at breast height and cross sections (n=7) from post oak stumps and snags. All increment cores and cross sections were sanded with progressively finer sandpaper to visualize cells under a microscope. To assign calendar years to each tree-ring, we cross dated samples using the computer program COFECHA and graphically. We dated seven living trees to the 1820's. There were six non-living trees that dated from 1822 to 1827. The oldest living tree we discovered dated to 1774 (248 y.o.). The oldest non-living tree dated to 1822. One cross section had potential fire scars that dated at 1835 and 1841, suggesting that surface fires were likely present at Turkey Mountain. These preliminary findings suggest that the Cross Timbers forest at Turkey Mountain Urban Wilderness Area contains living post oak trees that are 200+ years old. Further samples are being collected in 2022 and 2023 to identify other old post oaks in this urban setting.

Derek McGuire, Joshua Baer, Shania Do, Tiffany Jones, Abigail Kee, Karissa LeHew, Sarah Soliman, Sydney Spillane, Monica Vuong, Cari Marshall, and Ipe Paramel (Oklahoma State University Center for Health Sciences)

Poster 16

****LEAN HEALTHCARE: EVALUATION OF BED THROUGHPUT AT OSU MEDICAL CENTER**

Several factors play a role in an organization's success to function on a daily basis. For example, one factor being the application of efficient protocols to produce effective and consistent results. There is a specific procedure, called LEAN, that has been increasingly employed throughout various types of corporate professions due to its favorable outcomes. Originally, LEAN practices were created to enhance workflow and manufacturing processes in the automobile industry. After other industries observed the success rates from applying these certain methods, LEAN has been progressively adapted by many businesses to achieve similar effects. By adopting the LEAN methodologies, corporations have been able to increase their productivity, value, and client satisfaction. An example of how versatile and beneficial the LEAN approach can be in other fields, besides manufacturing, can be portrayed within a healthcare setting. There have been multiple healthcare organizations that have applied LEAN strategies to their systems in order to amplify quality improvement, with an end goal to better patient care. In this poster, a model is presented on how to apply and replicate LEAN tactics in an effort to advance bed throughput within a hospital setting. In the summer of 2022, a team of medical students from Oklahoma State University College of Osteopathic Medicine (OSU-COM) applied LEAN tools and techniques to examine the delayed process of bed throughput from the Emergency Department to the hospital floors. In doing so, possible solutions were developed in hopes to improve workflow, culture, and most importantly, patient outcomes.

Daniel McInnes and Charles Crittall (East Central University)

Poster 7

MOLECULES OF NATURE: A SUMMER ACADEMY FOR RISING 8TH AND 9TH GRADERS

The Molecules of Nature Summer Academy is a residential summer camp sponsored by the Oklahoma State Regents for Higher Education. The camp serves twenty rising eighth and ninth graders from Oklahoma, and is held on the campus of East Central University. The primary goal of the Academy is to demonstrate to participants that they can thrive while living and learning in a campus environment.

Madeline McTigue and William P. Ranahan II (Oral Roberts University)

8:30-8:45 in 353 Tandy

*TURMERIC FOR CANCER PREVENTION

Most chemotherapy, though advancing in its complexity, is killing healthy cells, and harming patients while generally providing low efficacy against tumor suppression. Given that many of the successful drugs on the market today are naturally occurring or designed from natural sources, a holistic cancer prevention model will be fundamental to fighting this disease, and plants are our best bet in preventing such an elusive illness. In 2011, scientists Douglas Hanahan and Robert Weinberg consolidated our understanding of cancer progression into ten “hallmarks of cancer”. The ten hallmarks of cancer describe the ten steps required for a normal or healthy cell to become tumorigenic. It is in these ten areas that cancer must be addressed to properly treat and prevent the disease from occurring. Medicinal plants and herbs were identified that biochemically interact with each of these hallmarks to prevent cancer progression. Of the identified plants, turmeric root was found to interact with the most hallmarks via its polyphenolic pigment curcumin. As such, we began to deduce the process of sterilization and tissue culturing the turmeric root. Once this process was successful, a callus was induced, providing the future site for epigenetic modification using a biolistic particle delivery system. The aim of such epigenetic modification is to upregulate turmeric’s expression of curcumin for a more potent anti-cancer product.

Zachary M. Mearse¹, William J. Moss², Caitlyn E. Rivera², Alexander K. Jochmans³, and Kevin M. Brown² (¹Oklahoma Christian University; ²University of Oklahoma Health Science Center; ³Rogers State University)

9:45-10:00 in D107 Lecture Hall

*EXPLORING PAIRWISE INTERACTIONS BETWEEN ENZYMES THAT REGULATE CYCLIC NUCLEOTIDE TURNOVER IN *TOXOPLASMA GONDII*

Toxoplasma gondii is an obligate-intracellular apicomplexan parasite that infects one-third of humans worldwide and causes the disease toxoplasmosis. *T. gondii* expresses a collection of phosphodiesterases (TgPDEs) to degrade the cyclic nucleotides cAMP and cGMP, which are required for the parasite’s lytic life cycle. Of the 18 TgPDEs, only 4 have been shown to be important for parasite growth. TgPDE2 is indispensable for cAMP turnover, but cGMP appears to be regulated by multiple TgPDEs. We hypothesize that cGMP is primarily degraded by TgPDE1 in cooperation with TgPDE5 and TgPDE9. Previously, we found that TgPDE1 does not physically associate with other TgPDEs. Here we developed new tools and tested whether combinatorial deletion of TgPDE1/5 and TgPDE1/9 is lethal in *T. gondii*. Previously, we generated a conditional knockdown mutant of TgPDE1. In this background, we used CRISPR genome editing to replace TgPDE5 and TgPDE9 with a drug selectable marker. Knockouts were validated by diagnostic PCR. To determine whether conditional loss of TgPDE1/5 or TgPDE1/9 is lethal, we performed plaquing assays on host cell monolayers as a measure of complete lytic parasite growth. We were able to generate a variety of new knockout plasmids by PCR and HiFi assembly. Using these constructs, we successfully generated and validated the TgPDE1/5 and TgPDE1/9 mutants. Ongoing plaquing assays are addressing the effect of combinatorial deletion of TgPDE1/5 and TgPDE1/9 on *T. gondii* growth. The new tools and data generated here provide the foundation for further studies investigating the role of TgPDEs in regulation of cyclic nucleotides required for host cell infection. Funding: Summer Undergraduate Research Experience (SURE), OUHSC.

Tyler Merrill, Logan Seeley, Yanel Otero, and Joel Sierra (University of Central Oklahoma)

8:45-9:00 in D107 Lecture Hall

*DECIBEL DETECTING DEVICE

Most hearing loss is gradual, though the rate is greatest during the first ten years of exposure. Continued exposure causes hearing loss of frequencies needed to hear speech. The average construction site noise level is around 85dBA. CDC reports that 51 percent of construction workers have been exposed to hazardous noise and 31 percent of those workers report not wearing hearing protection. Furthermore, approximately 14 percent of all construction workers have hearing difficulty. This piece of equipment will measure the soundwaves near these workers and alert them when it reaches an unsafe level. Many people don't know what “too loud” is, so by alerting you instead, this device will be the perfect solution. Once notified the workers can seek personal protective equipment, PPE, for their safety. Workers usually have ear-protection with them, but they simply don't wear them: due to bad habits, company culture, or lack of knowledge. The company will be receiving data to analyze for their own convenience. With this data they can identify areas of higher volumes and how long workers are exposed to dangerous levels. This way, supervisors can rotate workers, so the same group is not exposed to that unsafe level for extended periods. This device

will be of significant use for the user and consumer, making the work environment safer. This will be an extremely valuable tool to minimize lawsuits for companies from issues like this. Our decibel detecting device will reduce company lawsuits, increase hearing aid safety, and provide valuable data for their company. This project is very feasible physically, the more challenging aspect would be programming and getting these internet features to function properly. Our plan is to make this as general use, but with the research and studies gathered we will use industrial jobs as a reference to express the importance.

Joe Moberly and Janaki K. Iyer (Northeastern State University)

8:45-9:00 in D107 Lecture Hall

****DIFFERENT UROPATHOGENS INDUCE DIFFERENT INNATE IMMUNE RESPONSES IN BLADDER CELLS**

Urinary tract infections (UTIs) are a common bacterial disease. The most common uropathogen to cause a UTI is *Escherichia coli* (*E. coli*), followed by *Klebsiella pneumoniae* (*K. pneumoniae*). Treatment of UTIs involves an antibiotic regimen, but due to an increase in antibiotic resistance, antibiotic treatments are becoming less efficient. Increase in resistance among uropathogens creates a need for novel therapies and strategies to treat UTIs. The aim of this study was to determine whether different uropathogens elicit the same or different innate immune responses in bladder cells upon infection. Since uropathogens differ in the kind of virulent factors they express, we hypothesize that infection with different uropathogens will result in the expression of different inflammatory genes in bladder cells. We used strains of uropathogenic *E. coli* or *K. pneumoniae* as our uropathogens and human 5637 bladder cells as our host cell model. Total RNA from bladder cells infected with the uropathogens for 6 hours was purified and submitted to the Laboratory of Molecular Biology and Cytometry Research at OUHSC to evaluate the expression of inflammatory cytokines by Nanostring technology. nSolver software was utilized to analyze the data obtained, and we found that there was a differential relationship in the cytokines expressed by bladder cells in response to *E. coli* and *K. pneumoniae*. Evaluation of protein levels of some of these cytokines, like IL-6, showed that *E. coli* induced significantly more IL-6 secretion in bladder cells while *K. pneumoniae* inhibited IL-6 secretion. The results support the hypothesis that infection with different uropathogens results in the expression of different inflammatory genes in bladder cells. These findings provide the foundation for further studies to determine if modulation of cytokine production upon infection can be used to develop novel therapies for the treatment of UTIs.

Jay Modi and Trevor Magee (Oklahoma State University Center for Health Sciences)

Poster 58

****AN ANALYSIS OF HARMS REPORTING IN SYSTEMATIC REVIEWS REGARDING KETOROLAC FOR MANAGEMENT OF PERIOPERATIVE PAIN**

Due to the frequent perioperative use of ketorolac tromethamine and its ability to minimize postoperative opioid requirements, it is important to continually reassess harms associated with its use. Our primary objective was to investigate the extent of harms reporting in systematic reviews (SRs) on ketorolac for perioperative pain. In May 2022, we conducted a search of major databases, MEDLINE (Pubmed and Ovid), Embase, Epistemonikos, and the Cochrane Database of Systematic Reviews to identify eligible SRs on ketorolac for perioperative pain. Screening and data extraction was performed in masked, duplicate fashion. AMSTAR-2 was used to appraise the methodological quality of included SRs. Corrected covered area (CCA) was calculated to determine overlap of primary studies between SR dyads. A total of 28 SRs evaluating 630 primary studies met inclusion criteria. Seven SRs (7/28, 25%) reported no harms and 17 SRs (17/28, 60.7%) reported $\leq 50\%$ of harms items. A significant association was found between completeness of harms reporting and whether harms were specified as a primary outcome (P 50% but neither reported harms). The extent of harms reporting in SRs was inadequate. Given the importance that SRs have on guiding perioperative decision-making, it is essential to improve the completeness of harms reporting.

Jose Montalva (East Central University)

10:15-10:30 in 331 Tandy

TALES FROM THE GARDEN: CARBON FARMING A SUSTAINABLE ALTERNATIVE TO FIGHT GLOBAL WARMING

Some of the main elements responsible for global warming are greenhouse gasses: such as carbon dioxide (CO₂), methane (CH₄), and nitrous oxide (N₂O). One solution to this problem is to prevent these gasses from being released into the atmosphere. By composting, organic waste is turned into rich soil rather than sitting in a landfill. Organic waste in landfills is generally broken down over time anaerobically, conditions that tend to release large amounts of CH₄, a gas more potent than CO₂ in terms of trapping heat and thereby leading more rapidly to increased global temperatures. In addition, organic "trash" can mix with other elements in the landfill, creating toxic percolates that can leak into aquifers polluting water reserves. Recycling food scraps into compost generates rich and nutrient soil that does not require amendments or commercial fertilizers; the production of commercial fertilizers generates N₂O, another greenhouse gas. Moreover, the overuse of fertilizers often leads to the contamination of water sources with nitrates and phosphates. During the current season we started a composting program at the "OLE" Student Community and Experimental Garden. We have generated roughly 6 tons of soil so far during the research

season. The materials came from the following sources: Two tons came from recycled paper and cardboard collected at ECU, two tons of grass clippings were collected from the "OLE " Student Community and Experimental Garden. About 15 hundred pounds of food waste from Ada food Bank and 1 ton approximately of wood chip (horse bedding). It is estimated that 500 pounds of the overall compost weight was lost as water vapor during the entire procedure. We expect including the ECU cafeteria's food waste in the near future. Our compost pile towers' thermal energy is another source of future research.

