

**110<sup>th</sup> ANNUAL TECHNICAL MEETING**  
**OKLAHOMA ACADEMY OF SCIENCE**  
**EAST CENTRAL UNIVERSITY, ADA**

**PROGRAM SUMMARY**

**Thursday, 4 November 2021**

6:30 p.m. Executive Council Dinner/Meeting ..... CBCC Foundation Hall

**Friday, 5 November 2021**

7:30 a.m. Registration for Technical Meeting ..... PES Lounge 2nd Floor South Side

**Concurrent Scientific Paper Sessions (8:30 - 11:00 a.m.)**

Section A Biological Sciences (Botany & Zoology) ..... PES 206  
Section C Physical Sciences ..... PES 228  
Section D Social Sciences ..... PES 228  
Section E Science Communication and Education ..... PES 206  
Section G Applied Ecology and Conservation ..... PES 228  
Section H Microbiology ..... PES 240  
Section J Biochemistry and Molecular Biology ..... PES 166  
Section L Mathematics, Statistics, & Computer Science..... PES 156  
Section N Biomedical Sciences ..... PES 106

**Section Business Meetings (either 11:00 or 11:15)**

Section A Biological Sciences – Botany & Zoology ..... 11:00-11:15 PES 206  
Section B Geology ..... 11:15-11:30, PES 156  
Section C Physical Sciences ..... 11:15-11:30, PES 228  
Section D Social Sciences ..... 11:00-11:15, PES 228  
Section E Science Communication and Education ..... 11:15-11:30, PES 206  
Section F Geography ..... 11:15-11:30, PES 154  
Section G Applied Ecology and Conservation ..... 11:15-11:30, PES 240  
Section H Microbiology ..... 11:00-11:15, PES 240  
Section I Engineering Sciences ..... 11:00-11:15, PES 154  
Section J Biochemistry and Molecular Biology ..... 11:00-11:15, PES 166  
Section K Microscopy ..... 11:15-11:30, PES 106  
Section L Mathematics, Stats, & Comp. Science ..... 11:00-11:15, PES 156  
Section M Environmental Sciences ..... 11:15-11:30, PES 166  
Section N Biomedical Sciences ..... 11:00-11:15, PES 106

11:30 a.m. Academy Business Meeting..... CBCC Foundation Hall

All OAS members are encouraged to attend. Visitors are welcome.

12:00 p.m..... Academy Luncheon & Speaker  
CBCC Foundation Hall  
(Admission by ticket only)

1:30-3:30 p.m. ....Poster Session for All Sections, Hallways of PES

## REFRESHMENTS

Light refreshments will be served in PES 203.

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## LUNCHEON SPEAKER

### **“Clonal and transcriptional dynamics of direct-lineage reprogramming at single-cell resolution.” Brent Bidy**

Brent Bidy is from Seminole, OK. He attended East Central University where he participated in research with Dr. Stephen Fields and presented his research at Research Day at the Capital among many other presentations. He earned a BS in Molecular Biology in 2014. He attended graduate school at the Washington University in St Louis, MO where he expects to earn his PhD in December of 2020.

Bidy earned the distinction of having a first author paper in *Nature* in Dec. 2018 from research that developed a novel lineage-tracing technique that enables the parallel capture of lineage and gene expression information at the single-cell level. These techniques led to mapping the dynamic lineal and transcriptional landscape of the direct reprogramming of fibroblasts into hepatocytes. Brent A. Bidy, Wenjun Kong, Kenji Kamimoto, Chuner Guo, Sarah E. Waye, Tao Sun & Samantha A. Morris. **Single-cell mapping of lineage and identity in direct reprogramming.** *Nature*. 2018 Dec 13; 564(7735):219-224. doi: 10.1038/s41586-018-0744-4.

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## SPECIAL THANKS

Dr. Karen Williams for coordinating this year's meeting; College of Health and Science Dean, Dr. Kenneth Andrews and his secretary Kelly Payne for their support in hosting this event; Dr. Alisha Howard; Dr. Sanjiv Jha; Dr. Charles Crittall; Dr. April Nesbit; Dr. Charlie Biles; Dr. Nick Jacob; Dr. George Wang; Dr. Randall Maples; Dr. Douglas Bryhan; Dr. Bruce Moring for his leadership for the poster session; to those involved in IT room support and planning; David, the PES custodian, who helps clean up; to all the students who helped; Rick Haight with food service for the meals and snacks; and Stephanie Cooper for assisting with the conference center arrangements.

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## UPCOMING MEETINGS

2022 Fall Field Meeting, Lake Murray State Park (joint meeting with the Oklahoma Native Plant Society)  
2022 Annual Technical Meeting TBA

## GENERAL INFORMATION

**Name Badges:** Name badges, provided upon registration, must be worn at all times by all individuals attending Academy section programs, business meetings, and luncheon. If your badge is not visible, you may be asked to leave by the persons in charge. Lost badges may be replaced at the registration desk upon verification of your registration documents. **All presenters must register and wear an official name badge.**

**On-site Registration Fees:**

- Member - \$30.00
- Non-member - \$45.00
- Student - \$15.00
- ECU Students - free
- Luncheon tickets (if available) - \$20.00

**2021 and 2022 Dues are Payable:** The OAS registration desk will accept dues payments.

- Professional - \$30.00
- Graduate/Undergraduate Student - \$20.00
- Family - \$35.00
- Life - \$600.00

**Guidelines for Abstract Publication:** Abstracts may be published in the *Proceedings of the Oklahoma Academy of Science*, subject to the editorial policies as stated in the most recent issue of the *POAS* and the review of the Editorial Board. Specific formatting instructions for abstracts may be found at [www.oklahomaacademyofscience.org](http://www.oklahomaacademyofscience.org). Abstract publication fee is \$38. *POAS* editor is Dr. Mostafa S. Elshahed, [mostafa@okstate.edu](mailto:mostafa@okstate.edu).

**Executive Director:** Inquiries concerning upcoming OAS activities and membership may be directed to Dr. Adam Ryburn, OAS Executive Director, 2501 N. Blackwelder Ave, OKC, OK 73106, (405) 208-5044, [aryburn@okcu.edu](mailto:aryburn@okcu.edu).

## PROFESSIONAL DEVELOPMENT WORKSHOPS

Professional Development opportunities are available for faculty (and interested graduate students) and run concurrent with the poster session in the afternoon (1:30-3:00). See the list of workshops below.

**Title:** Implementation of a computer-based research project in lower and upper division Biology courses

**Location:** PES 156

**Time:** 1:30-2:00 PM and 2:00-2:30 PM

**Presenters:** Lindsey Long, Oklahoma Christian University and Alisha Howard, East Central University

**Description:** The Genomics Education Partnership (GEP) is a nation-wide collaboration of 100+ institutions that integrates active learning into the undergraduate curriculum through Course-based Undergraduate Research Experiences (CUREs) centered in bioinformatics and genomics. GEP faculty are provided training, curriculum, technical, intellectual, and TA support, professional development, and a community of faculty to serve as mentors. This workshop will provide an overview of the GEP and demonstrate different examples of how GEP research projects were implemented in the classroom.

**Title:** Alternatives To Final Exams: Unessays, Lightning Talks, and Epic Finales

**Time:** 1:30-2:00 PM and 2:15-2:45 PM

**Location:** PES 166

**Presenters:** Laurie Kauffman, Oklahoma City University

**Description:** Does a typical final exam really demonstrate and celebrate how much students have learned in a course? I will explain my use of, and experience with, alternative assessments that allow students to demonstrate their learning in ways that can be more memorable than a traditional final exam.

**Title:** Programming in the Cloud

**Location:** PES 154

**Time:** 2:15-2:45 PM

**Presenters:** Nicholas Jacob, East Central University

**Description:** Utilizing free, open source resources, it is easier than ever to integrate programming into your courses. We will examine coding in python and R using cloud computing. We will show how students can create reports and share them with class or the world with just an internet connection.

**Title:** Using online polling platforms in classes

**Time:** 1:30-2:00 PM and 2:00-2:30 PM

**Location:** PES 106

**Presenters:** Janaki Iyer, Northeastern State University

**Description:** The workshop will be geared towards using online polling platforms in face-to-face or synchronous virtual classes. Participants will become familiar with platforms like TopHat, the Zoom polling feature, and poll everywhere and how they can be used for engaging students. We will also cover how these platforms can be used for assessment purposes.

## SECTION A: BIOLOGICAL SCIENCES

PES 206

Section Chair: Rachel Jones; Vice-Chair: Jason Shaw

- 9:30-9:45 \*A COMPARISON OF TICK ABUNDANCE ON DISC GOLF COURSES IN URBAN AND SUBURBAN CENTRAL OKLAHOMA PARKS. Jessie Merrifield. University of Oklahoma.
- 9:45-10:00 \*PRELIMINARY TRENDS IN SMALL MAMMAL POPULATIONS AFTER THREE YEARS OF MARK-RECAPTURE RESEARCH IN THE GYPSUM HILLS OF WESTERN OKLAHOMA. C. Claire Smith. University of Central Oklahoma.
- 10:00-10:15 \*\*THE POTENTIAL FOR USING CERVIDS AS PROXIES FOR PALEOECOLOGICAL RECONSTRUCTION THROUGH STABLE ISOTOPE ANALYSIS: IMPLICATIONS FOR OUT OF AFRICA I. Forrest Valkai. University of Tulsa.
- 10:15-10:30 \*\*ANALYSIS OF THE SPATIAL DISTRIBUTION OF GEOREFERENCED HERBARIUM RECORDS IN OKLAHOMA AND TEXAS. Sierra Hubbard. Oklahoma State University.
- 10:30-10:45 THREE SISTER POLYCULTURE AND INSECT VISITATION. Leah S. Dudley. East Central University.
- 10:45-11:00 FLORA OF OKLAHOMA INC. (Annual Meeting). Mark Fishbein (Oklahoma State University) Coordin.
- 11:00-11:15 BIOLOGICAL SCIENCES SECTION MEETING

### Posters

- Poster 1 \*BEE POLLINATION PATTERNS WITHIN A THREE SISTERS GARDEN. Hallie Reed. East Central University.
- Poster 2 \*LEAF WEIGHT AND SURFACE AREA OF THE THREE SISTERS IN MONOCULTURES AND POLYCULTURES. Jamian Maxwell. East Central University.
- Poster 3 \*NURSE PLANT EFFECT INCREASES PLANT SIZE AND INSECT ABUNDANCE ON *SOLANUM CAMPYLACANTHUM* ON AN AFRICAN SAVANNAH. Sudikshya Budhathoki. East Central University.

## SECTION C: PHYSICAL SCIENCES

PES 228

Section Chair, Randall D. Maples; Vice-Chair: Benjamin Tayo

- 10:00-10:15 \*INTERACTION OF DNA NUCLEOBASES WITH ARMCHAIR GRAPHENE NANORIBBONS: A VAN DER WAALS DENSITY FUNCTIONAL THEORY INVESTIGATION. Pujan Khatri. East Central University.
- 10:15-10:30 SINGLE-MOLECULE ANALYSIS OF DNA NUCLEOBASES USING VAN DER WAALS HETEROSTRUCTURES: A COMPUTATIONAL STUDY. Benjamin O. Tayo. University of Central Oklahoma.
- 11:15-11:30 PHYSICAL SCIENCES SECTION MEETING

### Posters

- Poster 4 G3MP2 COMPUTATIONAL STUDY OF GASEOUS BORON AND ALUMINUM HYDROXIDES. Dwight L. Myers. East Central University.
- Poster 5 GLOBAL REACTIVITY DESCRIPTORS OF CHLOROFLUOROPYRROLES. Daniel McInnes. East Central University.
- Poster 6 RECOVERY STUDY OF SILVER NANOPARTICLES THROUGH LIMESTONE AND DOLOMITE PACKED COLUMNS. Randall Maples. East Central University.
- Poster 7 \*A DENSITY FUNCTIONAL THEORY STUDY OF THE INTERACTION OF DNA NUCLEOBASES WITH PRISTINE AND DEFECTIVE GRAPHENE NANORIBBONS. Sagar Ghimire. East Central University.
- Poster 8 \*AN ANALYSIS OF 400-450NM COMPONENTS OF SEMICONDUCTOR AND UV ILLUMINATION. Andrew Seeberger and Ethan Strickler. East Central University.

\* Undergraduate \*\* Graduate

**SECTION D: SOCIAL SCIENCES**  
**PES 228**

**Section Chair: Jeff Seger; Vice-Chair: William Stern**

- 10:45-11:00 CONCEPTUALIZING SOFT SKILLS OF HEALTHCARE PROVIDERS. Nidaa AbuJbara. Tulsa Community College.
- 11:00-11:15 SOCIAL SCIENCES SECTION MEETING

**Posters**

- Poster 9 \*THE NEAR SIGNIFICANCE OF THE RELATIONSHIP AMONG CHILDHOOD TRAUMA, ATTACHMENT STYLE, AND RELATIONSHIP SATISFACTION. Kaylee Thoma. East Central University.
- Poster 10 SECONDARY SCHOOLING TYPE AND DIFFERENCES IN ACADEMIC SELF-EFFICACY AND SELF-REGULATION. LaDonna Autrey. East Central University.
- Poster 11 WORKPLACE CIVILITY AND THE WORK-FAMILY INTERFACE: AN EXAMINATION OF MEDIATORS. Jennifer Kisamore. University of Oklahoma-Tulsa.

**SECTION E: SCIENCE COMMUNICATION & EDUCATION**  
**PES 206**

**Section Chair: Kathleen Coughlan**

- 8:30-8:45 DEVELOPING A VECTOR-BORNE DISEASE RESEARCH PROGRAM AND EDUCATION PROGRAM: A REVIEW. Eric Howard. East Central University.
- 8:45-9:00 VIRTUAL TWIN STUDY: EFFECTS ON PARENTING EFFICACY. Robin Roberson. East Central University.
- 9:00-9:15 FIRST-GENERATION STUDENT NEEDS IN STEM "WEED-OUT" COURSES. Darcy Tessman. East Central University.
- 11:15-11:30 SCIENCE COMMUNICATION & EDU. SECTION MEETING

**SECTION G: APPLIED ECOLOGY & CONSERVATION**  
**PES 228**

**Section Chair: Mark Peaden; Vice-Chair: Julia Reid**

- 8:30-8:45 \*SEASONAL VARIATION OF ARTHROPODS COLONIZING DECOMPOSING MAMMALIAN CARCASSES. Sam Ray. East Central University.
- 8:45-9:00 \*\*THE PALEOECOLOGY OF YAHUAI CAVE IN GUANGXI, CHINA AT 120 KYA: IMPLICATIONS FOR EARLY MODERN HUMAN DISPERSAL INTO EAST ASIA. Kathleen Kelley. University of Tulsa.
- 9:00-9:15 \*\*NICHE FIGHTING: EXPLORING THE DISTRIBUTION OF NATIVE AND INVASIVE SPECIES OF BUMBLE BEES (HYMENOPTERA: APIDAE) IN CHILE, USING CITIZEN SCIENCE DATA. Jose Montalva. East Central University.
- 9:15-9:30 \*\*INVESTIGATION OF THE ECOLOGY OF HARRIS MUD CRAB IN LAKE TEXOMA. Shelbie Weaver. University of Central Oklahoma.
- 9:30-9:45 DIETARY PB IMPAIRS SONG DEVELOPMENT AND ALTERS SEXUAL TRAITS IN MALE ZEBRA FINCHES (*TAENIOPYGIA GUTTATA*). Christopher Goodchild. University of Central Oklahoma.
- 11:15-11:30 APPLIED ECOLOGY & CONSERVATION SECTION MEETING (**PES 240**)

**Posters**

- Poster 12 \*A PRELIMINARY ANALYSIS OF THE EMBRYOTOXICITY OF MULTIPLE POLYCYCLIC AROMATIC HYDROCARBONS IN CHICKEN EGGS. Hallum Ewbank. University of Central Oklahoma.
- Poster 13 \*EFFECTS OF HERBIVORY ON GROWTH OF OVERSTORY GREEN ASH (*FRAXINUS PENNSYLVANICA*, MARSHALL) AT ARCADIA LAKE, OKLAHOMA COUNTY, OKLAHOMA. Valeria Escareno. University of Central Oklahoma.

**SECTION H: MICROBIOLOGY**  
**PES 240**

**Section Chair: Charlie Biles; Vice-Chair: Avi Mitra**

- 8:30-8:45 \*THE ROLE OF THE CALCIUM SIGNALING IN QUORUM SENSING OF *PSEUDOMONAS AERUGINOSA*. Myriam Achour. Oklahoma State University.
- 8:45-9:00 \*ANTIBIOTIC RESISTANT AND GROWTH PATTERNS OF INVASIVE SPECIES IMPORTED ON MELONS FROM CENTRAL AMERICA. Katlyn Hampton. East Central University.
- 9:00-9:15 \*NOVEL MELANIN INSPIRED COMPOUND POSSESSES MEMBRANE-DIRECTED ANTIBACTERIAL MECHANISM FOR GRAM-POSITIVE BACTERIA. Daniel Reed. Oklahoma State University.
- 9:15-9:30 \*EXAMINATION OF DICTYOSTELIUM G PROTEIN FUNCTION IN RESPONSES TO THE CHEMOATTRACTANT CAMP. Nicholas Kiger. Oklahoma State University.
- 9:45-10:00 CHARACTERIZING THE ROLE OF PA2803 PROTEIN IN ANTIBIOTIC RESISTANCE IN BACTERIA. Anna Khanov. Stillwater High School.
- 10:00-10:15 \*HOW DOES *MYCOBACTERIUM TUBERCULOSIS* ACQUIRE HEME IRON?. November Sankey. Oklahoma State University.
- 10:15-10:30 \*\*ISOLATION AND CHARACTERIZATION OF *ACINETOBACTER BAUMANNII* BACTERIOPHAGE VB\_AB\_SCL1 FROM OKLAHOMA WASTE-WATER. Samantha Coplen. University of Central Oklahoma.
- 10:30-10:45 BIOFILM SIGNALING BY GLYCEROL IN *PSEUDOMONAS AERUGINOSA*. Simon A.M. Underhill. Oklahoma State University.
- 11:00-11:15 MICROBIOLOGY SECTION MEETING

**Posters**

- Poster 14 \*BACTERIAL TWO HYBRID ANALYSIS OF *CHLAMYDIA TRACHOMATIS* PROTEINS. Kayli Nail. Oklahoma State University.
- Poster 15 \*PURIFICATION AND CHARACTERIZATION OF TWO HEME INDUCED GENES IN *MYCOBACTERIUM TUBERCULOSIS*. Genesis Terrazas Valero. Oklahoma State University.
- Poster 16 \*ISOLATION AND CHARACTERIZATION OF ARTHROBACTERIOPHAGE GIPSYDANGER FROM OKLAHOMA SOIL. Kateri Gebhart. University of Central Oklahoma.
- Poster 17 \*MOLECULAR AND MORPHOLOGICAL CHARACTERISTICS OF PATHOGENIC FUNGAL SPECIES IMPORTED FROM CENTRAL AMERICA. Dylan Melton. East Central University.
- Poster 18 \*NOVEL ANTIBIOTICS FROM OKLAHOMA SOIL. Elizabeth Gwartney. Oklahoma City University.

**SECTION J: BIOCHEMISTRY AND MOLECULAR BIOLOGY**  
**PES 166**

**Section Chair: Shelley Xia; Vice-Chair: April Nesbit**

- 8:30-8:45 \*VECTORBORNE DISEASE IDENTIFICATION AND ANALYSIS. Alejandro Arriaga. East Central University.
- 8:45-9:00 \*CONSERVATION OF KINASE DOMAINS WITHIN THE INSULIN/TOR SIGNALING PATHWAY OF *DROSOPHILA*. Aidan Long. Oklahoma Christian University.
- 9:00-9:15 \*DNA POLYMERASE EPSILON MUTANTS EXHIBIT DELAYED RECOVERY AFTER DNA DAMAGE. Ostmo Lydia. Northeastern State University.
- 9:15-9:30 \*ANALYSIS OF EFFECTS OF CANNABINOIDS ON GENE EXPRESSIONS IN TRIPLE NEGATIVE BREAST CANCER. Anastasia Smith. Oral Roberts University.
- 9:45-10:00 \*\**BACILLUS SUBTILIS* RETAINS CHARACTERISTIC ENVIRONMENTAL STRESS RESPONSES ACROSS DIVERSE STRESSORS. Christopher Hamm. Oklahoma State University.
- 10:00-10:15 \*\*UNDERSTANDING EPIGENETIC MECHANISM: A NOVEL WAY TO APPROACH THERAPEUTIC TARGETS FOR THE TREATMENT OF COLITIS. Radhika Pande. Oklahoma State University Center for Health Sciences.
- 10:15-10:30 \*\*FUNCTIONAL STUDY OF C1Q/TNF-RELATED PROTEIN 6 (CTRP6) IN OBESITY AND DIABETES. Jeevotham Senthil Kumar. Oklahoma State University.

\* Undergraduate \*\* Graduate

## SECTION J: BIOCHEMISTRY AND MOLECULAR BIOLOGY (CONTINUED)

10:30-10:45 \*\*CO-LOCALIZATION STUDIES REVEAL DISTINCT PATTERNS OF POLE: MCM10 ASSOCIATION DURING CELL CYCLE IN HUMAN CELLS. Sarah Woller. Northeastern State University.

11:00-11:15 BIOCHEMISTRY AND MOLECULAR BIOLOGY SECTION MEETING

### **Posters**

- Poster 19 \*3H04 KINETIC ANALYSIS. Taje' Woods. Oklahoma Christian University.
- Poster 20 \*A COMPARISON OF THE EVOLUTIONARY CONSTRAINTS ON IMPL2 AND SLMB. Lucas Martinez. Oklahoma Christian University.
- Poster 21 \*ANALYSIS OF GENE EXPRESSION IN TRIPLE-NEGATIVE BREAST CANCER EPITHELIA AFTER TREATMENT WITH FULL-SPECTRUM CBD OIL. Nathaniel Hunter. Oral Roberts University.
- Poster 22 \*ANALYZING DNA BINDING OF YFAX IN *ESCHERICHIA COLI*. Mary Chambless. East Central University.
- Poster 23 \*ANALYZING KINASE DOMAIN CONSERVATION IN *DROSOPHILA*. James O'Brien. Oklahoma Christian University.
- Poster 24 \*COMPARING DIVERGENCE AND CONSERVATION IN THE SLMB GENE BASED ON GENOMIC NEIGHBORHOODS. Reagan Stephens. Oklahoma Christian University.
- Poster 25 \*DETERMINING OPTIMAL EXTRACTION CONDITIONS TO ISOLATE A PEPTIDE CONTAINING POLYSACCHARIDE WITH ANTI-CANCER PROPERTIES FROM *GANODERMA LUCIDUM*. Sneha Jacob. Oral Roberts University.
- Poster 26 \*EVALUATION OF SLMB AND ROC1A CONSERVATION WITHIN THE E3 UBIQUITINATION LIGASE OF THE INSULIN/TOR PATHWAY. Joseph Zajac. Oklahoma Christian University.
- Poster 27 \*EVOLUTIONARY CONSERVATION OF ROC1A AND SLMB IN THE INSULIN/TOR PATHWAY IN *DROSOPHILA*. Dusenge Shaida Kamali. Oklahoma Christian University.
- Poster 28 \*HEXOKINASE II INHIBITION IN THE PRESENCE OF FENBENDAZOLE. Mary Hang Nguyen. Northeastern State University.
- Poster 29 \*INVESTIGATION OF BOVINE LEUKEMIA VIRUS PREVALENCE IN OKLAHOMA HERDS. Jordan Odell. East Central University.
- Poster 30 \*MARTY MCFLY: A GENE ANNOTATION STORY. Andrew J. Sims. Oklahoma Christian University.
- Poster 31 \*PRELIMINARY BIOCHEMICAL AND STRUCTURAL CHARACTERIZATION OF A TYPE-II BETA-CARBONIC ANHYDRASE FROM *RHODOCOCCUS EQUI*. Camille Goerend. Southwestern Oklahoma State University.
- Poster 32 \*PRELIMINARY CRYSTALLIZATION AND STRUCTURAL CHARACTERIZATION OF A RO0101, A DPS HOMOLOG FROM *RHODOCOCCUS JOSTII*. Nicholas Bauer. Southwestern Oklahoma State University.
- Poster 33 \*DSOR1 CONSERVATION WITHIN THE INSULIN/TOR PATHWAY OF *DROSOPHILA*. Zachary Mearse. Oklahoma Christian University.
- Poster 34 \*EVOLUTIONARY CONSERVATION OF DSOR1 IN SPECIES OF *DROSOPHILA*. Sommers Bowker and Harmony Hysten. Oklahoma Christian University.
- Poster 35 \*HIGH EVOLUTIONARY CONSERVATION OF DSOR1 AS COMPARED TO ROC1A. Bridgiet Alvarado. Oklahoma Christian University.
- Poster 36 \*INCREASING DIVERGENCE OF IMPL2 AMONG SPECIES. Brooklynn Franks and Tyler Godsey. Oklahoma Christian University.

**SECTION L: MATHEMATICS, COMPUTER SCIENCE, AND STATISTICS**  
**PES 156**

**Section Chair: Mehmet Aktas; Vice-Chair: Esra Akbas**

- 8:30-8:45 \*THE VIEW ON VACCINES. Brenden P. Latham. East Central University.
- 8:45-9:00 \*UNDERSTANDING MATHEMATICAL COMPONENTS OF DEEP LEARNING. Jacob Mantooth. East Central University.
- 9:00-9:15 APPROXIMATING RELU NEURAL NETWORK SOLUTIONS USING LINEAR REGRESSION. Maxim Khanov. Stillwater High School.
- 9:15-9:30 \*HYPERGRAPH LAPLACIANS IN DIFFUSION FRAMEWORK. Rakin Riza. University of Central Oklahoma.
- 9:45-10:00 \*IDENTIFYING CRITICAL HIGHER-ORDER INTERACTIONS IN COMPLEX NETWORKS. Sidra Jawaaid. University of Central Oklahoma.
- 10:00-10:15 HOMOLOGY PRESERVING GRAPH COMPRESSION. Mehmet Aktas. University of Central Oklahoma.
- 10:15-10:30 AN INTRODUCTION TO EVENQUADS: CELEBRATING WOMEN IN MATH. Michelle Lastrina. East Central University.
- 10:30-10:45 CLASSIFYING NBA PLAYER POSITION FROM BOXSCORE STATISTICS. Andrew Wells. East Central University.
- 11:00-11:15 MATHEMATICS, COMPUTER SCIENCE, AND STATISTICS SECTION MEETING

**SECTION M: ENVIRONMENTAL SCIENCES**  
**PES 166**

**Section Chair: Dan McInnes; Vice-Chair: Charles Crittall**

- 11:15-11:30 ENVIRONMENTAL SCIENCES SECTION MEETING

**Posters**

- Poster 37 \*\*ENVIRONMENTAL STEWARDSHIP IN CITIZEN SCIENCE PARTICIPANTS. Cheyanne Olson. Rogers State University.
- Poster 38 \*EFFECTS OF LIGHT INTENSITY ON THE MORPHOLOGY, GROWTH RATE, AND PHENOLIC CONTENT OF *ZYGNEMA*. Ethan C. Long. Southwestern Oklahoma State University.
- Poster 39 \*OBSERVATION OF LAND USE, SOIL QUALITY, AND ECOSYSTEM SERVICES. Leonard Cole Davis. East Central University.
- Poster 40 \*SYSTEM MODELS FOR LONG-TERM REGIONAL WATERSHED MANAGEMENT: A PRELIMINARY LAKE MODEL. Ann McNairn. East Central University.
- Poster 41 \*VECTOR-BORNE DISEASE ASSESSMENT. Sarah Gault. East Central University.



## SECTION N: BIOMEDICAL SCIENCES

### PES 106

**Section Chair: Lindsey Long; Vice-Chair: Nikki Seagraves**

- 8:30-8:45 \*AFFORDANCE BASED ENGINEERING APPLIED TO RENAL FAILURE. Mackenzie Edwards. Oral Roberts University.
- 8:45-9:00 \*BIOLOGICAL CHARACTERIZATION OF THE CYTOTOXIC EFFECTS OF NOVEL LACTATE DEHYDROGENASE INHIBITORS IN MIA PACA-2 CELLS. Hanna Hill. Southwestern Oklahoma State University.
- 9:00-9:15 \*MOLECULAR ANALYSIS OF THE ANTITUMOR EFFECTS OF CANNABINOIDS ON U87-MG CELL LINE. Min Kim. Oral Roberts University.
- 9:15-9:30 \*ANTI-CANCER EFFECTS OF DANDELION'S EXTRACT ON CERVICAL CANCER CELLS. Kayley McBride. University of Central Oklahoma.
- 9:45-10:00 \*EFFECTS OF PRETREATMENT OF MICE WITH A SERIES OF KETONE COMPOUNDS ON IN VIVO HEPATIC MICROSOMAL GLUCURONYLTRANSFERASE ACTIVITY—IMPLICATIONS FOR KETONE-DRUG INTERACTIONS. Brittany L. Moehnke. Oklahoma Christian University.
- 10:00-10:15 \*CELLUS: DIGITALIZED, LOW-COST SUPER-RESOLUTION MICROSCOPE. Daniel Oforji. Oral Roberts University.
- 10:15-10:30 \*\*EPIGENETIC REGULATION IN COLON INFLAMMATION. Christy Eslinger. Oklahoma State University Center for Health Sciences.
- 10:30-10:45 \*\*PLATELETS STIMULATE OVARIAN CANCER SPHEROIDS IN EPTIFIBATIDE-SENSITIVE MANNER. Zitha Redempta Isingizwe. University of Oklahoma Health Sciences Center.
- 10:45-11:00 CLONING, SEQUENCING AND IDENTIFICATION OF TWO CLINICAL ENTEROVIRUS ISOLATES FROM OKLAHOMA. Earl Blewett. Oklahoma State University Center for Health Sciences.
- 11:00-11:15 BIOMEDICAL SCIENCES SECTION MEETING

### Posters

- Poster 42 DIFFERENT RESISTANCE STRATEGIES FOR *PSEUDOMONAS AERUGINOSA* AND *SERRATIA MARCESCENS* STRAINS WHEN EXPOSED TO SUB-MIC CONCENTRATIONS OF TRICLOSAN. Sue D. Katz Amburn. Oklahoma State University Center for Health Sciences.
- Poster 43 \*CHARACTERIZATION OF PATHOGENIC *FUSARIUM* SPECIES IMPORTED FROM CENTRAL AMERICA ON MELONS. Angeela Gauchan. East Central University.
- Poster 44 \*PHENOTYPICAL ANALYSIS OF OLD AND YOUNG DUPUYTREN'S DISEASE CELLS. Austin Segrest. University of Central Oklahoma.
- Poster 45 \*TARGETING THE MOLECULAR SWEET TOOTH OF CANCER. Matthew Ahlemeier. Southwestern Oklahoma State University.