Daniel Moore, Chase Sanders, and Daryll Burns (University of Central Oklahoma)

10:30-10:45 in E378 Forensic

***SMART 3D PRINTED CAP FOR DISORDERED NEURAL PATIENT**

The project's goal is to design a product that will provide real time data that relays the health of a disordered neural patient to a medical professional who would be able to initiate therapy through a LPEMF that would be low cost and non-invasive. To do this we followed 4 deliverables; design a setup that will record temperature, bpm, and brainwave values with Bluetooth compatibility, develop an app that will relay sensor values in real time, design a customizable 3D printed device to hold the LPEMF, sensors, and microcontroller, and lastly to design a low profile LPEMF to generate desired magnetic field. Depending on how the therapy device is utilized, it might find use in sports, medicine, defense, and any other profession where there is a danger of head damage. Having this apparatus in these areas can allow for a more immediate response from a doctor. By having a constant stream of data concerning the health of the patient there can be more deductions taken and can allow for more precision in the application of a treatment plan. This in turn will allow for a speedier recovery through the use of the LPEMF.

Rohaana Muhammad and Kyle Fitzgerald (Oklahoma State University Center for Health Sciences)

Poster 52

****ASSESSMENT OF THE REPORTING OF HARMS IN SYSTEMATIC REVIEWS FOCUSED ON CAR-T CELL THERAPY: A CROSS-SECTIONAL STUDY**

Our primary objective was to investigate complete reporting of harms in systematic reviews (SRs) on CAR-T therapy. Eligible SRs evaluating the effects of CAR-T therapy were identified by performing a search of major databases including MEDLINE (Pubmed and Ovid), EMBASE, Epistemonikos and Cochrane Databases for Systematic Reviews in May 2022. Investigators conducted screening and data extraction in a masked, duplicate fashion. AMSTAR-2 was used to assess the methodological quality of included SRs. Corrected covered area (CCA) was calculated for overlap of primary studies between SR dyads. Inclusion criteria was met for 45 SRs consisting of 929 primary studies. We found 13 SRs reported no harms, and reported less than 50% of harms items. AMSTAR-2 appraised 41 SRs as 'critically low' (41/45, 91.1%) and 4 SRs as 'low' (4/45, 8.9%). A significant association was found between completeness of harms reporting and whether harms were specified as an outcome. No other statistically significant associations were found. Three CCA dyads had a CCA > 50% and were compared to investigate shared or different harms reported. The assessment of harms reporting was found to be insufficient. Because of the importance of SRs in clinical therapy decision-making, it is essential to enhance reporting of harms in every aspect.

Stephanie Myers, Daniel J. Buck, Kelly McCracken, J. Thomas Curtis, and Randall L. Davis (Oklahoma State University Center for Health Sciences)

Poster 63

****B-FUNALTREXAMINE IS PROTECTIVE AGAINST LPS-INDUCED CXCL10 EXPRESSION AND BEHAVIORAL IMPAIRMENTS**

Inflammation plays a pivotal role in neurological and peripheral disorders. Specifically, inflammation is one of the common factors in diseases such as anxiety, stress, depression, Alzheimer's disease (AD), Parkinson's disease (PD), and inflammatory bowel disease (IBD). Thus, exploring potential treatments geared toward the assessment of inflammation is crucial to the continuation of treatment development. One pharmacological agent researched for its anti-inflammatory effects is β -funaltrexamine (β -FNA), a selective mu-opioid receptor antagonist. Preclinical studies using in vitro human astroglial cells showed that β -FNA inhibited inflammatory signaling, NF- κ B signaling, and chemokine expression in a mechanism unrelated to MOR. Also, β -funaltrexamines neuroprotective effects were discovered in a preclinical model of lipopolysaccharide (LPS)-induced neuroinflammation and sickness-like behavior when administered before LPS. This study determines the effects of β -FNA (50 mg/kg, i.p.) on LPS-induced (0.83 mg/kg, i.p.) sickness-like behavior using a 10 min open field test, and anxiety-like behavior, using a 5 min elevated plus maze in male and female C57BL/6J. It also assesses the effects on LPS-induced neuro and peripheral inflammation when β -FNA is administered immediately or 10 h post-LPS. Tissue collected included whole brain, hippocampus, prefrontal cortex, cerebellum/brain stem, spleen, liver, small intestine, large intestine, and plasma. Levels of inflammatory chemokine interferon gamma-induced protein 10 (IP-10, also known as CXCL10) was measured using an enzyme-linked immunosorbent assay (ELISA). Also, to our knowledge, this is the first time β -FNAs effect on female mice has been assessed. Differential effects of β -FNA were found between the whole brain vs. brain regions, central vs. peripheral, and sexes. This study provides insight into the inflammatory protection offered by β -FNA in both the central and peripheral systems and further knowledge of potential therapeutic options for neurological disorders.

Ayesha Nair, Ashlee N. Hawkins, and Karen L. Wozniak (Oklahoma State University - Stillwater Campus)

10:00-10:15 in D107 Lecture Hall

****THE ROLE OF DIFFERENTIALLY-REGULATED GENES IN THE OUTCOME OF MURINE PHAGOCYTE-CRYPTOCOCCAL INTERACTION**

Cryptococcus neoformans is a causative agent of cryptococcosis and can survive intracellularly, leading to cryptococcal meningitis. The primary route of infection is inhalation. The pathogen first interacts with pulmonary macrophages and dendritic cells (DCs). These have been purified from the lungs of naïve mice: alveolar macrophages, interstitial macrophages, Ly6c⁺ and Ly6c⁻ monocyte-like macrophages, CD11b⁺ and CD103⁺ DCs. Following interactions of each subset with *C. neoformans*, the Ly6c⁻ monocyte-like macrophages from female mice significantly inhibit fungal growth, while CD11b⁺ DCs from male mice significantly enhance fungal growth. RNA sequencing revealed that MHC I gene H2-K1 and Cyp1b1 gene were differentially regulated. We hypothesize that differentially-regulated genes and pathways are integral in determining the outcome of *C. neoformans* intracellular interaction with pulmonary macrophage and DC subsets. For these studies, we examined antifungal activity of Cyp1b1 KO bone marrow-derived DCs (BMDCs) against *C. neoformans*. We examined gene expression over time of H2-K1 in macrophage cell lines following exposure to *C. neoformans* strain H99 to determine optimum time points for gene silencing. Additionally, we examined H2-K1 gene expression in macrophage cell lines at different timepoints following exposure to UV-killed and heat-killed H99. We also looked at the expression of MHC-I protein in *C. neoformans* treated macrophages by flow cytometry. Results showed that incubation with Cyp1b1 KO BMDCs resulted in significantly greater cryptococcal growth compared to WT BMDCs, suggesting a role for this gene in antifungal activity. We also observed induction of H2-K1 gene expression following incubation with live, heat-killed and UV-killed H99. Future studies will continue to examine the roles of MHC I and CYP1B1 in antifungal activity thereby being potential therapeutic targets for preventing cryptococcal dissemination to the brain.

Jacob Nakanashi¹, Mubaraak Akinbola¹, Nesreen Alsbou¹, and Imad Ali² (¹University of Central Oklahoma; ²University of Oklahoma Health Science Center)

9:30-9:45 in E378 Forensic

***INCREASING THE NUMBER OF ANTENNAS AND SWEEPING DIFFERENT FREQUENCIES TO ENHANCE MICROWAVE IMAGING SYSTEM RESOLUTION**

This research aims to enhance the resolution of images obtained using a microwave imaging system for different phantoms representing different parts of the human body. The Microwave Imaging System is considered more advantageous than other available imaging systems like x-rays, CT scans, and MRIs. CT scans are preferred for identifying specific cancers, such as lung, and liver, but CT scans expose the patient to ionizing radiation which can cause damage to healthy tissues while MRI consumes more power and a huge equipment setup. The microwave imaging system used in the lab consists of a vector network analyzer, antennas for transmitting and receiving RF signals, SPDT and SP8T switches to allow for multiple antennas to be added to the system to increase the image resolution. Microwave Imaging equipment is not expensive compared to other Imaging techniques, making microwave imaging a cost-effective technique. The immediate objective of this research project is to get images of different objects with a different frequency range using vector network analyzer to sweep over different frequencies and different kinds of antennas to determine what range or antenna array configuration is best used to get clearer and better images for each scan. The system used is portable which makes it easily move to scan different objects at different locations compared to the currently available huge imaging modality. The system will be characterized and the data collected will be analyzed to find the relation between the different types of antennas, increased number of antennas, different frequency ranges used and the quality of images obtained.

Katherine Nehmzow, Abby S. Rigsbee, Christopher Godman, Sam Hudgeons, Sue Katz Amburn, and Franklin R. Champlin (Northeastern State University)

Poster 23

***CELL SURFACE HYDROPHOBICITY PROPERTIES AND BIOFILM ADHESION IN OPPORTUNISTIC *SERRATIA* SPECIES HAVING DISPARATE SUSCEPTIVITY TO TRICLOSAN SENSITIZATION**

We have shown all but one of 10 *Serratia* species capable of opportunistic pathogenicity to be intrinsically resistant to the hydrophobic biocide triclosan. However, they differed markedly regarding their susceptibility to triclosan sensitization by outer membrane permeabilization using the cationic detergent compound 48/80. Representative organisms exhibiting slight (*Serratia marcescens*), complete (*Serratia fonticola*), transitorily complete (*Serratia liquefaciens*), and intermediate (*Serratia rubidaea*) susceptibility were selected for further analysis. The purpose of the present study was to determine if cell surface hydrophobicity properties of these phenotypically disparate *Serratia* species are related to susceptibility to triclosan sensitization and the initial adhesion stage of biofilm formation. NPN fluorescent probe and hydrocarbon adherence assays were employed to quantitatively determine cell surface hydrophobicity properties, while an in vitro biofilm assay was used to assess adhesion of planktonic cells to a solid substrate. While *S. rubidaea* was seen to be extremely hydrophobic, *S. marcescens* and *S. liquefaciens* were only

slightly to moderately hydrophobic, and *S. fonticola* was seen to be hydrophilic to slightly hydrophobic. These data do not appear to support the notion that the degree of susceptibility to triclosan sensitization by outer membrane permeabilization is directly related to cell surface hydrophobicity. However, the initial adhesion stage of biofilm formation appears to be influenced to some degree by cell surface hydrophobicity properties.

Ashley Nguyen, Kayla Nguyen, Stephanie Rojas, Lindsey Morris, and Christina Hendrickson (Oklahoma City University)
Poster 21

***INVESTIGATING ANTIMICROBIAL EFFECTS OF AQUEOUS DANDELION EXTRACT**

Certain plant-derived products have pharmaceutical uses due to their anti-inflammatory and anti-cancer effects. Dandelion (*Taraxacum officinale*) is one of them. 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 DWE. The disk diffusion method was utilized to test various concentrations (5 - 100 mg/mL) of DWE on bacterial growth. DWE was tested on six bacteria: *Escherichia coli*, *Citrobacter freundii*, *Morganella morganii*, *Salmonella typhi*, *Staphylococcus aureus*, and *Neisseria sicca*. All bacterial cultures were incubated at 37 °C for 24 hours. Isolated bacterial colonies were 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. A Mueller-Hinton Agar plate devoid of bacteria was treated with DWE disks to serve as a control to ensure the DWE disks did not introduce contamination. After incubation, all plates were visualized for indication of DWE impact on bacterial growth. The results showed no zone of inhibition; indicating all six bacteria were resistant to aqueous DWE in this method. In the future, broth dilution antibiogram assays will be conducted utilizing additional bacterial species and different formulations of dandelion extracts.

Kayla Nguyen, Ashley Nguyen, Stephanie Rojas, Lindsey Morris, and Christina Hendrickson (Oklahoma City University)
Poster 21

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Jordan Odell-Brown and Alisha Howard (East Central University)
Poster 38

***INVESTIGATION OF BOVINE LEUKEMIA VIRUS (BLV) PREVALENCE IN OKLAHOMA HERDS**

Bovine leukemia virus (BLV) is an oncological retrovirus infecting a significant number of cattle globally. The economic consequences of BLV infection in cattle herds are sizable, with both direct and indirect costs of BLV infection cutting into already slim profit margins. It is estimated that \$283 is lost per milking cow infected with BLV, which accounts for a \$2.7 billion national deficit.¹ While the clinical presentation of BLV in the form of B-cell leukemia affects only a small number within the infected population (1-5%), the virus is also known to cause widespread immunological deficiencies leading to a decreased ability to resist infection by other pathogens. These immunocompromised individuals experience decreased production, lifetime in the herd, and reproductive success. Despite the potential economic impact, the prevalence of BLV infection in many herds is unknown. Residual BLV particles also have the potential to impact human health. This was supported by previous findings of BLV reactive antibodies in human tissue, BLV DNA in human blood, and the presence of BLV DNA in human breast tissue.² The purpose of this research is to determine the prevalence of BLV in dairy and beef products for human consumption. This can be done by assaying the presence of BLV RNA, DNA, or protein in raw milk samples. Milk specimen collections are ideal for both convenience and follow established BLV transmission routes. This work will establish impact of this virus in food sources and lay the groundwork for understanding any potential infectivity of BLV viral particles or cross-reactivity of BLV proteins in human systems.