## ABSTRACTS

(sorted by presenter's last name)

Nidaa AbuJbara (Tulsa Community College)

### CONCEPTUALIZING SOFT SKILLS OF HEALTHCARE PROVIDERS

Soft skills are set of competencies that contributes to building the relationship between healthcare providers and their patients. The literature reflects ambiguity and disagreement about the nature of soft skills which present limitations in their assessment. This research utilizes the Iceberg Model of Managerial Competencies to define the construct and develop a conceptual model of soft skills. The research discusses the diversity of definitions of soft skills in published research and their importance to healthcare providers. These varied definitions were evaluated and synthesized in order to present the conceptual and operational definition of soft skills for healthcare providers. This research can aid future development of assessment tools to measure soft skills and training efforts to improve provider-patient interactions.

Myriam Achour (Oklahoma State University)

### \*THE ROLE OF THE CALCIUM SIGNALING IN QUORUM SENSING OF *PSEUDOMONAS AERUGINOSA*

*Pseudomonas aeruginosa* has been a direct cause in a great deal of diseases, generating a distinct interest in the scientific research community. As a human pathogen, *P. aeruginosa* has been known to particularly settle in patients with cystic fibrosis, exposing them to lethal infections as well as those with wounds, severe burns and certain cancers. Since *P. aeruginosa* is the most prominent factor in deaths found in cystic fibrosis patients, it has become a priority to discover the reason behind it and how the situation can be avoided. There are many complications in finding treatments for *P. aeruginosa* infections due to its immense antibiotic resistance, making it difficult to fight against the pathogen. Calcium (Ca<sup>2+</sup>) has been shown to have a critical role in the way that these infections occur and, as the main focus of our research lab, cystic fibrosis patients have abnormally high concentrations of Ca<sup>2+</sup> in their cells and secreted fluids. These high Ca<sup>2+</sup> levels are rightfully suspected as one of the underlying causes for the disease. Therefore, in order to understand the mechanisms of *P. aeruginosa* infections more effectively, one must utilize varying Ca<sup>2+</sup> concentrations in their virulence studies of the bacterium and establish a root to the infection. My research has been aimed at determining whether or not an increase in Ca<sup>2+</sup> concentration exemplifies *P. aeruginosa*'s virulence factors by focusing primarily on quorum sensing (QS) and the type III secretion system (T3SS).

Matthew Ahlemeier and Pragya Sharma (Southwestern Oklahoma State University)

### TARGETING THE MOLECULAR SWEET TOOTH OF CANCER

In the attempt to develop innovative anticancer treatments, growing interest has recently focused on the peculiar metabolic properties of cancer cells. Cancer cells undergo metabolic rewiring to support their growth and proliferation. Altered cellular metabolism, including increased dependence on aerobic glycolysis, is a hallmark of cancer cells. In this poster, we will summarize the dysregulated and reprogrammed cancer metabolism. Finally, we will review the role of the enzyme Lactate dehydrogenase-A in cancer progression and its potential as an anticancer drug target.

Mehmet Aktas, Thu Nguyen, and Esra Akbas (University of Central Oklahoma)

### HOMOLOGY PRESERVING GRAPH COMPRESSION

Recently, topological data analysis (TDA) that studies the shape of data by extracting its topological features has become popular in applied network science. Although recent methods show promising performance for various applications, enormous sizes of real-world networks make the existing TDA solutions for graph mining problems hard to adapt with the high computation and space costs. In this talk, we present a graph compression method to reduce the size of the graph while preserving homology and persistent homology, which are the popular tools in TDA. The experimental studies in real-world large-scale graphs validate the efficiency of the proposed compression method.

Bridgiet Alvarado, Tanner German, Lindsey J. Long, and Laura Reed (Oklahoma Christian University)

### \*HIGH EVOLUTIONARY CONSERVATION OF DSOR1 AS COMPARED TO ROC1A

The evolutionary conservation of genes in the insulin/TOR pathway has not been completely studied. In this research, the Roc1a gene was annotated in various species of *Drosophila* and used *D. melanogaster* as a comparison. It was hypothesized that out of the genes taken into consideration, including Roc1a, Dsor1 was the most conserved in the insulin/TOR pathway. This reasoning is based on the number of interactions a gene has with different pathways regardless of its place in the gene. The number of interactions demonstrates how irreplaceable it becomes therefore how well it is conserved in evolution. Through annotation in *D. eugracilis*, *D. kikkawai*, and *D. virilis* our gene of interest, Roc1a, was compared to Dsor1 by its divergence. Roc1a demonstrated more divergence as compared to Dsor1. To compare divergence, scoring was done by taking various factors into account including genomic copies, gene structure, genomic neighborhood, protein sequence identity, protein sequence similarity, and nucleotide sequence similarity. This was evident in the increasing difference in genomic neighborhoods as Roc1a was annotated in species moving down the evolutionary tree. Throughout the research, isoform PC was not found in species past *D. melanogaster*. This could be due to it not being conserved or the isoform could be very weakly expressed in a specific developmental stage. These various observations are in agreement with coinciding research on other genes in the insulin/TOR pathway that support Dsor1 being the most conserved.

Alejandro Arriaga (East Central University)

**\*VECTORBORNE DISEASE IDENTIFICATION AND ANALYSIS**

Community health insufficiencies are prevalent across rural Oklahoma and data centered around numerous factors associated with them are limited. It is essential to determine the severity of current pathogenic vectors in order to devise a plan of action that will better the overall health of rural Oklahoma communities. The research project that was conducted looked into the prevalence of vector borne diseases, such as the West Nile Virus, in an effort to determine the amount of risk mosquitoes pose to civilians in the city of Ada Oklahoma. Collected species of mosquitoes were identified and sorted by using a dichotomous key. The sorted specimen were then sequenced to determine the exact species. With the species identified, the project will continue to test the DNA extracted from the specimen to determine if the specimen are positive for the tested pathogens. Once frequency of pathogen occurrence is calculated, a health reports will be made for the city of Ada in an effort to improve overall community health.

LaDonna Autrey (East Central University)

**SECONDARY SCHOOLING TYPE AND DIFFERENCES IN ACADEMIC SELF-EFFICACY AND SELF-REGULATION**

College students who received secondary education of homeschooling or traditional schooling were compared using self-efficacy for learning and academic self-regulation ability. A quantitative nonexperimental study was used with a convenience sample of 184 traditional undergraduate college students (44 homeschooled and 140 traditionally schooled) from 18 to 24 years of age. Participants completed the SELF, MSLQ, Parental Involvement-Student Section, and demographic questions. An ANCOVA found homeschooled students had significantly higher academic self-efficacy but found no significant differences in academic self-regulation when holding parental involvement and SES constant. No significant difference was found between participants' SES or parental involvement levels, so an ANOVA analysis was used and found homeschooled students had significantly higher academic self-efficacy but no significant difference from traditional students on academic self-regulation. Differences in academic self-efficacy could stem from differing pedagogical approaches and role students play in directing homeschool education not found in traditional schooling. Lack of difference found in academic self-regulation could stem from erratic answer patterns displayed on the MSLQ not found on the other surveys.

Nicholas Bauer (Southwestern Oklahoma State University)

**\*PRELIMINARY CRYSTALLIZATION AND STRUCTURAL CHARACTERIZATION OF A RO0101, A DPS HOMOLOG FROM *RHODOCOCCUS JOSTII***

Dps (DNA binding protein from starved cells) and related ferritin proteins are ubiquitous stress proteins expressed in eukaryotes and prokaryotes. Dps proteins are integral in stress tolerance and known for DNA binding and protection. Furthermore, Dps and related ferritin proteins have been tested extensively in bionanotechnological applications including nanocages, biocontrast agents in medical imaging and in drug delivery. We have identified a Dps homolog, Ro00101 referred as Dps1, from *Rhodococcus jostii*, a soil dwelling bacteria with unparalleled metabolic potential. The dps1 gene encodes a 19.4 kDa protein with conserved domains typical of DNA-binding proteins with ferroxidase activity. The goal of this study is to characterize Rhodococcal Dps protein using biochemical and structural techniques. Cloning and over-expression were done using standard techniques. Protein purification was done using immobilized metal affinity chromatography. The purified protein was concentrated to 17 mg/ml before crystallization trials. Preliminary 96-well sitting-drop vapor diffusion crystallization revealed crystals in drops containing 0.1 M sodium acetate trihydrate pH 4.5. and 2M ammonium sulfate pH 4.5. A single, cryopreserved rhomboidal crystal obtained using hanging-drop method used for data collection diffracted at 1.85 Angstrom. The structure for Dps1 was solved by molecular replacement using *Mycobacterium smegmatis* Dps1 (PDB ID: 1VEI) as a model. The structure of Dps1 revealed a dodecameric protein with conserved ferritin-like and Dps-like trimeric interfaces involved in iron channeling and protein folding respectively. The dimeric interface that harbors the iron-binding active site is also conserved. The active site of Dps1 reveals twin histidine residues from one monomer and glutamine/aspartic acid residues from the second monomer contributing to the two ferroxidase site found in the dimeric interface. Interestingly, Dps1 crystallized without the bound ligand. Studies are underway to obtain ligand-bound structures and to determine the ferroxidase and DNA-binding properties of Dps1.

Earl Blewett, McKayla Muse, Brett Szymanski, and BJ Reddig (Oklahoma State University Center for Health Sciences)

**CLONING, SEQUENCING AND IDENTIFICATION OF TWO CLINICAL ENTEROVIRUS ISOLATES FROM OKLAHOMA**

We obtained clinical enterovirus isolates from the Oklahoma State Department of Health. Two isolates have proven very useful and have been studied in two publications (Brett, et al. 2019a, 2019b). We are continuing research on anti-viral drugs that act on a wide spectrum of viruses, using these isolates. To confirm the identity of the isolates, which were typed at the Department of Health, we are cloning, sequencing and analyzing the viral genomic nucleic acid sequence using bioinformatics. The isolate CoxA9-01 has been positively identified as a Cocksackie A Virus. Isolate Echo2-01 has been confirmed as an Echovirus 2.

Sommers Bowker<sup>1</sup>, Julia Davila<sup>1</sup>, Lindsey J. Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

**\*EVOLUTIONARY CONSERVATION OF DSOR1 IN SPECIES OF *DROSOPHILA***

This project contributed to the Genomics Education Partnership (GEP) Pathways Project. The Pathways Project is currently focused on the insulin pathway in species of *Drosophila*. Based on current data, it is believed that genes closer to the terminal end of the pathway are more conserved compared to genes near the beginning of the pathway. It is believed that genes near the terminal end of a pathway are connected and therefore impact more genes within the same pathway. Here, four genes in the insulin pathway (ImpL2, Dsor1, slmb, and Roc1a) were compared in five species of *Drosophila* (D.), using *D. melanogaster* as a baseline to observe evolutionary conservation. The Basic Local Alignment Search Tool (BLAST) was used to investigate similar

regions of nucleotides or proteins within these species to establish evolutionary relationships. Based on all observations collected from this experiment, Dsor1 is the most conserved gene compared to ImpL2, slmb, and Roc1a in all species studied.

Sudikshya Budhathoki and H. George Wang (East Central University)

**\*NURSE PLANT EFFECT INCREASES PLANT SIZE AND INSECT ABUNDANCE ON *SOLANUM CAMPYLACANTHUM* ON AN AFRICAN SAVANNAH**

Nurse plant effect is a type of plant-plant interaction that can facilitate the focal plant by microclimate modification or protection from herbivory. It also has the potential to affect the community pattern at other trophic levels. We conducted a controlled field experiment to examine the nurse plant effect of *Acacia etbaica* on a perennial shrub *Solanum campylacanthum* in an area frequented by large mammalian herbivores in Laikipia County, Kenya. Ninety *S. campylacanthum* saplings were randomly assigned to three treatments: Thorn, Non-thorn, and Control. The initial height, stem length, and number of leaves were recorded for each plant. Plants of the Thorn treatment were covered with branches of *A. etbaica*, plants of the Non-thorn treatment were covered with branches of *Croton dichogamous*, and plants of the Control treatment were not covered. The *Solanum* plants were allowed to grow for nine months. At the end of the experiment the plant sizes were measured again and the insects on the plants were sampled. We also collected five leaves from each plant and used ImageJ to quantify leaf damage from insect herbivory. We used generalized linear modeling to compare the plant growth and insect density between the treatments. We also used linear mixed-effects modeling to compare leaf damage between treatments. The nurse plant significantly increased the growth of the *Solanum* plants and the density of insects on them relative to the Control plants. *Solanum* plants in the Thorn treatment had more leaf damage than the Control plants. The nurse plants, especially the type with thorns (*A. etbaica*), appear to have reduced large mammalian herbivory on *S. campylacanthum*, which in turn facilitated insect herbivory on the focal plant.

Mary Chambless, Alisha Howard, and April Nesbit (East Central University)

**\*ANALYZING DNA BINDING OF YFAX IN *ESCHERICHIA COLI***

The bacteria *Escherichia coli* is found in most healthy humans, although *E. coli* is thought of as a bad bacterium. *E. coli* serves an important purpose with vitamin K production and might help prevent bad bacteria from growing in your intestines. The best-studied sugar used by *E. coli* is glucose. Studies show that *E. coli* does have favorite types of sugar and prefers lactose after glucose and before L-arabinose, and D-xylose. YfaX is encoded by the first gene in the yfaXWVU operon, and YfaX is a predicted helix-turn-helix transcription factor. The second and fourth genes (yfaW and yfaU, respectively) are thought to encode proteins for rhamnonate degradation. The third gene, yfaV, encodes a predicted sugar transport protein. Because YfaX is predicted to bind DNA with the helix-turn-helix motif, we wanted to study the DNA binding properties. To create my DNA logo I extracted the upstream promoters with 25% Yfax binding from the SELEX data available at <https://shigen.nig.ac.jp/ecoli/tcc/top/?jsessionid=43CEA2290172746257C15B5206675FA9>. Subsequently I retrieved 41 base pairs from between the left and right end positions of each promoter using [www.ecocyc.org](http://www.ecocyc.org). These promoters were then placed in Weblogo online tool to develop the DNA binding motif. To test binding in vivo, we wanted to make a reporter gene fusion using one of the promoters from the SELEX data. We chose to use the appY promoter fused to lacZ reporter gene. Unfortunately, the PCR to amplify the appY promoter was repeatedly unsuccessful. Future work will be to tweaking the PCR and trying alternate DNA motif programs.

Samantha Coplen (University of Central Oklahoma)

**\*\*ISOLATION AND CHARACTERIZATION OF *ACINETOBACTER BAUMANNII* BACTERIOPHAGE VB\_AB\_SCL1 FROM OKLAHOMA WASTE-WATER**

Felix d'Herelle discovered a bacteriolytic substance that he named bacteriophage (commonly called phage), which means eater of bacteria, that could induce lysis of bacterial cell cultures. This lysis releases the progeny phage particles produced inside the host cell and the phage reinfects subsequent bacteria susceptible to phage infectivity. In recent years, healthcare communities and hospital settings have seen the emergence of multi-drug resistant (MDR) *Acinetobacter baumannii* as an important nosocomial pathogen. Infection by MDR *A. baumannii* induces diseases such as bacteremia, meningitis, and pneumonia. Bacteriophage therapy is an important tool for the control and treatment of MDR *A. baumannii*. Isolation and characterization of *A. baumannii* bacteriophages also provide a comprehensive understanding of their biology and facilitate their use in phage therapy. This work describes the isolation, purification, and characterization of the novel *Acinetobacter* bacteriophage vB\_Ab\_SCL1. Sewage samples were collected from the Coffee Creek Waste Water Resource facility and screened for bacteriophages. We used host *Acinetobacter baumannii* isolate 1171 for the isolation of bacteriophages. Phage Purification was performed with three rounds of single plaque picks in conjunction with full titer plating. Webbed plates were used for generating low-titer-lysate (3.1x10<sup>9</sup> pfu/mL) and high-titer-lysate (1.98x10<sup>10</sup> pfu/mL). Genomic DNA extraction was performed using the PCI method, followed by restriction digest with Bam HI, Cla I, Hae II, Hind III, Sac I, and Sal II. TEM images revealed a siphoviridae morphotype, a head with a tail of ±690nm. The phage genome is being sequenced utilizing the Illumina platform. Our future work will involve further characterization of the phage and annotation of the phage genome.

Leonard Cole Davis and Jessica Brumley (East Central University)

**\*OBSERVATION OF LAND USE, SOIL QUALITY, AND ECOSYSTEM SERVICES**

This summer, samples of soil were collected from various farms across Pontotoc county. The pH, infiltration rate, and biomass of these soil samples were analyzed. The purpose of this analysis was to compare the soil quality, land management, and ecosystem services. Our research has suggested that there is a slight correlation between soil pH and biomass and a slight negative correlation between biomass and the infiltration rate.

Leah S. Dudley (East Central University)

### THREE SISTER POLY CULTURE AND INSECT VISITATION

Crop pollination by native insects has been shown to be effective and important for crop yield. As the European honey bee becomes more imperiled, the importance of recruiting native pollinators has become even more of a priority. However, crop-pollinator interactions are affected by the environment. Plant water-status has been shown to impact floral rewards to pollinators in nectar volume and flower abundance in wild plants. In particular, drought stressed plants may reduce rewards corresponded resulting in fewer visits. Crop diversity has also been shown to have positive effects on pollinator abundance and plant yield. In the current study, the culturally relevant Three Sisters (corn, bean and squash) was grown within mounds containing only one sister type or all three sisters. Location within the garden was randomly selected across watering treatments (control, medium addition and high addition) and culture system (monoculture or polyculture). Observations of all visitors to each mound were monitored across the flowering season. Water availability was assessed for all plants towards the end of the flowering season. Total visits and visitor networks were compared across treatments. Results support that mound diversity was the greatest predictor in pollinator visitor abundance and diversity. Our study supports the growing body of work indicating that monoculture agricultural systems are negatively impacting local insect diversity.

Mackenzie Edwards and Dominic Halsmer (Oral Roberts University)

### \*AFFORDANCE BASED ENGINEERING APPLIED TO RENAL FAILURE

Medicine currently requires physicians to go through years of vigorous training to gain the necessary understanding needed to diagnose and treat patients. Patients are often misdiagnosed or can be subject to the bias of the doctor. In this project a program that will be able to offer a predictive objective diagnosis using AI and network mathematics. This program would allow for a creation of a network model of an organ, and by creating a healthy network and using computer and mathematical diagnostics to characterize the network. Then an unhealthy network model of the organ can be characterized by adding the 'unhealthy' relationships or the patient symptoms that would identify the unhealthy organ or sub organ parts in the body. For simple models this information only highlights what part of the organ is involved in various biological functions. Due to increases in our understanding of graph theory and networks, this model can be scaled to include any relevant research and create a highly comprehensive model of the body and the relationship between form and function. Further the mathematical structure allows for AI to be applied and the possibility of a powerful diagnostic tool becomes possible. This is further supported by the key feature of networks being modeled over time as the relationships change with changing conditions. These exciting possibilities highlight the importance of interdisciplinary problem solving and utilizing the strengths of other fields of study to medicine. In this project this model is applied to a kidney in renal failure, where a fully functional kidney network can be compared to an unhealthy kidney network to test the viability of the program.

Valeria Escareno, Chris Castillo, and Chad King (University of Central Oklahoma)

### \*EFFECTS OF HERBIVORY ON GROWTH OF OVERSTORY GREEN ASH (*FRAXINUS PENNSYLVANICA*, MARSHALL) AT ARCADIA LAKE, OKLAHOMA COUNTY, OKLAHOMA

North American beaver (*Castor canadensis*) and wood-boring insects demonstrate repeated herbivory on green ash (*Fraxinus pennsylvanica*) at Arcadia Lake, Oklahoma County, Oklahoma. This interaction increases stress levels in green ash, but it is unknown if herbivory reduces overall growth and subjects trees to increased mortality. The potential exists for herbivory to alter tree species composition of the forest and influence successional trajectory. We hypothesized that trees exhibiting signs of herbivory would have a significantly different growth rate than trees without evidence of herbivory. Increment cores were collected from control trees (n = 20) and trees exhibiting signs of herbivory (n = 26). All green ash trees were sampled in the same habitat and subject to repeated flooding at Arcadia Lake. To assess growth rates, tree-ring measurements (mm) were recorded using a binocular microscope and Measure J2X software. Tree-ring series were crossdated using COFECHA and graphical software. Raw ring-width was converted to basal area increment (BAI). No significant differences were detected in mean diameter (1-tailed t-test, t = 1.69, p = 0.38) and mean BAI over the past 10 years (1-tailed t-test, t = 1.64, p = 0.38) between herbivory trees and control trees. Using linear regression, approximately 20% (n = 4) of control trees and 38.5% (n = 10) of herbivory trees exhibited a declining growth pattern. Collectively, most of the herbivory trees were exhibiting constant or increasing growth rates similar to the control trees. One possible explanation for the lack of growth decline in herbivory trees may be due to their ages. Most green ash at the site are relatively young (mean age = 30 years) and are likely to recover from herbivory effects more quickly. The site is saturated making it easier for green ash to obtain nutrients and maximize resource allocation in order to overcome herbivory.

Christy Eslinger and Subhas Das (Oklahoma State University Center for Health Sciences)

### \*\*EPIGENETIC REGULATION IN COLON INFLAMMATION

Inflammatory bowel disease (IBD) encompasses both ulcerative colitis and Chron's disease which are known to cause chronic inflammation, severe visceral pain, and recurring flares that are life debilitating. The latest statistics indicate over 80,000 inflammatory bowel diseases are in children under the age of 18, and 70,000 new cases being diagnosed every year. We seek to understand the initial inflammatory response through targeting DNA hypermethylation activation of glutaminase (GLS) gene in 2,4, 6-trinitrobenzenesulfonic acid (TNBS) induced colitis in rats. Located in the promoter of GLS gene is a CpG island that is hypermethylated subsequent to colitis induction resulting in overexpression of GLS. Treatment with Azacitidine (Aza), a hypomethylating drug, resulted in significant decrease in the hypermethylation activation of GLS gene in TNBS induced colitis. Methyl-CpG binding protein 2 (MeCP2) proteins are known to be interacting with methylated CpG dinucleotides. With the help of modified chromatin immunoprecipitation assay (ChIP) followed by a bisulfide conversion and a methylation specific PCR (MSP), we confirmed that MeCP2 directly interacts with the methylated CpG dinucleotides in the promoter region of GLS gene. These results confirmed that TNBS induced colitis resulted in hypermethylation of CpG island in the promoter region leading to

\* Undergraduate \*\* Graduate

recruitment of MeCP2 proteins to interact with methylated CpG dinucleotides thus resulting in increased expression of GLS. Pretreatment with Aza resulted in decreased hypermethylation and thus decreased expression of GLS due to decreased interaction with MeCP2 in the promoter region. These results suggest that demethylating agent, Aza, can be potentially used for reducing inflammation and alleviating pain in IBD patients

Hallum Ewbank and Christopher G. Goodchild (University of Central Oklahoma)

#### \*A PRELIMINARY ANALYSIS OF THE EMBRYOTOXICITY OF MULTIPLE POLYCYCLIC AROMATIC HYDROCARBONS IN CHICKEN EGGS

Polycyclic aromatic hydrocarbons (PAHs) from oil spills are highly toxic to birds and can cause death and other sublethal pathological conditions. Additionally, previous studies in other organisms (e.g., fish) have found embryonic exposure to PAHs causes embryotoxicity and interferes with cardiovascular development. However, the embryotoxicity of in ovo exposure to PAHs has been less well studied in avian embryos. Developmental effects from in ovo exposure to PAHs could have long-lasting effects for post-hatch survival and fitness, especially if impaired cardiac function impairs ability to fly long distances. Previous studies explored lethal doses of certain PAHs and sublethal effects of whole crude oil on avian embryos, but more investigation is necessary to determine sublethal effects of individual PAHs. This study aims to find the impact of sublethal in ovo exposure of six PAHs (anthracene, phenanthrene, pyrene, benzo[a]pyrene, chrysene, fluoranthene) on avian embryonic heart rate and development. To do so, we monitored heart rate of developing chicken embryos at days 10, 14, and 18 after injection with five different concentrations of each PAH tested. On day 18, we collected morphometric variables and organ mass (brain, liver, heart). Here, we present preliminary data from our experiment. The results will provide insight into which PAHs are causing embryotoxicity and cardiovascular damage in order to better assess the sublethal damage caused by oil spills.

Brooklynn Franks<sup>1</sup>, Tyler Godsey<sup>1</sup>, Lindsey Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

#### \*INCREASING DIVERGENCE OF IMPL2 AMONG SPECIES

The insulin/TOR pathway in *Drosophila* species is crucial due to its role in nutrient storage, whole body growth, and innate immune system interactions. In collaboration with the Genomics Education Partnership, four genes involved in this pathway were analyzed in various *Drosophila* species to see the evolutionary divergence and conservation of these genes. The gene ImpL2 is located early in the pathway and therefore has fewer genetic connections when compared to the other three genes. This observation was used to predict that ImpL2 was the least conserved gene out of the four researched in the insulin pathway. Annotations were conducted for the genes in several *Drosophila* species, and the degree of sequence conservation across species was measured. Sequence conservation analyses supported the hypothesis that ImpL2 is less well conserved than the other genes that were investigated.

Angeela Gauchan, Dylan Melton, Katlyn Hampton, Charlie Biles, and Alisha Howard (East Central University)

#### \*CHARACTERIZATION OF PATHOGENIC *FUSARIUM* SPECIES IMPORTED FROM CENTRAL AMERICA ON MELONS

*Fusarium* species are some of the most economically damaging and prevalent pre-harvest and post-harvest diseases of numerous fruits, particularly cucurbits. Besides agricultural damage, the *Fusarium* also has the potential for human infection. *Fusarium solani*, a prominent fungus species, has been found in the eyes, nails, skin, bone, nasal cavities, systemically infecting cancer patients, and HIV patients. At least one case of *F. proliferatum* has been reported as being responsible for the death of both immunocompromised and healthy humans (F. Leslie, et al., 2006). Melon (*Cucumis melo* L. var. *cantalupensis* Naudin) is an economically important fresh fruit that is imported from several parts of Central America. Melon imports are potentially an important contributor to phytopathogens and animal pathogens in the USA. The main goal of this research is to identify *Fusarium* species imported from Central America on the melons. Phylogenetic analyses utilizing various genetic loci in combination with morphological markers were used to identify species. DNA extracted from these isolates and amplified using barcoding primers. BLAST results of TUB confirmed the presence of a diverse set of *Fusarium* species imported on the melons. Koch's postulates confirmed that *F. sacchari* and *F. incarnatum* were pathogenic on melons. Morphological characteristics further confirmed their identity. Additional loci and *Fusarium* isolates are being investigated.

Sarah Gault (East Central University)

#### \*VECTOR-BORNE DISEASE ASSESSMENT

Vector-borne disease (VBD) assessments have generally been limited to larger municipal areas. Identification of disease competent vectors is an initial step in determining risk of VBD. Around the campus of East Central University, in Ada, Oklahoma, ovipositional mosquito traps were set out for a four-week period during the summer of 2021. Frommer updraft gravid traps were placed, after being assembled with a battery to operate the fan that held the mosquitos in the structure of the trap. There is a metal wire funnel within the trap that helped to get the mosquitos in the trap. The 117 mosquitos were retrieved and sorted. Competent disease vectors were identified via a dichotomous tree. This research provides a basis for a continuation of vector-borne disease assessment in Ada, Oklahoma.

Kateri Gebhart (University of Central Oklahoma)

#### \*ISOLATION AND CHARACTERIZATION OF ARTHROBACTERIOPHAGE GIPSYDANGER FROM OKLAHOMA SOIL

Drug resistant bacteria are becoming more persistent in healthcare facilities due to overuse of antibiotics resulting in resistance to antibiotics. In an effort to search for new alternatives to combat this issue, the use of bacteriophages is being investigated as a possible solution. A bacteriophage is a virus that specifically infects and kills bacteria. These phages can hijack the bacterial host's replication machinery to manufacture more phage particles. This results in lysis of host bacteria and release of more

\* Undergraduate \*\* Graduate

phages into the surrounding environment to target more bacteria. This lytic process is what makes bacteriophages of interest to researchers to use in phage therapy. The purpose of this research is to isolate and characterize an Arthrobacteriophage from Oklahoma soil sample. We used *Arthrobacter* sp. KY3901 as host bacteria. The phage, GipsyDanger, was isolated from soil found near Lost Lake located in the Wildlife Refuge of Lawton, Oklahoma, the latitude is 34.7109 and the longitude is -98.6747. GipsyDanger was isolated from a plaque using direct method and then purified through three sets of plaque purification to obtain a clonal phage population. We obtained a high-titer-lysate using webbed plates. The phage was concentrated with polyethylene glycol (PEG) and prepared for DNA extraction. Our future work will involve further characterization and sequencing of our phage genome.

Sagar Ghimire, Pujan Khatri, Benjamin O. Tayo, and Sanjiv K. Jha (East Central University)

**\*A DENSITY FUNCTIONAL THEORY STUDY OF THE INTERACTION OF DNA NUCLEOBASES WITH PRISTINE AND DEFECTIVE GRAPHENE NANORIBBONS**

Graphene is a promising material for a wide range of applications, including the sensing and detecting various biomolecules, and DNA sequencing. In this study, we computationally investigated the interaction mechanism of four DNA nucleobases [Adenine (A), Cytosine (C), Guanine (G), and Thymine (T)] with graphene nanoribbons (GNRs). Our calculations were performed using the van der Waals corrected density functional theory (via the vdW-DF2 and semi-empirical Grimme's-D2 methods), as implemented in Quantum Espresso electronic structure package. N-Armchair graphene nanoribbons (AGNRs) with three different widths corresponding to the indices  $N = 13, 14$ , and  $15$ , passivated with the hydrogen atoms were considered in this study. The binding energies of DNA nucleobases on GNRs were examined for GNRs containing no surface defects, containing Stone-Wales (SW) defects, and containing di-vacancy (DV) defects. The binding energies of DNA nucleobases on GNRs were examined for GNRs containing no surface defects, containing Stone-Wales (SW) defects, and containing di-vacancy (DV) defects. Our results revealed that DNA nucleobases form stable complexes with GNRs. The computed binding energies of DNA nucleobases on GNRs showed the following sequence:  $G > A > T > C$ . The presence of structural defects on the GNRs showed no significant effect on the computed binding energies between the DNA and GNRs. The computing for this project was performed at the OU Supercomputing Center for Education & Research (OSCER) at the University of Oklahoma (OU).