Olabode Victor Olayode, Anabelle Mamie Hawkins, and Renan Bosque (Southwestern Oklahoma State University)
Poster 6

***THE INTERPLAY BETWEEN LIGHT AVAILABILITY, WARNING SIGNALS AND PREDATION RATES ON WESTERN DIAMONDBACK RATTLESNAKE**

Most Research into the adaptative significance of visual warning signals has focused on the coloration and pattern of animals. However, the perception and interpretation of visual warning signals by predators can be affected by the amount of light available, a topic often overlooked by scientists. The western Diamondback Rattlesnake (*Crotalus atrox*) has a diamond-like pattern on the dorsal portion of its body, which is hypothesized to act as a warning signal, reducing the predator's willingness to attack. To date, no study has been performed in the wild to test the effect of light conditions on the attack rates of snakes that have diamond shapes as a warning signal. Predation of snakes can be conducted in the wild using clay-model replicas resembling different snake phenotypes. In our project, we will use these replicas to assess the effect of the amount of light and willingness to attack snakes with diamond patterns. The replicas will be released into various locations and the light availability will be recorded with data loggers. Every two days, we will check the imprint on the replicas to evaluate the rate at which the replicas have been attacked by predators. Our study will help to elucidate whether light influences the effectiveness of the warning signal present in the western diamondback rattlesnake.

Moses Omeneki¹, Kwabena Boateng¹, Imad Ali², and Nesreen Alsbou¹ (¹University of Central Oklahoma; ²University of Oklahoma Health Sciences Center)

10:15-10:30 in E378 Forensic

****MICROWAVE IMAGING SYSTEM (PASCO SYSTEM) MOTION DETECTION AND TRACKING OF MOBILE PHANTOM FOR HUMAN TISSUE**

Breast cancer is a disease that occurs mostly in female cancer patients and is the leading cause of cancer-related death among females worldwide. Breast screening and early detection are currently the most successful, most common method for the management, reduction, and treatment of this disease or mortality rate. Various imaging methods such as X-ray and MRI are currently utilized for detecting breast cancer. Microwave Imaging is gaining quite a lot of attention as a promising diagnostic tool for early breast cancer detection. MWI is inexpensive, fast, convenient, and a safe screening tool. The purpose of this research is to use a specially designed object that is utilized as a human tissue equivalent material and can be scanned/imaged to evaluate, analyze, and fine-tuned the performance of an imaging device. This is an effort to provide an update on the principles, developments, and current research status of MWI for breast cancer detection. The project is structured to provide an overview of MWI system techniques used for detecting the motion of fourteen different human tissue equivalents to provide reliable and quantitative data to determine how effective an imaging system is compared to imaging systems used in a real-world setting. For this project, a Pasco system consists of a transmitter, a receiver, a breadboard circuit, an Arduino, a stepper motor driver, a computer, and a DC power supply. The innovative technique of the MWI system is significant in that it has the potential to provide a safe and reliable method of enhancing the overall performance of imaging systems in a very safe, cost-effective, and non-invasive way before it can be applied in a clinical setting.

Lydia Ostmo and Sapna Das-Bradoo (Northeastern State University)

10:00-10:15 in 333 Tandy

****INVESTIGATING THE EFFECTS OF A POLE GENE MUTATION ON PROTEIN-PROTEIN INTERACTION IN FILS SYNDROME**

Accurate DNA replication in human cells is crucial to our health and survival. Errors during the process can lead to disease and genomic instability. One of the crucial proteins involved in the DNA replication process is Polymerase Epsilon, or POLE, which performs leading strand DNA synthesis. POLE has four subunits, with POLE1 being the catalytic subunit. Mutations in the C-terminus of POLE1 have been linked to FILS Syndrome, which stands for facial dysmorphism, immunodeficiency, livedo, and short stature. Our lab has shown that mutations in the C-terminus of POLE1 disrupt its interaction with Minichromosome Maintenance Protein 10 (MCM10), another protein involved in DNA replication and repair. The goal of this project was to investigate POLE1 and MCM10 interaction in mammalian cells and study the effects of the POLE1 FILS mutant on this interaction. We employed fluorescence microscopy, immunoprecipitation and western blot analysis to examine the expression of plasmid-based POLE1 and the POLE1-FILS mutant within HEK293T cells. We also used siRNA to knock down the endogenous expression of POLE1, and analyzed the extent of that knockdown using qPCR. Fluorescence microscopy confirmed the expression of POLE1-RFP and GFP-MCM10 in the nucleus of HEK293T cells. Expression of truncated POLE1 FILS protein was observed by western blot. Co-immunoprecipitation experiments confirmed that POLE1 and MCM10 interact in mammalian cells. In addition, our preliminary data demonstrates that the FILS truncated protein still interacts with MCM10. qPCR and western blot analysis confirmed the knockdown of endogenous POLE using siRNA. Our data suggests that POLE1 and MCM10 interaction is conserved from yeast to humans. The FILS truncated mutant did not disrupt this interaction. Since the mutation is associated with a biological consequence in humans, we plan to further investigate the ability of this mutant to form a functional Pole complex and carry out error free DNA replication.

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

10:15-10:30 in 351 Tandy

*EFFECTS OF MULTIPLE POLYCYCLIC AROMATIC HYDROCARBONS ON CARDIAC DEVELOPMENT IN CHICK EMBRYOS

Following oil spills, avian embryos may be exposed to polycyclic aromatic hydrocarbons (PAHs) when crude oil is transferred from oiled nesting material or oiled feathers of brooding parents to the eggshell surface. While several studies have examined the effects of PAHs on adult birds, the developmental effects of embryonic exposure to PAHs remain unclear. In other taxa, like fish, embryonic exposure to PAHs causes cardiac impairments like bradycardia and a decline in cardiac output. Similar trends have been detected in avian embryos, specifically external application of crude oil to the eggshell reduces embryonic heart and metabolic rates. However, the mechanism and specific PAHs driving these effects in developing avian embryos are still poorly understood. This experiment investigated the effects of sublethal exposure of six PAHs (anthracene, phenanthrene, pyrene, chrysene, benzo[a]pyrene, and fluoranthene), at four concentrations (100, 200, 400, and 800 ng PAH / g egg mass), on avian embryonic heart rate, heart organ mass, morphology, and mRNA expression of phase I and phase II detoxification enzymes. We exposed chicken (*Gallus gallus*) embryos to PAHs on embryonic day (ED) 3 via egg-injection. We recorded heart rate on ED 10, 14, and 18, and collected heart organ mass, morphology, and transcriptional data on ED 18. Chick embryos exhibited a decrease in ED 18 heart rate at the highest concentrations for fluoranthene, phenanthrene, chrysene, and pyrene. Additionally, we found an increase in heart mass in chicks exposed to phenanthrene, pyrene, chrysene, and fluoranthene at intermediate concentrations. Preliminary results also indicate several transcriptional responses in chicks exposed to various PAHs. Collectively, these data indicate in ovo exposure to various PAHs interferes with avian embryonic development and may contribute to reduced hatchling survival, especially if these impaired cardiac functions continue post-hatch.

Somalisa Pan, Mary Erdmann, and Matthew Cabeen (Oklahoma State University - Stillwater Campus)

10:15-10:30 in 333 Tandy

A ROLE FOR A LIPASE IN PTSN-MEDIATED BIOFILM SUPPRESSION IN *PSEUDOMONAS AERUGINOSA*

Pseudomonas aeruginosa (PA) is an opportunistic pathogen that is widely known for infecting patients with underlying conditions – for example cystic fibrosis, chronic burn wounds, and immune disorders. What makes it even more concerning is its ability to resist many antibiotics by forming biofilms, in which cells produce a protective extracellular matrix. PA also produces numerous virulence factors that enhance its ability to infect and cause disease. One signaling pathway in PA that influences virulence is the Nitro-PTS. This phosphotransferase system that consists of a kinase, PtsP, a phosphocarrier, PtsO, and a terminal phosphate receptor, PtsN. The physiological role of the Nitro-PTS in PA is poorly understood. However, PtsN when deprived of its upstream kinase or phosphocarrier, has an antagonistic effect on biofilm formation, suggesting a suppressive effect of unphosphorylated PtsN on biofilm formation. We next hypothesized that the phospho-state of PtsN regulates biofilm formation via other factors. We thus conducted a transposon mutagenesis screen in an unphosphorylated PtsN background to identify downstream proteins with unacknowledged roles in PtsN-mediated biofilm suppression. We found an unnamed gene, 04030, whose disruption restored biofilm production. This gene encodes an alpha/beta hydrolase bearing a lipase signature motif with an active-site Ser residue. Deletion of this gene in an unphosphorylated PtsN background increased biofilm formation, suggesting 04030 might work with unphosphorylated PtsN to suppress biofilm formation. Moreover, substituting the putative catalytic Ser for Ala phenocopied 04030 deletion, indicating it is important for the activity of 04030 in vivo. As our preliminary data suggests that 04030 is a lipase, we did lipidomics to study any differences in the lipid profile between PA in the presence and absence of 04030. 04030 might represent a new element of biofilm signaling in this important human pathogen.

Radhika Pande and Subhas Das (Oklahoma State University Center for Health Sciences)

9:45-10:00 in 333 Tandy

**EPIGENETIC MECHANISMS HOLD THE KEY TO DEVELOPING NOVEL THERAPEUTIC TREATMENTS FOR ULCERATIVE COLITIS

Background: Inflammatory bowel disease (IBD) includes Crohn's disease (CD) and ulcerative colitis (UC) and is associated with symptoms like abdominal pain, diarrhea, fatigue, reduced appetite, and weight loss. According to CDC, approx. 3 million Americans are reportedly diagnosed with IBD. Compared to normal individuals, IBD patients are more prone to colorectal cancer and arthritis. The causes of IBD are unknown; however, environmental, nutritional, microbiological, and genetic factors have been suggested to play a role in disease development. Nerve Growth Factor (NGF), a neurotrophic factor, is significantly elevated during several inflammatory and autoimmune diseases, including IBD and is essential for a robust inflammatory response. Studies suggest the importance of epigenetic mechanisms in chronic gastrointestinal inflammation and colorectal cancer, offering important insights into IBD's molecular basis. Although epigenetic regulators are well-explored in IBD, the regulations controlling NGF gene expression are unknown. Epigenetic modifications, including DNA methylation and covalent histone modifications, influence gene expression at the transcription level without altering the DNA sequence. We found that colon inflammation causes hypermethylation of the NGF promoter, resulting in its activation. Hypermethylation recruits proteins containing methylated DNA binding domains (MBDs), such as MeCP2. The evidence suggests that MeCP2 links DNA methylation and histone modifications to control gene expression. Aim: To understand the involvement of MeCP2 and identify novel histone modifications associated with NGF transcription. Method: TNBS-induced colitis animal model was used for this study. After inflammation, colon tissue was collected to study the DNA-protein and protein-protein interactions by Chromatin-immunoprecipitation-assay and Immunoprecipitation-assay, respectively. Results and Conclusion: Our findings show that MeCP2 and tri-methylation of histone 3 lysine 4 (H3K4me3) are elevated during the TNBS-induced inflammation compared to

control animals. ChIP and pull-down assays prove that MeCP2 interacts with H3K4me3, and both are associated with the hypermethylated NGF gene promoter for the active transcription during colon inflammation.

Diya Patel (Oklahoma State University Center for Health Sciences)

Poster 30

TESTING THE ABILITY OF JETPEI REAGENT TO TRANSFORM BACTERIA AND *C. ELEGANS*

JetPEI(JP) is marketed as a transformation reagent for mammalian cells. This experiment tests the effectiveness of JP transformation on other types of organisms, specifically bacterial cells and *Caenorhabditis elegans*. Using worm plasmids KG#276 and pGLOW30, both of which contain genes that code for proteins which fluoresce when exposed to red light. KG#276 also contains a gene for ampicillin resistance. JP's ability to transform bacteria was tested on whether Top10 competent cells, *Pantoea nemovictus* (BIG0393), and lactic bacterial strain *Leuconostoc mesenteroides* (L.m) fluoresced. Amino acid glutamine (G) was added to L.m JP transformations to determine if it could enhance plasmid uptake. Further experimentation tested if the plasmids successfully integrated into bacterial genome could be transformed into *C. elegans*, thereby allowing them to fluoresce under the microscope. A separate rescue plasmid pBX was also tested to demonstrate the effectiveness of JP transformation on pha-1 mutant *C. elegans* strain RM2256. The gene mutation in this strain hinders growth at 25°C. Inserting pBX into their genome would enable them to survive at higher temperatures. Based on the experimental results, JP was able to transform all bacterial strains. pBX was able to transform in some *C. elegans*, but it was undetermined if pGLOW30 was transformed.