Tyler Godsey<sup>1</sup>, Brooklynn Franks<sup>1</sup>, Lindsey J. Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

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Camille Goerend (Southwestern Oklahoma State University)

**\*PRELIMINARY BIOCHEMICAL AND STRUCTURAL CHARACTERIZATION OF A TYPE-II BETA-CARBONIC ANHYDRASE FROM *RHODOCOCCLUS EQUI***

*Rhodococcus equi* is a soil dwelling bacteria that causes mucopurulent pneumonia in foals. Transmitted through inhalation or ingestion of contaminated soil, *R. equi* pneumonia is hard to detect initially with subsequent progression to critical infection. The endemic nature of this infection in equine farms, difficulty in treatment procedures combined with emergence of antibiotic resistance in *R. equi* has necessitated the search for new treatment options. Recently, in *Mycobacterium tuberculosis*, a close relative of *R. equi*, studies have shown that inhibition of beta-carbonic anhydrase (beta-CA) activity induces impaired growth and decreased virulence. Studies have established Mycobacterial beta-CA as a potential novel antimicrobial target which prompted us to search for the a beta-CA in *R. equi* genome using computational analysis. Our search retrieved a beta-CA from *R. equi* with 69% similarity to a well characterized *M. tuberculosis*  $\beta$ -CA, Rv3588c. Further computational analysis of the *R. equi* beta-CA homolog, called ReqCanB2, revealed extensive structural and active site homology to other well-studied beta-CA's. This led us to hypothesize that ReqCanB2 is a beta-CA homolog in *R. equi* capable of reversible CO<sub>2</sub> hydration activity. To prove that ReqCanB2 is a beta-CA, the gene was cloned, over-expressed, and purified using standard techniques. CA activity assay revealed that ReqCanB2 is a CA with typical CO<sub>2</sub> hydration activity. Preliminary crystal structure of ReqCanB2 was determined in its native form which revealed a tetrameric arrangement and zinc ion coordinated active site with cysteine and histidine residues typical of beta-CA's. The structure also revealed that ReqCanB2 is in a zinc bound inactive form indicating this enzyme may be pH regulated. Currently, we are continuing further structural and biochemical analysis to fully characterize ReqCanB2 with the goal of identifying inhibitors that can be used to treat *R. equi* infections.

Christopher Goodchild, Michelle L. Beck, Isaac VanDiest, Frankie N. Czesak, Samuel J. Lane, and Kendra B. Sewall (University of Central Oklahoma)

**DIETARY PB IMPAIRS SONG DEVELOPMENT AND ALTERS SEXUAL TRAITS IN MALE ZEBRA FINCHES (*TAENIOPYGIA GUTTATA*)**

Lead (Pb) is a pervasive global contaminant that interferes with sensitive windows for neurological development and causes oxidative damage to tissues. The effects of moderate and high exposure to Pb have been well-studied in birds, but whether low-level early-life exposure to Pb influences adult phenotype remains unclear. Female songbirds use a male's song and coloration to

discriminate between high- and low-quality males. Therefore, if early-life exposure to Pb disrupts song learning ability or shifts the allocation of antioxidant pigments away from colorful secondary sexual traits, male birds exposed to Pb may be less attractive to females. We exposed developing zebra finches (*Taeniopygia guttata*) to Pb-contaminated drinking water (100 or 1000 parts per billion [ppb]) after hatching (days 0–100). Once male finches reached adulthood (120–150 days post hatch), we measured song learning ability, coloration of bill and cheek patches, and volume of song nuclei in the brain. We also measured female preference for Pb-exposed males relative to control males. Finally, we measured motoric and spatial cognitive performance in male and female finches to assess whether cognitive traits differed in their sensitivity to Pb exposure. Male zebra finches exposed to 1000 ppb Pb had impaired song learning ability, reduced volume of song nuclei, bills with less redness and received less attention from females. Additionally, Pb exposure impaired motoric performance in both male and female finches but did not affect performance in a spatial cognitive task. Adult finches exposed to Pb-contaminated water had higher blood-Pb levels, though in all cases blood-Pb levels were below 7.0 µg dL<sup>-1</sup>. This study suggests that low-level exposure to Pb contributes to cognitive deficits that persist into adulthood and may indirectly influence fitness by altering secondary sexual traits and reducing male attractiveness.

Elizabeth Gwartney and Greg Mullen (Oklahoma City University)

**\*NOVEL ANTIBIOTICS FROM OKLAHOMA SOIL**

Recent statistics from the United States Centers for Disease Control and Prevention (CDC) state that more than 2.8 million antibiotic-resistant infections and 35,000 deaths occur in the U.S. annually. The solution to this health crisis includes better clinical practices and developing new antibiotic drugs. My research attempts to contribute to the ongoing race to discover new antibiotics. Microbes that inhabit soil often produce antibiotic substances to inhibit the growth of other microorganisms that compete for resources. Bacteria from garden soil in northeast Oklahoma were tested for the ability to inhibit growth of various pathogenic bacteria chosen based on their relationship to the pathogens identified by the CDC as serious threats and common infection-causing organisms. Four novel microorganisms (CRB1 – 4) were identified that secrete soluble substances which inhibit growth of common pathogens. A modified Kirby-Bauer assay was then used to define the spectrum of pathogens inhibited by each of these isolates. The antibiotic secreted by the CRB3 strain have an especially broad spectrum, inhibiting a wide range of Gram-positive and -negative organisms. Sequencing of the 16S and 23S rRNA genes was then used to determine the phylogenetic relationships of these isolates to known bacterial species. We conclude that CRB1 and 2 are closely related to *Bacillus subtilis* and CRB3 and 4 are species of *Streptomyces*. Both *Bacillus* and *Streptomyces* species are known to secrete antibiotic substances, including some of medical importance. Our current goal is to create cell-free extracts from these bacteria that can be used instead of living bacteria in our modified Kirby-Bauer assay. This is the first step in determining the chemical nature of the antibiotics. Ultimately, we seek to contribute to the body of research seeking to mitigate antibiotic resistant infections.

Christopher Hamm and Matthew T Cabeen (Oklahoma State University)

**\*\*BACILLUS SUBTILIS RETAINS CHARACTERISTIC ENVIRONMENTAL STRESS RESPONSES ACROSS DIVERSE STRESSORS**

The model organism *Bacillus subtilis* has a large protein complex known as the stressosome that is responsible for sensing stress through four RsbR (R) protein paralogs and activating a general stress response. Each of these R-proteins responds with a unique response pattern when presented with the same exact stressor. To study this phenomenon, strains isolating single R-proteins in cells were engineered. Using a fluorescent reporter in conjunction with microfluidics, which allows us to study multiple, individual cells growing under identical condition over hundreds of generations, allows us to visualize when the stress response is active. We discovered that each single R-protein responded with the same unique pattern irrespective of the stressor used, including ethanol, salt, oxidative stress, acidic stress, and antibiotics. This leads to the question of which region of the gene sequence is responsible for this unique response. Each R-protein contains a conserved region as well as a variable region unique to each single R-protein. Engineering hybrid proteins with a mix of these conserved and variable gene sequences allows us to ascertain which region of the protein is responsible for stress response by comparing the hybrid R-protein response profiles with the previously observed individual R protein responses.

Katlyn Hampton, D. Melton, A. Gauchan, and C. Biles (East Central University)

**\*ANTIBIOTIC RESISTANT AND GROWTH PATTERNS OF INVASIVE SPECIES IMPORTED ON MELONS FROM CENTRAL AMERICA**

Invasive species of fungi are commonly imported into the United States on fruits and vegetables. Our goal with this project was to establish what the differences were between the species imported locally. The 2 genera that we studied were *Fusarium* and *Diaporthe*. We investigated a range of physiological traits in order to better understand them including antibiotic resistance and growth characteristics. We performed a growth study where we used different kinds of media to observe species' specific growth rates across a range of 5 agar plates. We also performed an antibiotic study where we tested the isolate cultures to analyze resistance and susceptibility to 10 different antibiotics. Finally, we performed a temperature study to determine what the optimum temperature was for each species to grow. Results indicate that Czapek-Dox (CZD) and Corn Meal Agar (CMA) provided the best nutrients for growth for most species. The most effective antibiotic we tested on all isolates was econazole 10 mcg, and the least effective was fluconazole 25 mcg. The optimum temperatures were 23° C and 25° C. Invasive species threaten immunocompromised people as well as the environment. By better understanding what these species prefer, we can work towards minimizing their impact.



Hanna Hill, Horrick Sharma, and Pragya Sharma (Southwestern Oklahoma State University)

**\*BIOLOGICAL CHARACTERIZATION OF THE CYTOTOXIC EFFECTS OF NOVEL LACTATE DEHYDROGENASE INHIBITORS IN MIA PACA-2 CELLS**

Pancreatic ductal adenocarcinoma cancer (PDAC) is one of the most lethal cancers, with a 5-year survival rate of ~8% and a median survival duration of fewer than six months. Therefore, identifying new biological drug targets is urgent. In the attempt to develop innovative anticancer treatments and selectively target cancer cells, growing interest has recently focused on the peculiar metabolic properties of cancer cells. One of the characteristic metabolic hallmarks of tumor metabolism is aerobic glycolysis. The Warburg effect in cancer cells is regulated by lactate dehydrogenase-A (LDH-A), which is shown to be overexpressed in many cancer types, including PDAC. Several studies have shown great potential in targeting this enzyme as a means of developing novel treatments. Our lab, in collaboration, has identified diverse novel lactate dehydrogenase inhibitors, which have shown promising anticancer activity against pancreatic cancer cells without having any cytotoxic effect in normal cells. We are currently investigating the mechanism of antiproliferative activity of lead LDHA inhibitors through Western blotting and Annexin V assays.

Eric Howard (East Central University)

**DEVELOPING A VECTOR-BORNE DISEASE RESEARCH PROGRAM AND EDUCATION PROGRAM: A REVIEW**

Efforts to design and develop an effective, productive, and sustainable vector-borne disease (VBD) research and education program have been underway at a Regional Oklahoman University since the summer of 2020. Both success and difficulties have been encountered over two summers in this unique cross-cutting undergraduate level program. Methods in the field and in the lab have improved with continued successes likely to result. Modification of expectations and acquisition of appropriate lab equipment will allow for more consistent and rapid results. An opportunity to gain real environmental health experience in the field and in the lab has been accomplished. Specific curriculum development may result in a more robust experience for the student and faculty. Future approaches involve a two-semester project commitment, community-based education and mosquito collection, advanced vector identification techniques, and enhanced map development for risk communication.

Sierra Hubbard (Oklahoma State University)

**\*\*ANALYSIS OF THE SPATIAL DISTRIBUTION OF GEOREFERENCED HERBARIUM RECORDS IN OKLAHOMA AND TEXAS**

Digitized and georeferenced herbarium collections are invaluable for research focused on spatial distributions of plants. However, herbarium data are often spatially biased; easily accessible locations are often overrepresented in herbaria, while remote locations are underrepresented. These spatial biases are compounded by the lack of digitization and georeferencing efforts in certain areas. The Texas Oklahoma Regional Consortium of Herbaria (TORCH) database currently houses 1.2 million vascular plant records, but only ~30% have been assigned geographic coordinates. Additional georeferencing improves data accessibility for researchers and can help address spatial bias, but it is necessary to develop methods for prioritizing locations for georeferencing. My objective is to analyze the spatial distributions of herbarium collections in Oklahoma and Texas to identify underrepresented locations that should be targeted for georeferencing efforts. My dataset is made up of ~300,000 georeferenced vascular plant records from Oklahoma and Texas. Examining the abundance of herbarium records from each county and the proportions of georeferenced records revealed that there are very few herbarium records from many counties in north and northwest Texas. The majority of these records do not have coordinates. Additionally, many counties of eastern and east-central Texas and one county in central Oklahoma have less than 15% of specimens georeferenced. Based on these findings, I recommend that TORCH georeferencing efforts should first focus on plant collections from the west-northwest and eastern-central regions of Texas. More specifically, locations in and near Haskell, Midland, Roberts, and Robertson counties appear to be in greatest need of attention.

Nathaniel Hunter, Anastasia Smith, Mary Claire Cooperrider, Ashton Hogue, Courtney Gillespie, and William P. Ranahan II (Oral Roberts University)

**\*ANALYSIS OF GENE EXPRESSION IN TRIPLE-NEGATIVE BREAST CANCER EPITHELIA AFTER TREATMENT WITH FULL-SPECTRUM CBD OIL**

In recent years, cannabinoids and endocannabinoids have emerged as potent modulators of cellular signaling pathways. Furthermore, the revelation that malfunction of cannabinoid receptors leads to pathological states warrants further investigation into cannabinoid signaling. Interestingly, recent research indicates that treating breast cancer cells with exogenous cannabinoids promotes anti-tumor responses through alterations in gene expression. However, the full extent of exogenous cannabinoids' effect on breast cancer gene expression remains unclear. Here, we treated triple-negative breast cancer cells with full spectrum CBD oil and observed alterations in the expression of 96 different genes through preparation and isolation of RNA and RT-qPCR. Analysis of the data revealed at least a two-fold increase in expression of CDK4, ERCC1, HRAS, KDR, MAP2K2, NOTCH1, THBS1, TIMP2, and WNT5A. Moreover, MUC1 and PDGFRA experienced at least a 50% reduction in expression.

Harmony Hysten<sup>1</sup>, Cameron Arogon<sup>1</sup>, D. Shaida Kamali<sup>1</sup>, Lindsey J. Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

**\*EVOLUTIONARY CONSERVATION OF ROC1A AND SLMB IN THE INSULIN/TOR PATHWAY IN *DROSOPHILA***

Roc1a and slmb are both downstream genes in the Insulin/Tor (IT) pathway and are negative regulators in the E3 ubiquitin ligase complex. The purpose of this study was to analyze how regulatory regions of Roc1a and slmb evolve in the context of their position in the IT pathway. Previous studies have shown that the evolution of the species conserves these complex networks because of the interconnections of multiple genes, selective constraint, and their position in the pathway. Therefore, we hypothesized that Roc1a and slmb are highly conserved because they both function in the E3 ubiquitin ligase complex, and will

\* Undergraduate \*\* Graduate

equally diverge within the evolutionary tree of *Drosophila*. Performed tblastn of the translated *D. melanogaster* protein against the whole-genome assembly of the target species, to obtain regions in the target species genome that had similarities with the protein sequence of *D. melanogaster*. Gene record finder: A web tool that enables us to identify exons for a given gene, the Coding DNA Sequences (CDS's). Gene model checker: verifies that the proposed model follows a list of set criteria like the presence of a start and stop codon for each exon, and verifies the acceptor and donor sites at the splice junctions. The genomic neighborhood and protein-coding isoforms in *Roc1a* caused the increased divergence of the gene compared to *slmb*. Generated divergence scores indicate that *slmb* and *roc1a* are not conserved equally in the IT pathway. In the IT pathway, genes located in the downstream position tend to have more interactions and functional roles within a system which explains our findings that *slmb* is conserved because it has more connections and is involved in multiple pathways, which is not the case for *Roc1a*.

Zitha Redempta Isingizwe and Doris M. Benbrook (University of Oklahoma Health Sciences Center)

#### **\*\*PLATELETS STIMULATE OVARIAN CANCER SPHEROIDS IN EPTIFIBATIDE-SENSITIVE MANNER**

A third of ovarian cancer patients have high platelet counts at diagnosis resulting in reduced survival compared to patients with low/normal platelet counts. Current studies suggest that platelets and ovarian cancer induce each other in a feed-forward loop. The objectives were to: 1) evaluate differences in platelet counts and aggregation between healthy and newly-diagnosed ovarian cancer patients; 2) develop an experimental model of the pathological interactions between platelets and ovarian cancer spheroids; and 3) identify pathways affected by these interactions. Our hypothesis is that high platelet counts of ovarian cancer patients are associated with hypercoagulability and inhibiting platelet aggregation reduces platelet-mediated effects on ovarian cancer spheroids. Complete blood count including platelet count was evaluated between healthy controls and newly-diagnosed ovarian cancer patients before treatment. A platelet aggregation assay was performed to assess platelet physiology between the two groups. The molecular mechanism of platelet effects on ovarian cancer spheroid properties was evaluated using mass spectrometry and bioinformatic analysis of a magnetic 3D cancer spheroid assay, in the presence and absence of eptifibatide, a platelet inhibitor. While ovarian cancer patients had significantly higher platelet counts than healthy controls, platelet aggregation profiles and parameters were similar between the two groups. Incubation of platelets with cancer spheroids altered spheroid size and density in an eptifibatide-sensitive manner. Co-incubation of platelets with ovarian cancer spheroids activated the LXR/RXR pathway, a known down-stream effector of the integrin receptor that eptifibatide targets. Platelet count does not predict platelet hypercoagulability in ovarian cancer patients. Pathological interaction between platelets and cancer cells can be mimicked in co-culture, and eptifibatide inhibits these pathological interactions. The LXR/RXR pathway is a likely mediator of the eptifibatide interference in platelet-cancer interaction, and represents a candidate target for reducing platelet-mediated adverse events in ovarian cancer patients.

Sneha Jacob and William P Ranahan (Oral Roberts University)

#### **\*DETERMINING OPTIMAL EXTRACTION CONDITIONS TO ISOLATE A PEPTIDE CONTAINING POLYSACCHARIDE WITH ANTI-CANCER PROPERTIES FROM *GANODERMA LUCIDUM***

*Ganoderma lucidum*, commonly known as Reishi, is a popular mushroom used in Asian countries for promotion of health and longevity. It was therefore called the “Mushroom of Immortality”. In ancient Chinese medicine, *G. lucidum* has been used to treat various human diseases like bronchitis, chronic hepatitis, hyperglycemia, inflammation, and cancer. In our research, a peptide containing polysaccharide, Felix, isolated from *G. lucidum* showed cytotoxicity in triple-negative breast cancer cells. However, because of the availability of *G. lucidum* from different sources, the biological activity and concentration of the isolated compound (Felix) varied. To determine the optimal conditions, temperature and time, needed to extract the compound of interest, we took extraction from *G. lucidum* mycelia grown at six different conditions (varying temperature and time). We found that extraction at 37 degree Celsius for 48 hours gave the highest concentration of Felix (peptide containing polysaccharide). We also found that once the extraction is done on the mycelium plate, they are no longer alive. This means we need to have a constant supply of fresh mycelium each time for the extraction and isolation of Felix. The isolated Felix was then tested on triple-negative breast cancer cells for cytotoxicity. We are still working on finding the concentration of Felix needed to produce the cytotoxic effect and also the mechanism pathway.

Sidra Jawaid, Mehmet Aktas, Thu Nguyen, Rakin Riza, and Esra Akbas (University of Central Oklahoma)

#### **\*IDENTIFYING CRITICAL HIGHER-ORDER INTERACTIONS IN COMPLEX NETWORKS**

Diffusion on networks is an important concept in network science observed in many situations such as information spreading and rumor controlling in social networks, disease contagion between individuals, and cascading failures in power grids. The critical interactions in networks play critical roles in diffusion and primarily affect network structure and functions. While interactions can occur between two nodes as pairwise interactions, i.e., edges, they can also occur between three or more nodes, which are described as higher-order interactions. In this talk, we present a novel method to identify critical higher-order interactions in complex networks. We propose two new Laplacians to generalize standard graph centrality measures for higher-order interactions. We then compare the performances of the generalized centrality measures using the size of giant component and the Susceptible-Infected-Recovered (SIR) simulation model to show the effectiveness of using higher-order interactions. We further compare them with the first-order interactions (i.e., edges). Experimental results suggest that higher-order interactions play more critical roles than edges based on both the size of giant component and SIR, and the proposed methods are promising in identifying critical higher-order interactions.

Dusenge Shaida Kamali<sup>1</sup>, Harmony Hysten<sup>1</sup>, Lindsey J. Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

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Sue D. Katz Amburn, Gerwald A. Köhler, and Franklin R. Champlin (Oklahoma State University Center for Health Sciences)

**DIFFERENT RESISTANCE STRATEGIES FOR *PSEUDOMONAS AERUGINOSA* AND *SERRATIA MARCESCENS* STRAINS WHEN EXPOSED TO SUB-MIC CONCENTRATIONS OF TRICLOSAN**

*Serratia marcescens* and *Pseudomonas aeruginosa* are intrinsically resistant to the biocide triclosan, requiring outer membrane permeabilization for the agent to inhibit enoyl-acyl carrier protein reductase (FabI). Our laboratory has shown this is due primarily to outer membrane impermeability for hydrophobic molecules, and that this results in the induction of efflux pump expression in *P. aeruginosa*. Recent work indicated when permeabilizer treated, growth of both organisms was inhibited by 30 minutes post inoculation, with growth resumed at 150 minutes, so these time points were selected for analysis by RNA-seq. This experiment used the *S. marcescens* type strain ATCC 13880, and a *P. aeruginosa* quality control strain, ATCC 27853, treating only with a sub-MIC concentration of triclosan. The Oklahoma State University core facility in Stillwater, OK prepared and sequenced the libraries. Data analysis was performed using Qiagen CLC Workbench. GenBank annotations (ncbi.nlm.nih.gov) for the genomes were downloaded and confirmed using BLAST (blast.ncbi.nlm.nih.gov), BioCyc (biocyc.org), and UniProt (uniprot.org). Analysis indicated that at 30 minutes, the organisms responded disparately to triclosan. For example, *S. marcescens* induced osmoprotectants and detoxification mechanisms, while *P. aeruginosa* induced transporters, and inhibited various metabolic activities. At 150 minutes, both induced resistance proteins (YhjX in *S. marcescens* and ArpC and MexA in *P. aeruginosa*). In addition, the *S. marcescens* response included induction of stress proteins, while *P. aeruginosa* repressed quorum sensing and osmoprotectant synthesis and induced DNA and protein manipulation enzymes (topoisomerase, polymerase, peptidase). The growth of neither organism was measurably altered by triclosan. This leads to the conclusion that these two species have different response menus to low levels of triclosan exposure in the absence of triclosan sensitization by outer membrane permeabilization. Future qPCR experiments will allow us to determine a finer timeline for gene expression, as well as whether *S. marcescens* constitutively expresses efflux pumps.

Kathleen Kelley (University of Tulsa)

**\*\*THE PALEOECOLOGY OF YAHUAI CAVE IN GUANGXI, CHINA AT 120 KYA: IMPLICATIONS FOR EARLY MODERN HUMAN DISPERSAL INTO EAST ASIA**

One of the main questions in human evolution is the dispersal of modern humans across a range of ecological niches. Given that today South China is situated in a tropical environment, the question remains, if early modern humans dispersing into this region could penetrate the rainforest to forage for food and if the environment in that area was suitable for early hominins to seek out during their exodus out of Africa around 100kya. As a case study we present the small mammal remains from Yahuai Cave, Guangxi, China, dated to around 120,000 years ago as they dispersed into East Asia. The study aims to identify the paleoecology of the area by utilizing Middle Range and Niche Construction theories to make an analogous comparison between extant and the extinct micromammals around the region of the Yahuai cave. Reconstruction of the paleoecology will include a three-step process: taxonomic identification, quantification and a taphonomic study. The study will look at similar comparisons at other sites that were along the path of hominin's exit, to further solidify the paleoecological finding and the probability that early hominins would have utilized this novel ecosystem.

Anna Khanov, Marianna Patrauchan, and Tarosha Salpadoru (Stillwater High School)

**\*CHARACTERIZING THE ROLE OF PA2803 PROTEIN IN ANTIBIOTIC RESISTANCE IN BACTERIA**

With increasing model sizes and more complex problems, training neural network models has become a significantly resource-intensive task taking up to hundreds of hours. In this paper, we propose a new efficient model to train dense ReLU-based neural networks. Our method estimates a layer's weight matrix using linear regression. We evaluate our models on regression and classification tasks using the UCI Machine Learning Repository's Auto MPG Data Set and MNIST and compare our results to traditional gradient-based optimization methods. In both shallow (3 layers) and wide (10 hidden neurons) networks, this method significantly outperforms traditional gradient descent methods like AdaGrad in terms of speed, generalization, and accuracy.

Maxim Khanov (Stillwater High School)

#### \*APPROXIMATING RELU NEURAL NETWORK SOLUTIONS USING LINEAR REGRESSION

*Pseudomonas aeruginosa* is a bacterial pathogen that causes severe infections, including lethal infections of the airways in patients with Cystic Fibrosis (CF) [1]. Due to the ever-growing antibiotic resistance of this organism, the infections it causes are becoming increasingly difficult to treat [2]; therefore, there is a critical need of developing novel effective treatment strategies. To do so, however, requires a better understanding of the molecular mechanisms of how this organism becomes resistant to antibiotics and immune defenses. Dr. Patrauchan's research group studies the impact of calcium (Ca) on the ability of *P. aeruginosa* to survive the presence of antimicrobial compounds. One of the reasons for such interest is the importance of Ca in the health of humans; during diseases such as CF, the levels of Ca in the lungs and other body liquids are elevated. This condition may be recognized by the invading pathogens and signal to increase their resistance against immune defenses. Supporting this idea, the group showed that adding higher levels of Ca to a growth medium of the bacterium increased its virulence, which is the ability to cause an infection [3, 4]. Furthermore, the researchers observed that, when grown at elevated Ca, the pathogen becomes more resistant to several antibiotics, including polymyxin B (PolB). This antibiotic was recently considered "the last hope" and is commonly used in combination with other antibiotics to enhance their antimicrobial effect.

Pujan Khatr<sup>1</sup>, Sagar Ghimire<sup>1</sup>, Benjamin O. Tayo<sup>2</sup>, and Sanjiv K. Jha<sup>1</sup> (<sup>1</sup>East Central University, <sup>2</sup>University of Central Oklahoma)

#### \*INTERACTION OF DNA NUCLEOBASES WITH ARMCHAIR GRAPHENE NANORIBBONS: A VAN DER WAALS DENSITY FUNCTIONAL THEORY INVESTIGATION

Graphene is a suitable candidate for a wide spectrum of applications, including the biosensing and sequencing of DNA nucleobases. In this work, we computationally examined the interaction of four DNA bases [Adenine (A), Cytosine (C), Guanine (G), and Thymine (T)] with graphene nanoribbons (GNRs) using periodic density functional theory (DFT). Our calculations were performed using the van der Waals corrected DFT (vdW-DF2) and semi-empirical Grimme's-D2) methods, as implemented in Quantum Espresso simulation package. N-Armchair graphene nanoribbons (AGNRs) with three different widths corresponding to the indices N = 13, 14, and 15, passivated with the hydrogen atoms were considered in our study. The binding energies of nucleobases on GNRs were examined for GNRs containing no surface defects, containing Stone-Wales (SW) defects, and containing di-vacancy (DV) defects. Our results show that DNA nucleobases form stable complexes with GNRs. The DNA bases showed different interaction strengths on graphene nanoribbons, and their binding energies followed the order: G > A > T > C. It was found that the presence of structural defects on the GNRs has no significant effect on the computed binding energies of DNA bases on GNRs. The computing for this project was performed at the OU Supercomputing Center for Education & Research (OSCCER) at the University of Oklahoma (OU).

Nicholas Kiger and Jeffrey Hadwiger (Oklahoma State University)

#### \*EXAMINATION OF *DICTYOSTELIUM* G PROTEIN FUNCTION IN RESPONSES TO THE CHEMOATTRACTANT CAMP

The goal of our study is to elucidate the function of two G protein subunits-Gα1 and Gα2-in the *Dictyostelium* response to the chemoattractant cAMP. The Gα2 subunit is required for chemotaxis to cAMP during the aggregation phase of development (fig. 1) but this subunit is not essential for the activation of the MAP kinase Erk2, suggesting another G protein provides redundant function in Erk2 activation (fig. 2). The Gα1 subunit is structurally similar to Gα2, so we hypothesized that Gα1 might mediate redundant signaling to activate Erk2. The activation of Erk2 was measured using a reporter, GFP-GtaC, that translocates from the nucleus to the cytoplasm when phosphorylated by Erk2. Wild-type and a strain lacking the Gα1 subunit displayed translocation of the reporter in response to a low cAMP concentration. Strains lacking the Gα2 subunit or both Gα1 and Gα2 subunits did not translocate the reporter at low cAMP concentrations, however both strains exhibited comparable translocation of the reporter in response to higher cAMP concentrations. These results imply that the Gα2 subunit is required for this Erk2 mediated response, but that Gα1 function does not contribute to this response. We also tested the ability of Gα1 overexpression to rescue the aggregation defect of gα1-gα2- mutants. Our results indicate that Gα1 does not provide functional redundancy with Gα2 with respect to Erk2 activation. The analysis also indicated that translocation of the GtaC transcription factor is mediated by other mechanisms-possibly other G protein mediated signaling pathways at high concentrations of cAMP-suggesting low affinity cAMP receptors can also regulate this process at the onset of starvation.

Min Kim, Diego De La Torre, and William Ranahan (Oral Roberts University)

#### \*MOLECULAR ANALYSIS OF THE ANTITUMOR EFFECTS OF CANNABINOIDS ON U87-MG CELL LINE

Glioblastoma is a type of brain cancer that is known to be the most malignant and dangerous among the brain cancer known to develop in humans. The standard of care for GBM has been craniotomy followed by chemotherapy and radiotherapy, which was developed in 2005. Developing a novel therapy for glioblastoma has been an area of huge interest for medical researchers, and cannabinoids have been showing promising results in terms of its anti-tumor effects. To assess its anti-tumor effects on glioblastoma, U87MG glioma cell line was exposed to cannabinoids, and the anti-tumor effects was analyzed using RNA extraction, cDNA, and qPCR.