Asiah Powers¹, Madison Stephens¹, Lena Marcikic¹, G. Caroline Schwab¹, Tyler Godsey¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 36

*THE EVOLUTIONARY CONSERVATION OF DOCK AS COMPARED TO RICTOR IN THE INSULIN-LIKE RECEPTOR PATHWAY

The Insulin/TOR Signaling Pathway evolves in *Drosophila* as the species become further diverged from *Drosophila melanogaster*. In this study, a comparative genomics approach was used in order to determine the levels of conservation of two genes, rictor and dock, of the insulin pathway. A variety of genes from the *Drosophila* genus were annotated based on elements like genomic neighborhood and gene structure. Each gene annotated also had isoforms which varied in amino acid sequences and number of exons. We used this information to determine the organisms' evolutionary relationship to *D. melanogaster*. The scores were then compared using a bar graph which demonstrated divergence levels. The results demonstrated dramatically higher divergence scores of rictor than dock which was earlier on the pathway than rictor. Results indicated that dock was more conserved than rictor. Future research could be done to determine if other genes that are also early in the pathway are more conserved than those later in the pathway.

Toni Proctor, Logan Swope, Ashlee Bradley, Anil Kaul, and Rashmi Kaul (Oklahoma State University Center for Health Sciences)

Poster 57

**PREVALENCE OF *CHLAMYDIA TRACHOMATIS* AND *NEISSERIA GONORRHOEAE*: PRE AND POST COVID LOCKDOWN

Chlamydia trachomatis (CT) and *Neisseria gonorrhoeae* (NG) are two of the most common Sexually transmitted diseases (STDs) (Rowley et al., 2016) with almost 1.6 million CT cases reported in 2020 and an estimated 1.14 million NG cases yearly in the United States. The SARS-Cov-2 pandemic has infected ninety-six million Americans and caused over a million deaths (CDC). According to the American Society for Microbiology, focused efforts on SARS-Cov-2 had a negative impact on STD control measures. Further, Sars-COV-2 resulted in disruption of prevention and treatment to various infectious diseases such as tuberculosis, human HIV, and dengue fever (Downey et al., 2022). Restrictions due to the pandemic resulted in reduced routine STD testing. At the Oklahoma State University (OSU), regular STD testing is done in the OSU Clinical laboratory on the university campus in Tulsa. Test results were collected and analyzed to compare the prevalence of CT and NG cases, before and after the SARS-Cov-2 lockdown. We aimed to determine the impact pandemic lockdown protocols had on STD numbers, specifically CT and NG. Statistical analysis using an independent t-test and chi-squared test of independence showed that there was not a statistically significant ($p > 0.05$) difference in cases for CT when comparing pre- and post-lockdown measures for SARS-Cov-2. However, there was a statistically significant increase ($p < 0.05$) in NG rates when comparing pre-lockdown to post-lockdown. Future correlations can be done with data from recent months to further solidify the relationship that the pandemic has had on CT and NG numbers, and ultimately STD prevalence. This study explored the relationship SARS-Cov-2 lockdown measures had on CT and NG positivity rates. Our findings indicate the pandemic lockdown had an impact on NG rates potentially resulting from clinical service interruption due to the lockdown measures.

Huxley Rainwater (Northeastern State University)

Poster 43

*IDENTIFICATION OF THE CAUSATIVE AGENT OF BACTERIAL LEAF SPOT DISEASE IN PEPPER IN OKLAHOMA

Chili pepper (*Capsicum annuum*) is a cash crop that belongs to the family Solanaceae. In 2020, worldwide production of green chili production reached to be 36 million tons. Unfortunately, peppers are susceptible to many bacterial diseases, and among them, *Xanthomonas* leaf spot disease is considered one of the major bacterial diseases in pepper and tomato. Bacterial leaf spot disease is caused by *Xanthomonas campestris* pv. Vesicatoria and symptoms of the disease on above-ground parts of the plant include leaf spot, fruit spot, and stem canker. Symptomatic pepper leaf samples with water-soaked brown-to-back spots were collected from Oklahoma, and the causative agent of the spot disease was isolated by surface sterilizing isolated leaf spots and plating them on nutrient agar. Plates were incubated at 25°C for 48 hours, and five pure cultures of bacteria were isolated. All these bacterial isolates were subjected to staining, several biochemical test, and differential media to confirm the identity of the bacteria. Further PCR using universal primers for 16 S rRNA gene was carried out. All pepper isolates were gram negative, catalase positive, motile, utilize citrate, and are MacConkey positive lactose non-fermenting. We also used a previous squash isolate with similar morphology that had opposite results of no citrate utilization, negative MacConkey, and all samples varied for oxidase and triple sugar ion results. The five bacterial isolates were inoculated onto three-week-old pepper plants. Four out of the five peppers with isolates, including the squash isolate, are presenting symptoms of whitening of the injection spot, and curling of the leaves. This indicates that the original isolates were likely those that cause the infection in the original peppers and squash. The DNA of these isolates will be sent for sequencing to further identify the bacteria.

Lucy V. Ramirez, Luke M.D. Woodward, and Eric Howard (East Central University)

Poster 50

*STREAMLINING SPECIES ANALYSIS PROGRAM

Competent disease vectors in Pontotoc County remain mostly unidentified due to a traditional identification system with high labor and financial costs. A research process to ascertain a robust specimen identification method was developed and tested for use in longitudinal vector competence identification program in Pontotoc Co., OK. We hypothesize that with the use of competent vector-specific primer design, a mixed pool of multiple unidentified mosquitoes could be identified as containing known competent vectors; this would be a useful tool, leading to efficient hazardous vector identification. DNA was extracted from mosquito samples collected in Pontotoc county. This was followed by DNA amplification via polymerase chain reaction (PCR) using standardized barcoding primers. Gel electrophoresis was used to verify that sufficient amplification occurred prior to Sanger sequencing. Successful sequences were confirmed by forward and reverse assembly followed by species identification using NCBI BLAST. DNA from over 100 mosquito specimens have been successfully extracted, amplified, and sequenced. Of those samples the majority have been identified at the species level. These results have been sorted into vector competence categories. With a streamlined approach, disease risk can be more easily and consistently mitigated when the prevalence of competent disease vectors is identified. Being able to identify competent vectors quickly, will allow for increased public awareness concerning mosquito transmitted diseases. This project was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award P20GM103447. The content in this publication is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Jack Rea¹, Chase Lee¹, Micah Kee¹, Brayden Rucker¹, Holly Flores¹, Corbin Walters², Taryn Haney², Alicia Tomlin², & Matt Vassar¹ (¹Oklahoma State University Center for Health Sciences; ²School of Global Public Health, New York University)

Poster 55

**HARMS REPORTING ASSESSMENT REGARDING SYSTEMATIC REVIEWS FOCUSING ON DIRECT ORAL FACTOR XA INHIBITORS: A CROSS-SECTIONAL STUDY

Our primary objective is to evaluate the quality and completeness of harms reporting in systematic reviews (SRs) regarding factor Xa inhibitors through a cross-sectional analysis. We searched MEDLINE (PubMed and OVID), EMBASE, Epistemonikos, and Cochrane Database Systematic Reviews for SRs comprised of randomized control trials (RCTs) designed to evaluate direct oral factor Xa inhibitors. We performed screening and data extraction for harms among eligible SRs in a masked, duplicate fashion using a pilot-tested Google Form. This form, based on the published work of Qureshi and colleagues, quantified the reporting of harms among SRs. AMSTAR-2 was used to evaluate the methodological quality of the included SRs. Corrected covered area (CCA) was calculated for overlap of primary studies between SR dyads. Approximately 70 SRs comprising 242 unique primary studies met inclusion criteria and were included in the present study for analysis. Of these 70 SRs, 69 (69/70, 98.6%) reported harms as a primary outcome. Further, 23 SRs (23/70, 32.9%) completed 50% or less of harms items. Seven (7/70, 10%) SRs reported the total number of patient treatment discontinuations. Less than half of SRs (38/70, 54.3%) established severity scales to evaluate harms. CCA data showed 12 studies containing 50% or higher CCA values and many contained less than 50% overlap for harms. No statistically significant associations were found. We found the overall reporting of harms to be incomplete. Because SRs are often viewed for clinical practice, improvements must be made to better report harms.

Dixie Redman, Ghastin Harjo, Elijah Woodward, and April Nesbit (East Central University)

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*DETERMINE FUNCTION OF YFAX IN *ESCHERICHIA COLI*

Escherichia coli (*E. coli*) is most commonly thought of as a harmful bacterium. Contrary to this belief, *E. coli* is actually found in the gut microbiome of most healthy humans. The YfaX protein is hypothesized to be a transcription factor that regulates in

response to rhamnonate as part of the yfaXWVU operon. YfaW, YfaV, and YfaU are expected to transport and metabolize rhamnonate, which would create a feedback loop. To determine whether YfaX functions as a transcription factor in response to rhamnonate, we first had to create a promoter fused to the lacZ reporter gene on the chromosome, and we decided to use the *adiA* promoter and the *bluF* promoter for this because Shingen et. al. showed that YfaX binds these promoters in vitro. Initially, the promoter was placed on a plasmid next to a partial lacZ gene. Then we recombined the promoter-lacZ onto the chromosome using electroporation of the PCR product created by primer lacI-Kn at the 5' end and primer lacZ corr at the 3' end. We then performed a colony PCR in order to verify that desired promoter-lacZ fusion was inserted on the chromosome. Our PCR indicates that we successfully inserted the promoter-lacZ fusion onto the chromosome. The next step is to create strains with and without yfaX gene to determine whether there is a difference in regulation of these promoters.

Gwen Reilly, Senait Assefa, and Gerald Koehler (Oklahoma State University Center for Health Sciences)

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****BIOMARKER DISCOVERY IN MICROBIOME PROFILES**

Trillions of bacteria, archaea, fungi, and viruses comprise the human microbiome and virome. The composition and diversity of these complex communities have a profound impact on the health of their human or animal host. Embedded in these communities might be groupings such as individual bacterial species/strains or consortia that have key roles and could serve as biomarkers for host health and disease. We are collecting microbiota and microbiome profiles from humans and animals to identify such specific markers for dietary intake, inflammation, infection, and other health or disease related outcomes. Next-generation sequencing systems are used for 16S ribosomal RNA analyses and whole-genome shotgun metagenomics to determine taxonomic profiles and predict functional profiles of the microbial communities. Correlation of these profiles with host metadata will aid in the identification of potential biomarkers of health and disease. Examples of workflows and bioinformatic approaches will be presented that illustrate how biomarkers discovery could lead to novel diagnostic targets and preventative or therapeutic interventions.

Jessalyn Rivet-Tissot (Oklahoma State University Center for Health Sciences)

Poster 65

****CLOSTRIDIUM BUTYRICUM MAYAIRI BACTERIOCIN (CBMB) AGAINST CLOSTRIDIODES DIFFICILE**

Clostridioides difficile is the leading cause of antibiotic-associated diarrhea worldwide and infects approximately 200,000 people annually in the United States. *C. difficile* is a gram positive, anaerobic, spore forming bacterium that takes advantage of the disruption of the gut microflora during antibiotic treatment. *C. difficile* spores germinate in the small intestine and rapidly proliferate in the colon leading to infections that can lead to sepsis and death if left untreated. Vancomycin and metronidazole are the antibiotics of choice for *C. difficile* infections (CDIs). However, relapsing cases are often common while the risk of developing antibiotic resistance is high. Therefore, it is critical to develop alternative treatment strategies against *C. difficile*. Previously, our lab screened multiple non-pathogenic commensals for their ability to inhibit *C. difficile* in vitro. Currently commercialized as a probiotic, *Clostridium butyricum* Mayairi bacteriocin (CBMB) was shown to have the highest inhibitory effect on multiple strains of *C. difficile* in vitro. Currently we have successfully cloned and purified recombinant CBMB. Results from our laboratory show an equal to greater effectiveness of the bacteriocin compared to the current antibiotics. In this study, our goal is to assess the activity of the bacteriocin on several strains of *C. difficile* as well as other similar bacterium. The goal of the research would be to find a novel treatment for CDIs that would avoid reoccurring cases and antibiotic resistance risks.