Jennifer Kisamore<sup>1</sup> and Tago L. Mharapara<sup>2</sup> (<sup>1</sup>University of Oklahoma-Tulsa, <sup>2</sup>Auckland University of Technology, New Zealand)

#### WORKPLACE CIVILITY AND THE WORK-FAMILY INTERFACE: AN EXAMINATION OF MEDIATORS

Work-to-family spillover occurs when experiences in the workplace affect one's experiences at home. Specifically, the quality of workplace interactions can exhaust or assist individuals' abilities to fulfill their family roles. We predict that the quality of work interactions will predict the quality of family interactions and that specific personal states, namely physical symptoms and

\* Undergraduate \*\* Graduate

calling, will mediate these relationships. This is a secondary analysis of Time 1 data collected as part of the longitudinal New Zealand Midwifery Work and Wellbeing (NZ MidWoW) study. Self-report data was collected from 224 core midwives using Qualtrics. Mediation analyses were conducted using Hayes (2018) PROCESS macro. Both hypotheses were supported. Physical symptoms significantly mediated the positive relationship between workplace incivility and work-to-family conflict; percent mediation was 41%. Calling significantly mediated the positive relationship between workplace civility and work-to-family enrichment; percent mediation was 66%. The current study replicates and extends the extant research by investigating mediating mechanisms that help explain the work-to-family spillover process. The current study also extends the research literature by extending the generalization of previous findings to the field of midwifery. Ensuring that work and home roles enhance rather than undermine each other is essential for the well-being of individuals, families, organizations, and society. Results suggest negative workplace interactions are associated with greater experiences of stress-related physical ailments and a reduced ability to meet family responsibilities. Conversely, positive workplace interactions are related to an enhanced sense of purpose as well as a sense that one's work helps one be a better family member. Employees and organizations will benefit to the extent that they foster workplace cultures that are caring rather than unkind.

Michelle Lastrina (East Central University)

#### AN INTRODUCTION TO EVENQUADS: CELEBRATING WOMEN IN MATH

In honor of the 50th anniversary of the Association of Women in Mathematics (AWM) in 2021, members of the AWM and numerous volunteers researched, created, and published EvenQuads aka Notable Women in Math playing cards. Five different games can be played with these cards and each card includes a biography and portrait of a notable woman in mathematics. In this talk, I will describe the project, discuss my involvement, and go over some of the mathematics behind the corresponding games.

Brenden P. Latham (East Central University)

#### \*THE VIEW ON VACCINES

In recent years Twitter has made a name for itself as the leading social platform for sharing ideas and opinions. This trend has continued recently concerning the pandemic of COVID-19. One of the most controversial discussion topics as of late has been the COVID-19 vaccination. This paper wishes to explore the sentiment towards the COVID-19 vaccine held by the general population of Twitter users. All tweets posted between the dates 1/1/20 and 6/28/21 containing the word "vaccine" were scraped using Twint and loaded into Rstudio to explore characteristics such as user, hashtags, and word sentiment. A random sample of 100,000 tweets was taken and compared to tweets by subsets of users with similar behavior. All words were then individually rated as either having negative, positive or no connotation by comparison to a corpus within the "textdata" R package. A series of proportion tests determined that not only did the words from the sample hold significantly more negative connotation than positive, but they differed from other important subsets of users by as much as 40% more negative.

Aidan Long, Ryan Dufur, and Jimmy O'Brien (Oklahoma Christian University)

#### \*CONSERVATION OF KINASE DOMAINS WITHIN THE INSULIN/TOR SIGNALING PATHWAY OF *DROSOPHILA*

The insulin/TOR signaling pathway is a key pathway within organisms that contributes to maintaining homeostasis and allows the uptake of glucose into cells. This pathway has been found to be well conserved in *Drosophila* species when compared to humans. Sik3 and S6k are two proteins that both fall within the insulin/TOR pathway. Sik3 was found to be less connected within the pathway than S6k, so we hypothesized that S6k would be more highly conserved than Sik3 due to the number of interactions within the pathway. After confirming the higher conservation of S6k in comparison to Sik3, we shifted our focus to the conservation of kinase proteins. Kinases are proteins that catalyze the movement of a phosphate from ATP to another protein, these proteins have kinase domains that are the structural active site of the phosphorylation process. Due to these domains having more interactions when compared to the whole protein, we hypothesized that the kinase domains would show a higher level of conservation than the overall whole protein. It was shown that the kinase domains of Sik3 and S6k had a lower degree of percent change when compared to the whole protein sequence. The proteins Sik3 and S6k are more conserved in the kinase domain than the overall protein sequence due to the interactive active site that is key for the protein function.

Ethan C. Long and Steven W. O'Neal (Southwestern Oklahoma State University)

#### \*EFFECTS OF LIGHT INTENSITY ON THE MORPHOLOGY, GROWTH RATE, AND PHENOLIC CONTENT OF *ZYGNEMA*

Filamentous algae, such as *Zygnema*, form loose floating mats in shallow areas of lakes and streams where the mats are exposed to extreme light conditions and high levels of UVB radiation in sunlight. The algal cells located on the surface of the mat are exposed to the highest levels of light intensity, while the cells deeper within the mat are exposed to lower levels. Previous work in this lab has shown that *Zygnema* produces phenolic compounds in response to high light intensity and that these compounds seem to contribute to a significant increase in tolerance to UVB radiation. This study focused on the light intensities that trigger the production of phenolics, shrinkage in cell length, and the effect, if any, on the growth rate of *Zygnema*. Specifically, we aimed to find the critical light intensity needed to bring about these changes. We began by growing five plates of *Zygnema* samples at a low light intensity for one week. The samples were then exposed to several light intensities ranging from ~15.6 - ~159.7  $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$  and allowed to grow for an additional week. The phenolic content, growth rates, and cell lengths were measured. There were significantly more phenolic compounds produced when the samples were exposed to higher light intensities compared to the lower light intensities. The cell lengths were significantly shortened as the light intensity increased. The growth rates remained unchanged across the treatments. Additionally, progress was made to identify the types of phenolic compounds *Zygnema* is producing.

Ostmo Lydia and Michael Smith (Northeastern State University)

#### \*DNA POLYMERASE EPSILON MUTANTS EXHIBIT DELAYED RECOVERY AFTER DNA DAMAGE

DNA replication requires many proteins to interact together to keep copies of our DNA intact and free of errors. Recent work in our lab with budding yeast has shown that Mcm10 plays an integral role in DNA polymerase epsilon (Polε) functionality. Pole contains three structural subunits and one essential catalytic subunit known as POLE1 in mammals and Pol2 in budding yeast. The N-terminal half of Pol2 contains functionally characterized DNA polymerase and exonuclease domains but the C-terminal half contains no experimentally characterized domains aside from two putative Zn-finger modules that are conserved from yeast to humans. Previously, we have shown that the C-terminus of Pol2 interacts with Mcm10 in budding yeast. Expanding on this research, we constructed mutations in yeast Pol2 that interrupted interaction with Mcm10. The current project studied cell cycle progression in the yeast POL2 mutants after exposure to DNA damage. Our results suggest that the specific mutants of Pol2 take longer to complete chromosome replication when treated with hydroxyurea. Our second project investigated the interaction of MCM10 and POLE1 in human cells. Co-immunoprecipitation experiments confirmed the interaction in HEK293T cells. Current experiments are focused on exploring POLE1 C-terminus mutants and their interactions in human cells. Our work in yeast and human cells will shed light on Polymerase Epsilon and MCM10 interaction and the function of this interaction in the maintenance of genome stability.

Jacob Mantooth (East Central University)

#### \*UNDERSTANDING MATHEMATICAL COMPONENTS OF DEEP LEARNING

Utilizing the handwritten digits from the MNIST dataset, we examine the mathematics of deep learning. To develop this understanding, we look at the interplay of linear algebra and non-linear ReLU function. We also explore the PCA dimensional reduction, linear regression and how these work when interchanged. We create decision trees and highlight the differences between deep learning. All of these techniques are applied to the MNIST dataset.

Randall Maples, Rachel L Bley, and Jarett A Williams (East Central University)

#### RECOVERY STUDY OF SILVER NANOPARTICLES THROUGH LIMESTONE AND DOLOMITE PACKED COLUMNS

Nanomaterials have found use in diverse applications such as materials coatings and pharmaceuticals, among many others because of the unique properties they possess. Due to this increased usage in society, the fate of these engineered nanoparticles being released into the ecosystem is important as potential environmental contaminants when devices and materials containing these nanoparticles are disposed of. Studies of the behavior of various nanoparticles in the environment is not new and has been underway for some time. Still, however, the environmental toxicity of these materials has not been fully determined due to the sheer variety of engineered nanoparticles available and in use. It is important to be able to assess the short and long-term fate of these engineered materials and the distribution of various nanoparticles in groundwater. This preliminary study examines the percent recovery of water dispersible functionalized silver nanoparticles using columns packed with limestone or dolomite as a potential model for their behavior in the local groundwater environment.

Lucas Martinez<sup>1</sup>, Hannah Rouse<sup>1</sup>, James O'Brien<sup>1</sup>, Lindsey J. Long<sup>1</sup>, Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

#### \*A COMPARISON OF THE EVOLUTIONARY CONSTRAINTS ON IMPL2 AND SLMB

The insulin/TOR gene signaling pathway is one that helps regulate cell and organism growth, which is essential for developmental purposes. Although there are many genes involved in this pathway, this research focused on the comparison of the two genes known as ImpL2 and slmb to determine the evolutionary constraints on this particular pathway. *Drosophila* species were used in the gene annotation process, and many *Drosophila* species were compared to the baseline species *Drosophila melanogaster* to compare if genes upstream or downstream in the signaling pathway were more susceptible to mutations or epigenetic changes. It was previously believed that genes upstream in the pathway were less conserved than those downstream, therefore when comparing these two genes it was hypothesized that ImpL2 would be constrained less than slmb in the pathway because it is more upstream in the pathway. After further gathering data and analyzing the different annotations reported on the genes throughout many *Drosophila* species, it was concluded that the original hypothesis was supported due to ImpL2 displaying significant changes like missing isoforms and less matches from sequencing results than slmb. Future directions with this study include comparing ImpL2's evolutionary constraint to other genes in the insulin/TOR pathway and studying conservation of genes in this pathway to observed phenotypic differences in many species of *Drosophila*. Any genes involved in this pathway found between these two studied genes will also be studied in detail to determine if the conservation of genes increases or decreases throughout the pathway between ImpL2 and slmb.

Jamian Maxwell and Leah S. Dudley (East Central University)

#### \*LEAF WEIGHT AND SURFACE AREA OF THE THREE SISTERS IN MONOCULTURES AND POLYCULTURES

It has been shown that plants grown in polycultures can have increased productivity when comparing them to monocultures. Leaf weight and surface area were taken when looking at the three sisters (bean, corn, and squash) in both monocultures and polycultures. Looking at these factors in relation to each other can give some insight on whether the three sisters grow more effectively in a polyculture or a monoculture. Four varieties of each sister were grown in a factorial design in two culture treatments: monoculture (3 varieties of the same sister) or polyculture (one variety each of corn, bean, and squash). Three seeds were sown into a mound randomly located within a garden space. They were then randomly assigned one of three watering treatments: control, medium (5mL/day on average of rainwater added) and high (10mL/day). Leaves were haphazardly collected from each living plant at the end of the flowering season, pressed and later weighed and scanned for leaf area. The area was measured by using the program ImageJ. Surface area to leaf weight ratio has been linked to photosynthetic potential and yield in plants. We assess this ratio for the Three Sisters in monoculture compared to polyculture and hypothesize that plants in

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polyculture may benefit from the association compared to monoculture. If results support our hypothesis, then growing plants as a polyculture supports this long-held tradition.

Kayley McBride, Mahnoor Ahsan, Melville Vaughan, and Christina Hendrickson (University of Central Oklahoma)

#### \*ANTI-CANCER EFFECTS OF DANDELION'S EXTRACT ON CERVICAL CANCER CELLS

According to the American Cancer Society Journal, 1,806,590 new cancer cases and 606,520 cancer deaths are expected to occur in 2020 in the United States. Despite the development of many forms of cancer therapy, there continues to be a high rate of death among patients. Certain plant-derived products have pharmaceutical uses due to their anti-cancer effects. Dandelion (*Taraxacum officinale*) could be one of them. Dandelion is widely accessible, it grows throughout the world and has long been consumed safely as part of Middle Eastern and Ancient Chinese Medicine due to its anti-inflammatory and anti-carcinogenic properties. The mechanism of its effect on cancer cells is still unclear. This study investigated the anti-cancer effects of Dandelion on cervical cancer cells known as HeLa cells. It was hypothesized that the anti-cancer activity of dandelion extract acts by disrupting key cellular processes in tumor cells, which could result in growth inhibition, cell death and an overall decrease in their invasiveness. Dandelion Whole Extract (DWE) was prepared, filtered, freeze-dried and resuspended in cell-growth media. HeLa cells and normal human cervical cells (HCEC) were maintained under standard in vitro cell culture conditions, then treated with DWE concentrations between 8 to 0 mg/ml for 96 hours. Our results showed that DWE inhibited proliferation and invasion while promoting programmed cell death in HeLa cells, but did not have such effects on HCEC cells. This study supports the possible use of dandelion as a natural source of anti-cancer compounds against cervical cancer. This study could potentially improve cancer treatment by unveiling cellular and molecular mechanisms behind anti-proliferative and anti-invasion effects of dandelion that are getting popularized as a cancer treatment.

Daniel McInnes and Charles M. Crittall (East Central University)

#### GLOBAL REACTIVITY DESCRIPTORS OF CHLOROFLUOROPYRROLES

The global reactivity descriptors chemical potential ( $\mu$ ), chemical hardness ( $\eta$ ) and electrophilicity index ( $\omega$ ) were calculated for chlorofluoropyrrole isomers using the BLPY/6-311+G basis set. Geometries were optimized, and energy in Hartrees were calculated for each compound. This data can potentially be used in predicting reactivity and toxicity.

Ann McNairn and Jessica Brumley (East Central University)

#### \*SYSTEM MODELS FOR LONG-TERM REGIONAL WATERSHED MANAGEMENT: A PRELIMINARY LAKE MODEL

Water resource estimation is an integral part of long-term watershed planning, especially as climate change is expected to impact meteorological patterns. Studies have attempted to predict regional water resource availability due to climate change but lack reliability. Many current models do not apply a system dynamics approach, modeling techniques that include nonlinear behavior. STELLA simulation software was used to develop a common lake model to be incorporated into a future watershed model. Current model calibrations, based on Lake Thunderbird in Oklahoma, have successfully shown evaporation, runoff, precipitation, and outflow patterns that keep a lake at equilibrium for ~25 years. Future plans include incorporating climate change predictions for precipitation and droughts, soil management, and community impacts such as population growth.

Zachary Mearse<sup>1</sup>, Zachary Mearse<sup>1</sup>, Hannah Ewing<sup>1</sup>, Lindsey J. Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

#### \*DSOR1 CONSERVATION WITHIN THE INSULIN/TOR PATHWAY OF *DROSOPHILA*

The insulin/TOR pathway in *Drosophila* species consists of a network of genes that heavily regulate a cell's glucose metabolism and response mechanisms while contributing to overall growth and survival. The conservation of genes in this pathway is currently. Using resources from the Genomics Education Partnership (GEP) program, the evolutionary conservation of Dsor1 was annotated in multiple *Drosophila* species. Genes that are downstream in a pathway should have higher conservation levels than upstream genes because they have a higher number of connections with other genes. It was hypothesized that the gene Roc1a was further upstream than Dsor1 based on the number of connections each gene had. A divergence scoring system was used to give a numeric value to the divergence of different genes in species related to *Drosophila melanogaster*. Scoring between Dsor1 and Roc1a in *D. ananassae* supports that Roc1a has a higher level of divergence and that Dsor1 is a well-conserved gene due to its low divergence score. Divergence between species was mainly seen in varying genomic neighborhoods.