Daniel Rocha, Natalie Shreffler, Cait Hudgens, and Sydney Oliver (Southern Nazarene University)

10:30-10:45 in 351 Tandy

FACTORS THAT AFFECT AMAZONIAN TERRESTRIAL MAMMAL DISTRIBUTIONS

Tropical forests are among the most biologically diverse areas on the planet. The Amazon Rainforest represents about 50% of the remaining tropical forests and hosts over three million different species. Of these species, mammals play vital roles in ecosystems across the globe such as predators, prey, seed dispersers, ecological engineers, and therefore are of conservation importance. The decline in mammal populations, particular large bodied ones, is a pressing issue globally, including in the Amazon forest. The first step to mitigate and prevent mammal declines, is to understand factors that affect mammal distributions. In this study, we used data from 182 camera trap sites from four different protected areas (Samuel Ecological Station, Amana Nature Reserve, Corumbiara State Park, and Guaporé Biological Reserve) of three Amazonian terrestrial mammal species (paca *Cuniculus paca*, white-collared peccary *Pecari tajacu*, and mountain lion *Puma concolor*). We used camera trap data in combination with remote sensing satellite data and hierarchical occupancy modeling to identify environmental and anthropogenic factors that influence species distribution in the Brazilian Amazon. Our results suggest that puma was positively affected by elevation. Paca was negatively affected by elevation and human footprint index. White-collared peccary negatively affected by forest fragmentation. Net primary productivity had a positive effect on the three species studied. Our results support that species occurrence is related to habitat quality and that the increasing human presence in the Amazon will likely negatively affect species distributions, which might require active conservation management.

Kyler Rogers¹ and Oliver Beckers² (¹University of Central Oklahoma; ²Murray State University)

9:00-9:15 in 351 Tandy

DIFFERENTIAL HOST USAGE IMPACTS LIFE HISTORY STRATEGY IN A GENERALIST PARASITOID

Mating signals of insects are often conspicuous to attract their intended receivers, but these signals can also attract eavesdropping predators. Species interactions can be driven by selective pressures. Thus, signal exploitation can promote an arms race between signaler and receiver with a high potential for introducing diversity in the involved species. Here, we present data on the life history and host usage of the rarely studied tachinid fly *Ormia lineifrons* that uses *Neoconocephalus katydids* as hosts for larval development. We surveyed six *Neoconocephalus* species, of these, four were parasitized and subsequently killed by parasitoid development. Lab rearing of fly pupae indicated that the fly was multivoltine and synchronized each of its seasonal generations with the different host species seasons. The parasitism rate across differed among hosts and peaked between 38% and 100%. Parasitoid load and pupal development time did not differ among host species. However, fly development success was lowest for *N. triops*, the species that the fly likely has evolved with for the longest time. The parasitized host species' peak frequencies ranged from 6.9 kHz – 10.6 kHz. We discuss the importance of the synchronization between fly generations and their different host species as well as the potential counteradaptations of the hosts. The selective pressures in this system are acting in opposing directions with unique opportunities to understand how these species interactions can drive coevolution of parasitoids and their hosts.

Stephanie Rojas, Ashley Nguyen, Kayla Nguyen, Lindsey Morris, and Christina Hendrickson (Oklahoma City University)

Poster 21

*INVESTIGATING ANTIMICROBIAL EFFECTS OF AQUEOUS DANDELION EXTRACT

Certain plant-derived products have pharmaceutical uses due to their anti-inflammatory and anti-cancer effects. Dandelion (*Taraxacum officinale*) is one of them. 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 DWE. The disk diffusion method was utilized to test various concentrations (5 - 100 mg/mL) of DWE on bacterial growth. DWE was tested on six bacteria: *Escherichia coli*, *Citrobacter freundii*, *Morganella morganii*, *Salmonella typhi*, *Staphylococcus aureus*, and *Neisseria sicca*. All bacterial cultures were incubated at 37 °C for 24 hours. Isolated bacterial colonies were 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. A Mueller-Hinton Agar plate devoid of bacteria was treated with DWE disks to serve as a control to ensure the DWE disks did not introduce contamination. After incubation, all plates were visualized for indication of DWE impact on bacterial growth. The results showed no zone of inhibition; indicating all six bacteria were resistant to aqueous DWE in this method. In the future, broth dilution antibiogram assays will be conducted utilizing additional bacterial species and different formulations of dandelion extracts.

Brandon G. Roniss¹, Jamian Maxwell¹, Mathew T. Turnley², Derek P. Hahn², Michael J. Cherry³, M. Colter Chitwood², Marlin M. Dart³, Randall W. DeYoung³, W. Sue Fairbanks², Levi J. Heffelfinger³, Robert C. Lonsinger^{2,4}, Evan P. Tanner³, and H. (¹East Central University; ²Oklahoma State University; ³Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville; ⁴US Geological Survey, Oklahoma Cooperative Fish and Wildlife Research Unit)

Poster 18

*MONITORING THE POPULATION DEMOGRAPHY AND PARASITES OF PRONGHORNS IN WESTERN OKLAHOMA

The pronghorn antelope (*Antilocapra americana*) is the only extant species of Family Antilocapridae and is endemic to North America. The range of this species extends from southern Canada to northern Mexico, with populations existing in the Oklahoma Panhandle. The status of pronghorn populations in Oklahoma is poorly known, although annual surveys by the Oklahoma Department of Wildlife Conservation (ODWC) suggest that they are in decline. We are conducting a study of the pronghorn populations in Cimarron and Texas counties in western Oklahoma. Our goal is to assess the factors impacting the movement and population demography of Oklahoma pronghorns, and to devise methods to improve their monitoring. A major focus of this study is the fawning season, which occurs from early May to June in Oklahoma. A field crew composed of graduate students from Oklahoma State University (OSU) and Texas A&M University-Kingsville, as well as undergraduate technicians from OSU and East Central University (ECU) was tasked with fawn capturing in the summer of 2022. Primary duties involved (1) capturing of pronghorn fawns to install VHF collars and take morphological measurements, (2) daily monitoring of fawn collars via radio telemetry, and (3) investigating related mortality events. The team also collected fecal samples from adult pronghorns for energetics assessment and parasite monitoring. Currently we are processing the fecal samples using the McMaster egg counting method to quantify endoparasite eggs. This work will provide valuable information for understanding the population dynamics of pronghorns and the factors affecting them in the Oklahoma Panhandle.

Noelia Saldierna and William P Ranahan II (Oral Roberts University)

8:45-9:00 in 331 Tandy

*EFFECTS OF SHIITAKE MUSHROOM (*LENTINULA EDODES*) SECRETIONS ON TRIPLE-NEGATIVE BREAST CANCER CELLS

Before modern medicine, most ancient healing remedies came from nature. Medicinal mushrooms like *Lentinula edodes* have immunomodulatory properties that can potentially treat fatal diseases such as breast cancer when combined with current technological advances. Breast cancer is characterized by a malignant tumor in the ducts or lobules of the breast tissue and is a leading cause of death globally. One of the primary reasons for the high mortality rates of breast cancer is the body's dissociated response to treatment. Therefore, it is imperative to continue research on treatment alternatives to provide cancer patients with noninvasive options. To target this issue, *Lentinula edodes*' secretions were harvested, dehydrated, sampled through a Next Generation Chromatography system (NGC), and tested against triple-negative breast cancer cells via cell cytotoxicity assays. The assay results demonstrated that the cell viability of the abnormal cells diminished compared to the normal cells. Thus, it was concluded that the secretions captured from *Lentinula edodes* have the ability to stimulate cell death in cancerous breast cells and maintain healthy breast cells alive. Understanding the capabilities of medicinal mushrooms' secretions can be used to derive a more efficient, direct, cheaper, and personalized alternative to current treatment methods for cancer patients.

Andrew Seeberger and Douglas Bryhan (East Central University)

Poster 11

***A CONTINUING COMPARISON OF 400-450NM COMPONENTS OF FLUORESCENT, SEMICONDUCTOR, AND INCANDESCENT FILAMENT BASED ILLUMINATION**

Until recently, artificial illumination has been based on either the incandescent filament with its poor efficiency and high waste heat or mercury vapor fluorescent lamps with a somewhat elevated UV component and unnaturally blue color temperature. More recent lighting developments have included both compact fluorescent ("CF") lamps which can have a lower "warmer" color temperature than earlier industrial fluorescent lamps and semiconductor ("LED") lighting in a variety of color temperatures. However, there have been published claims that the compact fluorescents can produce potentially unsafe levels of near UV radiation and that semiconductor devices produce potentially unsafe levels of 450nm light. Levels of 400-450nm light are compared from an assortment of devices as a percentage of their total output from 400nm to 800nm. Several commercially available CF lamps are spectroscopically evaluated and compared to both incandescent and semiconductor illumination sources via an Ocean Optics Red Tide UV-VIS spectrometer.

Natalie Shreffler, Cait Hudgens, Sydney Oliver, and Daniel Rocha (Southern Nazarene University)

10:30-10:45 in 351 Tandy

***FACTORS THAT AFFECT AMAZONIAN TERRESTRIAL MAMMAL DISTRIBUTIONS**

Tropical forests are among the most biologically diverse areas on the planet. The Amazon Rainforest represents about 50% of the remaining tropical forests and hosts over three million different species. Of these species, mammals play vital roles in ecosystems across the globe such as predators, prey, seed dispersers, ecological engineers, and therefore are of conservation importance. The decline in mammal populations, particular large bodied ones, is a pressing issue globally, including in the Amazon forest. The first step to mitigate and prevent mammal declines, is to understand factors that affect mammal distributions. In this study, we used data from 182 camera trap sites from four different protected areas (Samuel Ecological Station, Amana Nature Reserve, Corumbiara State Park, and Guaporé Biological Reserve) of three Amazonian terrestrial mammal species (paca *Cuniculus paca*, white-collared peccary *Pecari tajacu*, and mountain lion *Puma concolor*). We used camera trap data in combination with remote sensing satellite data and hierarchical occupancy modeling to identify environmental and anthropogenic factors that influence species distribution in the Brazilian Amazon. Our results suggest that puma was positively affected by elevation. Paca was negatively affected by elevation and human footprint index. White-collared peccary negatively affected by forest fragmentation. Net primary productivity had a positive effect on the three species studied. Our results support that species occurrence is related to habitat quality and that the increasing human presence in the Amazon will likely negatively affect species distributions, which might require active conservation management.

Severin Simonsen and John F Geiger (Cameron University)

10:00-10:15 in E393 Forensic

***THE EFFECT OF A VERBAL AND VISUOSPATIAL SECONDARY TASK ON THE COMPREHENSION OF PROCEDURAL TEXT**

When reading procedural texts, individuals will usually form a mental model of the object described by the text. The present study examined the role that both verbal and visuospatial working memory play in text comprehension and mental model construction by employing a secondary task during reading. Seventeen participants read two narrative style and two list like procedural texts describing the construction of simple machines while performing a visuospatial tapping task, or a verbal secondary task. No main effects were significant, but the 2 x 2 interaction approached significance, $p = .23$. This interaction demonstrated that tapping secondary task reduced the proportion of idea units recalled from the narrative style texts, relative to the other three conditions. It appears that verbal working memory is most needed when reading a narrative style procedural text.

Phillip Sites, Joshua Dickey, Brady Combs, and Bryson Combs (University of Central Oklahoma)

9:00-9:15 in E378 Forensic

*IMPLEMENTATION OF A MINATARE ATOMIC CLOCK ONTO BUDDY SUPERCOMPUTER

We are living in a world with devices capable of accessing the internet with a click or touch of a button from anywhere. Many have experienced a long wait time or “Buffering”. This term can be described as the time it takes to receive enough data packets in the correct order to begin playing the video after requesting to stream. When networks are not communicating at the same speed, data can be lost or could be received out of order resulting in a corrupted file or an extremely long download time. Implementing an atomic clock on the Buddy Supercomputer will increase data transfer rate while decreasing the timing errors. The project requires an accurate timing source that will be received from a GPS (Global Positioning Satellite). When a network user connected to our network wants to transmit or receive a file, the atomic clock will send out the correct time to ensure the other side is transmitting or receiving at the same rate. The results of the improved clock will shorten the data transfer process, effectively increasing the speed of information to display on your device. To test our design, we will send packets of data before and after implementing the improved clock source from our supercomputer to a network across campus. By tracing the file, we can compare the time and accuracy of the data to determine our effectiveness across the network. Problems are to be expected and will play a critical role in the development of the long-term use of the atomic clock. The specific placement of the device, how the device is mounted, airflow, and cooling will all play a part in the final design phase of the project.

Jarrett Smith, Altherr (Joseph) Alcuitas, Rachel Uhlig, Ryan Agyemang, and Rickey Cothran (Southwestern Oklahoma State University)

Poster 4

*FEMALE AMPHIPODS ADJUST BROOD SEX RATIOS BASED ON MATE CHOICE

There are several determinants of sex ratios in nature all falling under two main categories genetic or environmental. The expectation from theory is that the sexes will be produced in a 1:1 ratio because investing in the rarer sex is expected to provide greater fitness returns. However, biased sex ratios are common in nature and can be the result of both genetic and environmental factors. We hypothesized that females bias the sex ratio of broods in favor of sons when allowed to choose their mate in the wild. We collected mating pairs of amphipods (*Hyaella* sp.) from two pools in the same natural spring system. Half of the females were separated and repaired with their original mate—i.e. they were allowed to choose their mate. The other half of the females were separated and assigned a new male at random. Each pair was placed in their own 50-ml jar and placed in an environmental chamber. We checked the pairs three times a week and recorded offspring sex ratios. We predicted females with a choice in their mate would pick higher quality males and in turn produce more male biased broods and females assigned a mate at random will produce more of an even brood sex ratio. Preliminary results show a non-statistically significant trend of females given a choice of a mate producing a higher proportion of sons in their broods than females mated at random. Such a strategy would allow females to maximize fitness by investing in sons only when high quality mates are present in a mating system characterized by strong sexual selection on males.

Sydney Spillane, Joshua Baer, Shania Do, Tiffany Jones, Abigail Kee, Karissa LeHew, Derek McGuire, Sarah Soliman, Monica Vuong, Cari Marshall, and Ipe Paramel (Oklahoma State University Center for Health Sciences)

Poster 16

**LEAN HEALTHCARE: EVALUATION OF BED THROUGHPUT AT OSU MEDICAL CENTER

Several factors play a role in an organization’s success to function on a daily basis. For example, one factor being the application of efficient protocols to produce effective and consistent results. There is a specific procedure, called LEAN, that has been increasingly employed throughout various types of corporate professions due to its favorable outcomes. Originally, LEAN practices were created to enhance workflow and manufacturing processes in the automobile industry. After other industries observed the success rates from applying these certain methods, LEAN has been progressively adapted by many businesses to achieve similar effects. By adopting the LEAN methodologies, corporations have been able to increase their productivity, value, and client satisfaction. An example of how versatile and beneficial the LEAN approach can be in other fields, besides manufacturing, can be portrayed within a healthcare setting. There have been multiple healthcare organizations that have applied LEAN strategies to their systems in order to amplify quality improvement, with an end goal to better patient care. In this poster, a model is presented on how to apply and replicate LEAN tactics in an effort to advance bed throughput within a hospital setting. In the summer of 2022, a team of medical students from Oklahoma State University College of Osteopathic Medicine (OSU-COM) applied LEAN tools and techniques to examine the delayed process of bed throughput from the Emergency Department to the hospital floors. In doing so, possible solutions were developed in hopes to improve workflow, culture, and most importantly, patient outcomes.

Madison Stephens¹, Asiah Powers¹, Lena Marcikic¹, G. Caroline Schwab¹, Tyler Godsey¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 36

*THE EVOLUTIONARY CONSERVATION OF DOCK AS COMPARED TO RICTOR IN THE INSULIN-LIKE RECEPTOR PATHWAY

The Insulin/TOR Signaling Pathway evolves in *Drosophila* as the species become further diverged from *Drosophila melanogaster*. In this study, a comparative genomics approach was used in order to determine the levels of conservation of two

genes, rictor and dock, of the insulin pathway. A variety of genes from the *Drosophila* genus were annotated based on elements like genomic neighborhood and gene structure. Each gene annotated also had isoforms which varied in amino acid sequences and number of exons. We used this information to determine the organisms' evolutionary relationship to *D. melanogaster*. The scores were then compared using a bar graph which demonstrated divergence levels. The results demonstrated dramatically higher divergence scores of rictor than dock which was earlier on the pathway than rictor. Results indicated that dock was more conserved than rictor. Future research could be done to determine if other genes that are also early in the pathway are more conserved than those later in the pathway.

Myliisa Stover, Sydney Marouk, Deole Ratnakar, and Jacob Manjarrez (Oklahoma State University Center for Health Sciences)

Poster 49

****PROBIOTIC CAPABILITY OF *LACTOCOCCUS LACTIS* AND *LEUCONOSTOC MESENTEROIDES* BACTERIAL STRAINS WHEN USED TO SUPPLEMENT THE DIET OF *CAENORHABDITIS ELEGANS* AND THE POTENTIAL EFFECTS ON WORM LONGEVITY, STRESS, AND DEVELOPMENT**

There are a variety of sources supporting the benefits of a diverse gut microbiome on longevity and quality of life across many species. A human diet supplemented with probiotics is found to promote digestion and support immune function. In this study, we propose to investigate the probiotic capabilities of *Lactococcus lactis* and *Leuconostoc mesenteroides* in the gut of *C. elegans* to understand if they have potential therapeutic applications. Preliminary lifespan studies suggest that worms given a diet closer to their natural microbiome (CeMBio) live longer than worms given the standard laboratory diet, OP50, *E. coli*. Our study has shown that when CeMBio is supplemented with *L. lactis* or *L. mesenteroides* the median lifespan decreases. This difference in longevity could be due to a decrease in variability introduced by the probiotic supplementation to an already healthy microbiome. To detect potential probiotic benefits of these microbes, lifespan and health span studies will be conducted using wild type worms and transgenic strains containing fluorescent stress reporters. Worms will be fed a standard laboratory diet of OP50, simulating an unhealthy and undiversified microbiome, supplemented with *L. lactis* and *L. mesenteroides*. The stress reporters used in this study will indicate metabolic, environmental, or chemical stress within the experimental system. Stress pathways will be studied along with classical development assays to see the range of potential therapeutic benefits provided by *L. lactis* or *L. mesenteroides* within an unhealthy and undiversified microbiome.

Logan Swope, Toni Proctor, Ashlee Bradley, Anil Kaul, and Rashmi Kaul (Oklahoma State University Center for Health Sciences)

Poster 57

****PREVALENCE OF *CHLAMYDIA TRACHOMATIS* AND *NEISSERIA GONORRHOEAE*: PRE AND POST COVID LOCKDOWN**

Chlamydia trachomatis (CT) and *Neisseria gonorrhoeae* (NG) are two of the most common Sexually transmitted diseases (STDs) (Rowley et al., 2016) with almost 1.6 million CT cases reported in 2020 and an estimated 1.14 million NG cases yearly in the United States. The SARS-Cov-2 pandemic has infected ninety-six million Americans and caused over a million deaths (CDC). According to the American Society for Microbiology, focused efforts on SARS-Cov-2 had a negative impact on STD control measures. Further, Sars-COV-2 resulted in disruption of prevention and treatment to various infectious diseases such as tuberculosis, human HIV, and dengue fever (Downey et al., 2022). Restrictions due to the pandemic resulted in reduced routine STD testing. At the Oklahoma State University (OSU), regular STD testing is done in the OSU Clinical laboratory on the university campus in Tulsa. Test results were collected and analyzed to compare the prevalence of CT and NG cases, before and after the SARS-Cov-2 lockdown. We aimed to determine the impact pandemic lockdown protocols had on STD numbers, specifically CT and NG. Statistical analysis using an independent t-test and chi-squared test of independence showed that there was not a statistically significant ($p > 0.05$) difference in cases for CT when comparing pre- and post-lockdown measures for SARS-Cov-2. However, there was a statistically significant increase ($p < 0.05$) in NG rates when comparing pre-lockdown to post-lockdown. Future correlations can be done with data from recent months to further solidify the relationship that the pandemic has had on CT and NG numbers, and ultimately STD prevalence. This study explored the relationship SARS-Cov-2 lockdown measures had on CT and NG positivity rates. Our findings indicate the pandemic lockdown had an impact on NG rates potentially resulting from clinical service interruption due to the lockdown measures.

Benjamin O. Tayo and Michael Walkup (University of Central Oklahoma)

8:45-9:00 in E393 Forensic

DETECTION OF DNA BASES USING MONOLAYER TWO-DIMENSIONAL MATERIALS: DENSITY FUNCTIONAL THEORY CALCULATIONS

Electronic DNA sequencing using monolayer-based nanodevices has recently emerged as the next-generation of DNA sequencing technology. Unlike protein nanopores, solid-state monolayer materials (graphene, silicene, phosphorene, MoS₂, hBN, Ti₃C₂) are nonbiological and thereby more tolerant to thermal, chemical, and mechanic stress. The subnanometer thickness of monolayer materials gives them the capability to detect DNA strands with single-base resolution and high signal-to-noise ratio (SNR). Due to their crystalline stability and conductive properties, monolayer materials can be processed into devices for

electronic DNA sequencing, which can produce signals that are several orders of magnitude greater than ionic current signals. The goal of our project is to carry out first-principle computational studies using density functional theory (DFT) to quantify the electronic interactions of the four DNA nucleobases (adenine, thymine, guanine, and cytosine) with monolayer crystals (graphene, silicene, phosphorene, MoS₂, hBN, Ti₃C₂, etc.). Our analysis will be carried out for several nanodevice configurations such as nanoribbon, nanogap, and nanopore. Our results and observations will be benchmarked against graphene, as it is the mostly widely studied 2D material for electronic DNA sequencing. The findings from this research will shed new insights that can help accelerate research in the field of electronic DNA sequencing using novel monolayer materials.

Melissa Testut¹ and Henry Shin² (¹Oklahoma Christian University; ²Excitant Therapeutics)

9:00-9:15 in 331 Tandy

***EXAMINING THERAPEUTIC EFFECTS OF EXT-4U ON NEOVASCULARIZATION AND FIBROSIS IN AMD**

EXT-4U is a novel small molecule that selectively activates Peroxisome Proliferator-Activated Receptor Alpha (PPAR- α). Here we show its therapeutic effects on retinal fibrosis and neovascularization in a mouse model of Age-related Macular Degeneration (AMD). To test the selectivity and potency of EXT-4U for PPAR- α agonism, we first performed a PPAR- α reporter assay. We then conducted a Cellular Thermal Shift Assay (CETSA) in ARPE19 cells to analyze the binding affinity of EXT-4U to human PPAR- α . We performed western blotting to examine the anti-fibrotic effects of EXT-4U in ARPE19 cells treated by TGF- β 2 and tested the anti-angiogenic effects by conducting an ex vivo choroidal sprout assay. Finally, we conducted in vivo efficacy tests in a mouse model of laser-induced Choroidal Neovascularization (CNV). The PPAR- α reporter assay confirmed that EXT-4U is a selective and potent PPAR- α agonist, and the CETSA assay further demonstrated PPAR- α binding affinity. In ARPE19 cells treated with TGF- β 2, co-treatment with EXT-4U downregulated levels of connective tissue growth factor. EXT-4U treatment also inhibited choroidal endothelial cell sprouting. Lastly, EXT-4U treatment in CNV mice decreased CNV lesion size. When considered together, these results demonstrate that EXT-4U exhibits a therapeutic effect on fibrosis and neovascularization.

Wyatt Thiel, Paul Crawford, and Lindsey Long (Oklahoma Christian University)

Poster 35

***THE DIFFERENCE IN EVOLUTIONARY CONSTRAINT BETWEEN SIMA AND PTP61F GENES IN *DROSOPHILA* SPECIES**

The Insulin-like receptor pathway influences the maintenance of blood glucose levels and progresses growth and development in multiple species, especially in *Drosophila* fruit flies. All genes located within this pathway evolved at differing rates. In this study, the *sima* and *Ptp61F* genes were tested for their level of evolutionary constraint. Using the UCSC Genome Browser, the location of the genes was identified in both the target species and *D. melanogaster* (*D. mel*). Once the location was determined, a Tblastn was performed, which tested the protein sequence in *D. mel* to the target species. All isoforms of the gene in the target species were annotated. The results of the annotation were verified using the GEP Model Checker, and the dot homology plot was recorded alongside the percent identity of the protein sequence. The evolutionary divergence scores were calculated for all tested species of *Drosophila*. From the data, *sima* shows more constraint in its evolutionary progress than *Ptp61F*.

MacKenzie Thomas (Oral Roberts University)

9:15-9:30 in 331 Tandy

***THE CYTOTOXICITY OF *GRIFOLA FRONDOSA* SECRETIONS ON TRIPLE-NEGATIVE MAMMARY EPITHELIA**

With cancer being the second deadliest killer in the world, trailing closely behind ischemic heart disease, it is no mystery why novel treatment options are constantly being researched. It is estimated that by the year 2060, cancer will become the leading cause of death, further increasing the urgency to find new cures. While there are many different types of cancer, breast cancer is the second most prevalent and is the deadliest malignancy among women. Common therapeutic strategies to combat breast cancer include surgery, radiotherapy, and chemotherapy. Unfortunately, these methods lack substantial specificity to target malignant growths and preserve healthy tissues. Mushrooms have long been used for medicinal purposes, and more recently, they have been studied for cancer suppression. *Grifola frondosa* (*G. frondosa*), also known as hen of the woods, is a Basidiomycetes fungus that provides many benefits, including antidiabetic, antioxidant, anti-inflammation, hepatoprotective, antiviral, and antitumor properties. Several studies have shown that *G. frondosa*'s bioactive macromolecules, such as polysaccharides and polypeptides, have the significant immunomodulatory effects of activating and upregulating many immune-related cells such as macrophages, natural killer cells, and cytotoxic T-cells. Also, *G. frondosa* biomolecules increase the release of cytokines, including interleukins (IL), interferons (IFN), lymphokines, and tumor necrosis factors (TNF). These factors promote apoptosis and have antiproliferative activity. Thus, the compounds that *G. frondosa* produces are a potential avenue for cancer research. Full spectrum *G. frondosa* secretions, as well as separated fractions, were tested on both MDA-MB-468 triple-negative mammary epithelia and MCF10A human breast epithelial cell lines. Cell viability assays were performed, yielding results that suggest *G. frondosa* secretions contain compounds that selectively kill breast cancer cells.

Triztan Thompson and Julianna Goelzer (Oral Roberts University)

Poster 2

*COMPARATIVE GENOMICS OF THE RBCL GENE IN *CANNABIS SATIVA* AND OTHER MEDICINAL PLANTS

The chloroplast is one of the major organelles inside plants; despite the fact that 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 chloroplast as a major organelle. Sequencing the chloroplast could help scientists understand how much the organelle contributes to the plant's unique properties. *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. Although medicinal plants like *C. sativa* have been used for thousands of years, their biochemistry and genetics are unknown. One area that would improve the overall medicinal qualities would be unlocking optimal growth through the plant's chemical factory. Several repetitive genes have been found on the plasmid of the chloroplast. One of these is the *rbcl* gene, which 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.

Rachel Uhlig, Altherr (Joseph) Alcuatas, Jarret Smith, Ryan Agyemang, and Rickey Cothran (Southwestern Oklahoma State University)

Poster 4

*FEMALE AMPHIPODS ADJUST BROOD SEX RATIOS BASED ON MATE CHOICE

There are several determinants of sex ratios in nature all falling under two main categories genetic or environmental. The expectation from theory is that the sexes will be produced in a 1:1 ratio because investing in the rarer sex is expected to provide greater fitness returns. However, biased sex ratios are common in nature and can be the result of both genetic and environmental factors. We hypothesized that females bias the sex ratio of broods in favor of sons when allowed to choose their mate in the wild. We collected mating pairs of amphipods (*Hyalella* sp.) from two pools in the same natural spring system. Half of the females were separated and repaired with their original mate—i.e. they were allowed to choose their mate. The other half of the females were separated and assigned a new male at random. Each pair was placed in their own 50-ml jar and placed in an environmental chamber. We checked the pairs three times a week and recorded offspring sex ratios. We predicted females with a choice in their mate would pick higher quality males and in turn produce more male biased broods and females assigned a mate at random will produce more of an even brood sex ratio. Preliminary results show a non-statistically significant trend of females given a choice of a mate producing a higher proportion of sons in their broods than females mated at random. Such a strategy would allow females to maximize fitness by investing in sons only when high quality mates are present in a mating system characterized by strong sexual selection on males.

Simon Underhill and Matthew T. Cabeen (Oklahoma State University - Stillwater Campus)

10:30-10:45 in 333 Tandy

REDUNDANCY IN CITRATE AND CIS-ACONITATE TRANSPORT IN *PSEUDOMONAS AERUGINOSA*

Tricarboxylates such as citrate are the preferred carbon sources for *Pseudomonas aeruginosa*, an opportunistic pathogen that causes chronic human infections. However, the membrane transport process for the TCA cycle intermediates citrate and cis-aconitate is poorly characterized. Transport is thought to be controlled by the TctDE two-component system, which mediates transcription of the putative major transporter OpdH. Loss of *tctDE* has been associated with sensitization to aminoglycosides, possibly linking tricarboxylate transport to enhanced antimicrobial resistance. In this work, we search for previously unidentified transporters of citrate and cis-aconitate using both protein homology and RNA sequencing approaches. We uncover new transporters and show that OpdH is dispensable for transport; instead, citrate transport primarily relies on the tripartite TctCBA system, which is encoded in the *opdH* operon. Deletion of *tctA* causes a growth lag on citrate and loss of growth on cis-aconitate. Combinatorial deletion of newly discovered transporters can fully block citrate and cis-aconitate utilization. We then characterize transcriptional control of the *opdH* operon in *tctDE* mutants and show that loss of *tctD* blocks citrate utilization due to its inability to express *opdH-tctCBA*. However, *tctE* and *tctDE* mutants evolve heritable adaptations that restore growth on citrate as the sole carbon source.

Landen Underwood and Alisha Howard (East Central University)

Poster 40

*HTLV-1 VIRAL PROMOTER NUCLEOSOME DYNAMICS

Human T-Cell Leukemia Virus Type 1, or HTLV-1, is a retrovirus infecting primarily T-cells. This viral infection is known to be the causative agent in a subset of patients into Adult T-Cell Leukemia (ATL), or if it crosses the blood-brain barrier into HTLV-1 associated myelopathy, or tropical spastic paraparesis (HAM/TSP). The virally-expressed transcription factor Tax has been found to be pivotal in the malignant transformation of infected cells. Control of viral expression by Tax from the proviral promoter varies with stage of infection. The association of the HTLV-1 viral promoter and the associated viral and host activators/co-activators within the context of the chromatin environment could provide insights into target interactions and interfaces leading to dynamic promoter control. To investigate this, a plasmid, pHTLV208-8, containing the HTLV promoter surrounded by 5S nucleosome positioning sequences was prepared. Four biotinylated oligos corresponding to complimentary regions near the 5S or

promoter sites along the plasmid were designed with various lengths and sent for synthesis with a 5' biotinylation modification included. Triplex strand invasions were performed to attach each specific biotinylated oligo and pHTLV208-8. Bead binding of the triplex strand mixtures were performed using streptavidin-bound magnetic beads. Restriction digests were then used to quantitatively analyze binding success and durability of the triplex-bound plasmids. Use of the stationary bound plasmid will allow analysis of Tax chromatin positioning effects as well as pulldowns from cell lysates in the absence of non-specific end-binding proteins.

Christelle Urujeni Wa-Mana¹, Lynda M. Bradley², Rachel Hartman², and David Civitello² (¹Oklahoma Christian University; ²Emory University)

Poster 48

***PREDICTING THE EFFECT OF RESOURCE PULSES ON HUMAN SCHISTOSOMIASIS INFECTION RATES**

Resource pulses are a result of excess nutrients from sources such as sewage overflow or agricultural sources accumulating in ecosystems such as lakes. One of the effects of resource pulses is that they can drastically change the dynamics of an existing ecosystem such as human and wildlife parasite infection rates. One such human disease, schistosomiasis, is caused by schistosome parasites and aquatic snails, which act as their intermediate hosts. In other snail-parasite systems, when agricultural wastes overflow into water bodies this causes an increase in parasite burden in the water, stemming from either an overall increase in the number of infected snail hosts present or by an increase in the number of parasites produced by each snail. If this is also true in the snail-schistosome system, such resource pulses would result in increased human schistosomiasis infection rates to the communities in proximity. Based on this, the project seeks to understand the repercussions that resource pulses have on individual snails and schistosome populations using *B. glabrata* snail hosts infected with *S. mansoni* schistosome parasites. To test the effects of resource nutrient supplementation, different groups of snails were fed synthetic food with varying amounts of nitrogen and phosphorus, which often accumulate in the water bodies following resource pulses. To do this we conducted a life-table experiment where we collected and analyzed snail life-history data, such as a snail's reproductive data (total eggs laid), growth (maximum shell size), and the number of parasites produced. Our hypothesis is that snails fed with synthetic food higher in nitrogen and phosphorous content will have greater growth, reproduction and parasite production. This would indicate higher risks of human schistosomiasis infection under nutrient supplementation.

Kathy Vo, Laurel Eze, Trung Le, and Christian Santizo (University of Central Oklahoma)

10:00-10:15 in E378 Forensic

***BIOHYBRID MICROSWIMMER FABRICATION AND CHARACTERIZATION**

The long-term objective of this project is to develop a novel drug delivery method in the form of biohybrid microswimmers with the purpose of improving and accelerating patient outcomes. Traditionally, drugs are delivered through the skin, mouth, veins, etc. in order to treat diseases, improve health, and extend lives. Usually, this treatment comes with a cost in the form of side effects due to the interactions between said drugs and healthy tissues. The background of this project stems from the need to develop a better and more precise way to deliver treatments and substances into the body exactly where they are needed. The biological part of the micro-swimmer is by establishing the green algae cells, which are created through a process called cell cultures that is done in labs. The algae cells will be tested with polystyrene beads that will ultimately contain drugs, and this will identify the most effective and efficient ratio of the beads to the cells. Subsequently, to ensure the beads are attached to the algae surface, the cells will be coated in an electropositive solution expected to attract the beads even more. The guidance of these cells will be placed in an experimental setup. There is possibly a light probe that will be emitting light with an ideal wavelength for the cell's reaction. As the cells are being guided by the light probe, another high intensity light operating in the 40mA range will be used for imaging, serving as a sort of PIV system to observe the movement on a more detailed level. The idea behind this project lies in the expansion of a safer, more effective drug delivery method that will utilize the motile flagella-powered-biohybrid microswimmers by transporting drugs to the targeted areas.

Monica Vuong, Jessica Gray, Joe McCreary, and I-Hsiu Huang (Oklahoma State University Center for Health Sciences)

Poster 53

****CHARACTERIZATION OF BIOFILM FORMATION BY ENVIRONMENTAL *CLOSTRIDIODES DIFFICILE* ISOLATES**

Clostridioides difficile is a gram-positive, spore-forming bacteria capable of causing disease, referred to as *Clostridioides difficile* Infections (CDI), which may include symptoms such as severe diarrhea and colitis. Every year in the United States, about half a million of these CDI cases result in approximately \$6 billion in medical costs. *C. difficile* is difficult to eradicate due to its antibiotic resistance, virulent properties, and the fact that there is no available vaccine. CDIs are thought to be iatrogenic, but accumulating evidence suggests that environmental transmission may play an important role as well. Previously, we were able to isolate multiple *C. difficile* samples from fish markets, hospital wastewater, and wastewater treatment plants in southern Taiwan. Genotypic analysis revealed the presence of toxigenic *C. difficile* isolates closely related to ones prevalent among humans and animals infected by *C. difficile*. To gain a better understanding of the virulence capabilities of these environmental isolates, a series of studies including growth rates, spore production, and cytotoxicity were performed; however, the biofilm forming abilities were not well characterized. In this study, biofilm formation ability of these isolates was observed over a 72-hour period, then biofilm mass was measured using a crystal violet staining assay. By using a One-Way ANOVA, results were compared to

the control lab strains 630 and R20291 to identify any significant differences. Further comparisons were made between isolates based on biofilm morphology. We observed a diverse range in biofilm formation abilities as well as biofilm morphology, but we did not detect any significant correlation between the robustness of the biofilms and the presence of toxin genes. Ongoing experiments focus on assessing the ability of these biofilms to resist antibiotics. In summary, our preliminary results contribute to the characterization of multiple environmental *C. difficile* isolates obtained from water and seafood samples in southern Taiwan.

Jue Wang and William P Ranahan II (Oral Roberts University)

Poster 66

***ANTI-CANCER EFFECTS OF *TRAMETES VERSICOLOR* SECRETIONS**

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.

Shaelyn Ward¹, Josh Autaubo¹, Philo Waters¹, Elizabeth Garrett¹, Kelsi Batioja¹, Reece Anderson¹, Debra Furr-Holden², and Matt Vassar¹³ (¹Oklahoma State University Center for Health Sciences; ²School of Global Public Health, New York University)

Poster 12

A SCOPING REVIEW OF HEALTH INEQUITIES IN ALCOHOL USE DISORDER

Alcohol Use Disorder (AUD) poses a significant health burden, especially in medically underserved, as well as underrepresented racial and sexual minority populations. Ameliorating health inequities are vital to improving patient-centered care. Given the heightened focus on narrowing the health disparities gap, evaluating health inequities for patients with AUD has become of utmost importance. More research is needed to understand health inequities in AUD and the disproportionate impact on already marginalized populations. The objective of this scoping review is to chart the existing evidence on health inequities related to AUD and identify existing knowledge gaps to guide future equity-centered research. We performed a literature search using Ovid (Embase) and MEDLINE (PubMed) databases for articles on AUD that were published in the 5-year period spanning from 2017-2021 and written in English. This scoping review followed guidelines from the Joanna Briggs Institute as well as the PRISMA extension for scoping reviews. All studies were screened and extracted in a masked, duplicate manner. Frequencies of each health inequity examined were analyzed and main findings from each included study were summarized. Following screening, our sample consisted of 72 studies for data extraction and analysis. Alcohol Use Disorder was more likely in historically marginalized groups, among sexual minorities and more common in men, though there are rising rates in women. Our findings indicate that significant research gaps exist in education, rural under-resourced populations, and LGBTQ+ communities with Alcohol Use Disorder. Scoping review highlights the gaps in research on inequities in AUD, as well as the conflicting findings across studies. To bridge the current gaps, we recommend research on the following: 1) triage screening tools and the use of telemedicine for rural, under-resourced populations; 2) interventions to increase treatment engagement and retention for women; and 3) community-based participatory methodologies for the LGBTQ+ communities.

Caitlin Wayland, Payden Farnsley, Nicholas Bauer, and Vijayakumar Somalinga (Southwestern Oklahoma State University)

Poster 20

IDENTIFICATION AND PRELIMINARY CHARACTERIZATION OF AN A-CARBONIC ANHYDRASE HOMOLOG FROM THE "BRAIN-EATING AMOEBEA", *NAEGLERIA FOWLERI

Naegleria fowleri is a thermophilic, free-living amoeba that inhabits aquatic ecosystems and water distribution systems. *N. fowleri* causes primary amoebic meningoencephalitis (PAM), a rare, fatal and rapidly destructive infection of the central nervous system. Current treatments consist of repurposed antimicrobial agents, which are not effective, leading to very high mortality rates. Therefore, identification of new and effective drug targets is imperative. Recent studies have shown that fatty acid utilization plays an important role in *N. fowleri* growth, and a central enzyme in fatty acid metabolism is a bicarbonate-requiring carboxylase. Carbonic anhydrases (CA's) are metalloenzymes that catalyze the reversible hydration of carbon dioxide into protons and bicarbonate, a ubiquitous reaction important for physiological functions. Bicarbonate produced by the catalytic activity of CA's are utilized by carboxylases for the synthesis of molecules essential for cellular activity. In addition, recent studies have shown that CA's may play a role in the virulence of bacterial pathogens. Surprisingly, CA's and their role in metabolism and virulence of eukaryotic pathogens remains largely uncharacterized. Using BLAST analysis, we recently

identified a protein, FDP41_009806, from *N. fowleri*, with 25% identity to human α -CAII. Both conserved domains and multiple sequence alignments analyses showed the presence of metal-coordinating histidine residues and catalytically important glutamate and threonine residues conserved in many closely related α -CA's. In addition, homology modeling of FDP41_009806 revealed conserved structural elements such as the central β -sheet core that harbors the metal binding residues essential for CA catalytic activity. Although FDP41_009806 shows all the hallmarks of an α -CA, phylogenetic analysis indicated that this *N. fowleri* homolog may represent a new type of α -CA. The structural and conserved active site homology led us to hypothesize that FDP41_009806, hereafter NfCA1 α , is an uncharacterized α -CA in *N. fowleri*. The goal of this project is to characterize NfCA1 α using biochemical and structural methods.

Alex Webb, Melville Vaughan, and Christopher Goodchild (University of Central Oklahoma)

Poster 19

***PRELIMINARY ANALYSIS OF IN VITRO EXPOSURE TO TWO 'ALTERNATIVE' FLAME RETARDANTS ON RAT AORTIC SMOOTH MUSCLE CELL MIGRATION**

Flame retardants are incorporated into commonly used household products (e.g., furniture, car seats, crib mattresses). In 2004, many traditional flame retardants (e.g., polybrominated diphenyl ethers) were removed due to toxicity concerns and replaced with 'alternative' flame retardants. However, the toxicity of these alternative flame retardants is unknown. A particular concern is the potential for maternal transfer to the embryo due to the fact that these flame retardants have been detected in breast milk and placental fluid of pregnant women. In utero exposure is an important aspect to consider, especially during the early stages of embryonic development in which many sensitive processes take place. More specifically, alternative flame retardants may impair cardiac development and angiogenesis. To test whether flame retardants interfere with arterial wall development, we exposed rat aortic smooth muscle cells to two alternative flame retardants, triphenyl phosphate (TPP) and tris 2-chloroethyl phosphate (TCEP). Using the wound scrape migration assay, we measured the rate at which these alternative flame retardants affect proliferation and fibrosis. If found that TPP and TCEP inhibit aortic smooth muscle cell migration, this may impact the heart's ability to develop and function properly.

Kobe White, Sean Laverty, Matthew Parks, James Long, and Andrew T. Taylor (University of Central Oklahoma)

9:45-10:00 in 351 Tandy

****HYBRID SWARMING OF NEOSHO BASS WITH NON-NATIVE SMALLMOUTH BASS IN THE UPPER ILLINOIS RIVER BASIN, OKLAHOMA**

Recent molecular investigations support the distinctiveness of the Neosho Bass (*Micropterus velox*) of the Ozark Highlands as a distinct species and evolutionary lineage from Smallmouth Bass (*M. dolomieu*). Like other endemic black basses, Neosho Bass are threatened by hybridization with non-native *Micropterus* forms. Non-native Smallmouth Bass were stocked in Lake Tenkiller in 1991 and 1992 to create better angling opportunities, resulting in introgressive hybridization with Neosho Bass in areas upstream of the impoundment, including the Illinois River. To inform management and conservation efforts, our objective was to characterize the spatial extent and directionality of introgressive hybridization, while also exploring the influences of abiotic landscape factors on hybridization. We sampled 622 individuals across the upper Illinois River Basin in April and May of 2019 and genotyped fish with a low-density SNP panel previously designed to identify Smallmouth Bass, Neosho Bass, and their hybrids. We characterized hybridization dynamics with several complementary approaches, including clustering assignment in Structure, hybrid class assignment with Newhybrids, and hybrid index estimation in Introgress. Highest rates of introgression were found in the largest watershed within our study system (Illinois River) with the lowest rates occurring in our smallest stream (Caney Creek). Percent deciduous forest was positively correlated with proportion of native alleles while watershed size was negatively correlated with proportion of native alleles. Future work will add an additional 650 specimens to increase spatial sampling coverage and include an mtDNA marker to examine symmetry of hybridization. Results from this study could help inform future conservation and management efforts for Neosho Bass in the region by identifying potential conservation priority areas and providing a better understanding of the conservation-genetic status of Neosho Bass.

Jacob O. Williams, Kohl D. Kirby, and Jacob T. LaMar (Oklahoma Christian University)

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***CONSERVATION OF DOCK AND RICTOR IN *DROSOPHILA* SPECIES**

This study examined the evolutionary conservation of the dock and rictor genes in various *Drosophila* species. Based on the conservation trends seen in the insulin/TOR pathway of *Drosophila*, it was hypothesized that the more connections a gene had the more conserved it would be. In this case, rictor was expected to be more conserved than dock. To compare the conservation of dock and rictor, each of the genes were first annotated in *Drosophila melanogaster*. The genes were then annotated in other *Drosophila* species. The sequence of amino acids that encoded each protein were compared in the different species, and then an evolutionary divergence score was calculated using a special formula. The results did not support the original hypothesis, and dock showed to be more conserved than rictor. However, this outcome could be due to a flaw in the divergence scoring system.

Lorelei Winton, Jacob Burch-Konda, and Marianna Patrauchan (Oklahoma State University - Stillwater Campus)

Poster 26

***NOVEL CA²⁺ SENSOR CONTROLLING IRON UPTAKE IN *P. AERUGINOSA*, A HUMAN PATHOGEN**

Pseudomonas aeruginosa is a Gram negative, opportunistic pathogen which causes a wide range of severe infections in humans. These infections are difficult to treat and, especially in the lungs of cystic fibrosis (CF) patients, often become chronic. Complicating eradication of *P. aeruginosa* is pyoverdine, a virulence factor which aids bacterial iron acquisition in iron-limited environments. Previous work has shown that pyoverdine production in *P. aeruginosa* strain PAO1 is increased under elevated levels of Ca²⁺, as are found in the pulmonary fluids of CF patients. A Ca²⁺-binding EF-hand protein, EfhP (PA4107), was demonstrated to be critical for the Ca²⁺-regulated virulence in PAO1. This study seeks to characterize EfhP regulation of the *P. aeruginosa* response to Ca²⁺, particularly pertaining to critical iron uptake pathways. We have established that deletion of efhP significantly hinders PAO1 pyoverdine production when grown at high Ca²⁺ in BMM8 medium. Pyoverdine is a fluorescent molecule quantified by measuring fluorescence at 400 nm excitation/460 nm emission and normalized by OD600. The presence of efhP in several CF clinical isolates was confirmed with PCR using efhP-specific primers. We observed that these clinical isolates also show increased pyoverdine production at 5 mM Ca²⁺ vs. the no Ca²⁺ condition. In the clinically relevant synthetic cystic fibrosis sputum medium (SCFM), PAO1 shows increased pyoverdine production with increasing Ca²⁺ concentrations. In the future, we aim to identify specific sequences in the efhP gene that are most important to the regulation of pyoverdine production by testing a series of strains expressing mutated EfhP. We also plan to evaluate expression of efhP in CF clinical isolates and test for their pyoverdine production when cultured in SCFM. The new knowledge gained can support further studies to develop novel efficient medications to improve the quality of life of CF patients who struggle with chronic *P. aeruginosa* infections.

Cameron Wood¹, Devon Chen¹, Lindsey J. Long¹, and Laura Reed² (¹Oklahoma Christian University; ²Genomics Education Program - University of Alabama)

Poster 37

***THE EVOLUTIONARY STATUS OF SIMA AND PTP61F**

The insulin/TOR pathway is responsible for maintaining homeostasis by regulating cell growth, blood glucose levels, and protein synthesis. This study focused on the synteny and conservation that occurred between the genes *sima* and *Ptp61F* in the insulin pathway. Within a gene, more physical interactions that are connected will consequently hinder the evolutionary alterations that occur. It was hypothesized that *sima* will be more conserved than *Ptp61F* because *sima* contains a higher number of physical interactions. This was tested by locating the genes *sima* and *Ptp61F* in multiple species in *Drosophila* and comparing them to the reference species *Drosophila melanogaster*. Annotations of each gene were performed using web-based resources and using data from other students and researchers, the divergence scores of multiple species were calculated. The results indicated that the gene *sima* was less evolutionary diverged than *Ptp61F* due to a higher number of physical interactions.

Elijah Woodward¹, Aaron Seto², Guoli Hu³, Yilin Yu³, and Courtney M Karner³ (¹East Central University; ²Brown University; ³ University of Texas Southwestern)

Poster 59

***GENERATION OF THREE NEW RUNX2 CYS-TO-ALA MUTANTS USING SITE-DIRECTED MUTAGENESIS**

The RUNX2 transcription factor plays an essential role in regulating mineral metabolism as it takes part in controlling calcium levels by facilitating osteoblast differentiation and bone development. RUNX2 contains five cysteine residues: C13, C123, C132, C357, and C473. C123 and C132 C473 exist inside the RUNX2 runt domain, an evolutionary conserved protein region that is important for RUNX2 and DNA binding. Since C123 and C132 C437 are highly conserved and directly involved in DNA binding, interaction with reactive oxygen species (ROS), which is produced from normal cell functions, such as mitochondrial metabolism is of much interest. With preliminary data indicating ROS oxidation rapidly reduces RUNX2 proteins, we hypothesized that oxidation of the RUNX2 transcription factor through its conserved cysteine residues interferes with the transcription factor's stability and capability. We employed site-directed mutagenesis induce the following mutations: C123A and C132A and C473A in an attempt to prevent oxidation, and by extension, protein degradation and loss of function.

Luke M.D. Woodward, Lucy V. Ramirez, and Eric Howard (East Central University)

Poster 50

***STREAMLINING SPECIES ANALYSIS PROGRAM**

Competent disease vectors in Pontotoc County remain mostly unidentified due to a traditional identification system with high labor and financial costs. A research process to ascertain a robust specimen identification method was developed and tested for use in longitudinal vector competence identification program in Pontotoc Co., OK. We hypothesize that with the use of competent vector-specific primer design, a mixed pool of multiple unidentified mosquitoes could be identified as containing known competent vectors; this would be a useful tool, leading to efficient hazardous vector identification. DNA was extracted from mosquito samples collected in Pontotoc county. This was followed by DNA amplification via polymerase chain reaction (PCR) using standardized barcoding primers. Gel electrophoresis was used to verify that sufficient amplification occurred prior to Sanger sequencing. Successful sequences were confirmed by forward and reverse assembly followed by species identification using NCBI BLAST. DNA from over 100 mosquito specimens have been successfully extracted, amplified, and sequenced. Of

those samples the majority have been identified at the species level. These results have been sorted into vector competence categories. With a streamlined approach, disease risk can be more easily and consistently mitigated when the prevalence of competent disease vectors is identified. Being able to identify competent vectors quickly, will allow for increased public awareness concerning mosquito transmitted diseases. This project was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award P20GM103447. The content in this publication is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.