Dylan Melton, Angeela Gauchan, Katlyn Hampton, Alisha Howard and Charles Biles (East Central University)

#### \*MOLECULAR AND MORPHOLOGICAL CHARACTERISTICS OF PATHOGENIC FUNGAL SPECIES IMPORTED FROM CENTRAL AMERICA

Plant pathogenic fungi are the leading cause of plant diseases in the world. The increasing discovery of plant pathogenic fungal species in the United States is, in many cases, due to the introduction of infected host crops via international trade. The genus *Diaporthe* (Phomopsis) is distributed to several geographical locations and many host crops as an endophyte or a latent pathogen, causing disease at the host crop's maturity. The purpose of this study was to identify the presence of *Diaporthe* spp. on specifically melons (*Cucumis melo* L. var. *cantalupensis* Naudin) being imported from Central America to Oklahoma. We purchased a total of 61 melons from 3 different markets in Ada, Oklahoma. Melons were imported from Honduras, Mexico, and Costa Rica. The melons were washed in a 10% bleach solution and set out on a clean surface for 4 to 6 days, until lesions were visible. Infected tissue was isolated from the mesocarp tissue of the melon and put onto acidic potato dextrose agar (APDA) to facilitate fungal growth and prevent any bacterial contamination. Once in pure culture, the DNA was extracted using an OmniPrep Fungal Kit and amplified using polymerase chain reaction (PCR). Three different loci were targeted during this study: Beta-tubulin (TUB), Transcription Elongation Factor 1-alpha (TEF), and HIS. Prior to analysis, Koch's postulates was conducted with each *Diaporthe* isolate using healthy melons to determine virulence. We found variation in the population of *Diaporthe* spp.

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being imported as well as some isolates that were of a different genus. This includes *Stagonosporopsis* spp. The information gathered indicates that there is a multitude of fungi being imported from Central America, increasing the variety of pathogenic fungi in the United States.

Jessie Merrifield and Heather R. Ketchum (University of Oklahoma)

#### \*A COMPARISON OF TICK ABUNDANCE ON DISC GOLF COURSES IN URBAN AND SUBURBAN CENTRAL OKLAHOMA PARKS

Tick surveillance is an important aspect of vector control because it provides necessary information about species abundance, the risk of a tick encounter, and the potential presence of pathogens. Risk assessment through flagging focuses on the possibility of a human coming into contact with a questing tick, one that is actively seeking a host, while carbon dioxide traps can be used to determine the presence and abundance of ticks in a defined area. For our project, we surveyed ticks on disc golf courses from two central Oklahoma parks, one urban and one suburban. Disc golf is an increasingly popular sport where players are exposed to a variety of environments where they could potentially encounter ticks. The fairways of disc golf courses are typically mowed and well maintained while the periphery of the fairway is relatively untouched. At each park, we flagged for ticks around the periphery and the fairway of disc golf courses to determine a player's risk of encountering a questing tick. Carbon dioxide traps were used around the park to determine tick abundance at each park. While ticks were present at both parks, the greatest abundance was at the suburban park. Generally, on the disc golf courses, there was a greater abundance of ticks around the periphery, which included unmanaged and wooded areas as well as tall grasses and shrubs. For less skilled players, chasing a disc into the periphery of the course could increase their risk of coming into contact with a tick.

Brittany L. Moehnke and William E. Luttrell (Oklahoma Christian University)

#### \*EFFECTS OF PRETREATMENT OF MICE WITH A SERIES OF KETONE COMPOUNDS ON IN VIVO HEPATIC MICROSOMAL GLUCURONYLTRANSFERASE ACTIVITY—IMPLICATIONS FOR KETONE-DRUG INTERACTIONS

Exposure to toxic chemicals in the workplace or environment can alter the way the body responds to the administration of therapeutic drugs. Studies have shown that ketones, such as acetone and pinacolone, can produce liver microsomal enzyme enhancement, thereby causing an increase in the rate of drug metabolism. The purpose of this study was to determine the effect of ketone exposure on the activity of microsomal glucuronyltransferase following pretreatment of mice with a series of ketone compounds. Five ketones of increasing molecular weight (acetone, 2-butanone, 2-pentanone, 2-hexanone, and pinacolone) were selected for pretreatment studies. Male CD-1 mice (n = 42) were pretreated by subcutaneous injection with 90% LD50 (median lethal dose) 12 hours before they were sacrificed and livers removed to provide microsomal tissue for a control and five ketone groups (n = 7). Liver microsomes were isolated and glucuronyltransferase activity was determined spectrophotometrically. When 2-aminophenol (2-AP) is glucuronidated, it forms 2-aminophenyl glucuronide (2-APG). Enzyme activities were expressed as  $\mu$ g 2-APG formed per milligram protein per minute. Using Lineweaver-Burk plots enzyme kinetic studies were completed with the determination of  $K_m$  and  $V_{max}$  values for glucuronyltransferase. Prism software was used for graphing and data analysis. All of the ketones, especially acetone, caused an increase in  $V_{max}$  values for glucuronyltransferase. In general, there was decreasing  $V_{max}$  values with increasing molecular weight of the ketone compounds. Pretreatment with ketone compounds of increasing molecular weight caused an increase in liver glucuronyltransferase activity in mice. This is consistent with our previous in vitro studies in which four of the five ketones stimulated the activity of glucuronyltransferase. This implies that workers exposed to these ketone compounds in high concentrations may be at risk for ketone-drug interactions due to enhancement of some Type II drug-metabolizing enzymes. Future studies will utilize sulfotransferase and glutathione S-transferase assays.

Jose Montalva<sup>1</sup>, Bruce Hoagland<sup>2</sup>, and Daniel Paiva Silva<sup>3</sup> (<sup>1</sup>East Central University, <sup>2</sup>University of Oklahoma, <sup>3</sup>Instituto Federal Goiano, Brazil)

#### \*\*NICHE FIGHTING: EXPLORING THE DISTRIBUTION OF NATIVE AND INVASIVE SPECIES OF BUMBLE BEES (HYMENOPTERA: APIDAE) IN CHILE, USING CITIZEN SCIENCE DATA

*Bombus terrestris* and *Bombus ruderatus* are invasive bumble bee species in South America. Several studies indicate that they are responsible for the sharp decline in the populations of the Patagonian bumble bee *Bombus dahlbomii* in Chile and Argentina. Here, we gathered a comprehensive database of occurrence records from museum and citizen science sources. Multivariate bioclimatic niche analyses and species distribution models were used to determine if niche overlap occurred between the invasive and the native species. We also analyzed the potential effect of current and future climatic scenarios on the distribution of these bumble bees. From the results, we concluded that there was niche overlap between the three bumble bee species, and most significantly between *B. terrestris* and *B. dahlbomii* (61%). The current distribution for *B. terrestris* is extensive in South America but the models also show a shrinking distribution for *B. ruderatus* and *B. dahlbomii* in the pessimistic future scenario. We discuss the consequences of the niche overlap between the introduced bumble bee species and the endangered *B. dahlbomii*.

Dwight L. Myers, Brenna S. Hefley, and Uendi Pustina (East Central University)

#### G3MP2 COMPUTATIONAL STUDY OF GASEOUS BORON AND ALUMINUM HYDROXIDES

Refractory oxides and nitrides are important materials in high temperature applications. In environments containing water vapor, hydroxides and oxyhydroxides are important reaction products, particularly in combustion environments, which can contain 3 – 10 % water vapor. Formation of gaseous hydroxides and oxyhydroxides is an important mode of corrosion. This study is a computational study of the thermodynamic stability of two of the gaseous hydroxides of boron and aluminum, boron(III) hydroxide and aluminum(III) hydroxide. Calculations were performed using composite methods at the G3MP2 level of theory. The geometries, vibrational frequencies, thermodynamics, and steps toward computations at higher levels will be discussed.



Kayli Nail, Christian Holcomb, and Erika Lutter (Oklahoma State University)

**\*BACTERIAL TWO HYBRID ANALYSIS OF *CHLAMYDIA TRACHOMATIS* PROTEINS**

*Chlamydia trachomatis* is an obligate intracellular bacterial pathogen which poses severe health problems throughout the world. There are over 90 million new cases annually, making it the most common sexually transmitted disease in the world. *Chlamydia* can pose significant problems during and after infection. It is imperative to understand how *Chlamydia* manipulates the host cell and potentially develop future treatments. The mechanisms by which *C. trachomatis* alters immune response is not well understood, but recent work has identified an interaction between the chlamydial inclusion membrane protein, CT226, and the potential interacting host proteins, Flightless homologue II (FLII), and Leucine Rich-Repeat Flightless-Interacting Proteins 1&2 (LRRFIP1 and LRRFIP2). FLII, LRRFIP1 and LRRFIP2 are known to interact as a complex and are upstream regulators of the inflammasome. Currently, it is unknown if CT226 interacts with one or all of the interacting partners and needs the actual interaction needs investigation. My hypothesis is that CT226 will directly interact with one of the 3 potential interacting partners (LRRFIP1, LRRFIP2, and FLII) and that we will be able to detect this interaction in the bacterial two hybrid system. Current efforts have focused on cloning CT226 into PUT18 and the three host proteins (FLII, LRRFIP1 and LRRFIP2) individually into PKNT25. PUT18 and PKNT25 are the bait and prey plasmids that have been adapted for use in the bacterial two hybrid system. Once each pair of plasmids are properly transformed (each *E. coli* strain will have two plasmids, one carrying CT226 and one carrying the potential interacting partner), they will be screened using traditional Beta-galactosidase assays or cAMP assays to determine the specific interactions.

Mary Hang Nguyen and Sung-Kun (Sean) Kim (Northeastern State University)

**\*HEXOKINASE II INHIBITION IN THE PRESENCE OF FENBENDAZOLE**

In both normal and cancer cells, glycolysis helps cells to grow. Requiring extensive amounts of energy for cancer cells' rapid growth causes promoting glycolysis. In an attempt to attenuate the cancer cells' growth, inhibition of hexokinases may be critical because the enzyme functions the conversion of glucose to glucose-6-phosphate irreversibly in glycolysis. We focused on the inhibition of human hexokinase II (HKII) among four different isozymes with the chemical Fenbendazole that is one of Benzimidazoles. Autodock program was used to identify possible binding locations on HKII and determine the binding affinity. The docking result showed that deltaG value between HKII and Fenbendazole was - 7.9 kcal/mol, which can be considered a strong interaction. We also performed HKII enzyme assays to determine an IC50 value, and the value was 2.5 microM. Based on these computational and experimental tests, Fenbendazole may be a potential cancer medicine; however, further experiments are warranted.

James O'Brien, Aidan Long, Ryan Dufur, and James O'Brien (Oklahoma Christian University)

**\*ANALYZING KINASE DOMAIN CONSERVATION IN *DROSOPHILA***

The Insulin/TOR signaling pathway is responsible for regulating insulin levels in *Drosophila*. It is understood that the genes in this pathway are more evolutionarily conserved if they have more connections within the pathway, but it is not entirely clear how this affects kinase domains. Kinase domains are binding sites on kinase proteins, which phosphorylate other proteins. Because the kinase domain has more interactions than the rest of the gene, it was hypothesized that the kinase domain would be more conserved. To test this, we analyzed the nucleotide similarity and protein similarity in two genes, Sik3 and S6k, between *Drosophila melanogaster* and five other *Drosophila* species. In both genes, the kinase domains were more conserved than the whole gene, which fit the hypothesis. It was also observed that the nucleotide sequence was more conserved than the protein sequence. This is probably due to the fact that many nucleotide mutations will be silent, coding for the same amino acid. Lastly, the gene S6k was found to be more conserved than Sik3, most likely because S6k has more connections.

Jordan Odell and Alisha Howard (East Central University)

**\*INVESTIGATION OF BOVINE LEUKEMIA VIRUS PREVALENCE IN OKLAHOMA HERDS**

Bovine leukemia virus (BLV) is an oncological retrovirus infecting a significant number of cattle globally causing B-cell leukemia in 1-5% of infected cattle. The economic consequences of BLV infection in cattle herds can be sizable, with both direct and indirect costs of BLV infection cutting into already slim profit margins. Direct costs of BLV are associated with clinical presentation in the form of lymphosarcoma resulting in loss of production. Other direct costs include decreased production in the sub-clinical presentation of BLV, such as veterinary costs associated with the identification of disease, and replacement costs associated with culling animals prematurely due to decreased production or death of animals. Indirect costs associated with BLV are connected to a loss of revenue related to export restrictions for cattle and cattle-related products. Despite the economic impact, the prevalence of BLV infection in many herds is unknown. BLV residual particles also has the potential impact on human health, as 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.<sup>1,2,3</sup> 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 samples are ideal since milk is one of the routes of transmission between cow and progeny. Another avenue is research understanding any potential infectivity of BLV viral particles or cross-reactivity of BLV proteins in human systems.

Daniel Oforji and Julianna Goelzer (Oral Roberts University)

**\*CELLUS: DIGITALIZED, LOW-COST SUPER-RESOLUTION MICROSCOPE**

Cellus is a fluorescence light microscopy project centered on a 3D printed microscope, based on our design and a design by the Openflexure project that uses low-cost components to perform super-resolution fluorescence imaging. This small footprint, multicolor fluorescent microscope is ideal for both diagnostic and research purposes. The system is sufficiently sensitive and mechanically stable to allow the use of the Super-Resolution Radial Fluctuations algorithm to obtain images with resolution better than the diffraction limit of 1 (approx. 140nm). This project also seeks to include a software interface that can connect

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professionals and nonprofessionals worldwide to share findings in real-time. We strive to include features such as remote monitoring of ongoing experiments and sharing of results in real-time with collaborators worldwide. These features will eliminate personnel issues typically seen in small research facilities and remote diagnostic labs. Due to the low-cost components, the entire system can be built for approximately \$1200, a considerable feat considering the new features proposed.

Cheyenne Olson (Rogers State University)

#### **\*\*ENVIRONMENTAL STEWARDSHIP IN CITIZEN SCIENCE PARTICIPANTS**

In recent years, citizen science programs have gained momentum and involved members of the public in active and ongoing science projects. Citizen science is often defined as a form of research collaboration that engages members of the public in scientific research projects that involve data collection, analysis, and dissemination (Haklay, 2013; Dickinson et al., 2012; Conrad & Hilchey, 2011; Wiggins & Crowston, 2011). In Oklahoma, Blue Thumb is a state-sponsored citizen science program that focuses on water quality monitoring. Blue Thumb has over 300 active volunteers monitoring 80 streams across Oklahoma annually. Focus on citizen science has turned to evaluation of participant outcomes. Behavior and stewardship is defined as “measurable behaviors that result from engagement in citizen science projects but are external to protocol or skills of the specific citizen science project” (Phillips et al., 2018). Behavior change is considered to be the “most sought-after outcome” for environmental citizen science program, but initial pro-environmental behaviors are not always documented before participation (Phillips et al., 2017). There is a need in Blue Thumb to evaluate whether volunteers change environmental behaviors as a direct result of participation in citizen science activities or if environmental behaviors already exist in their participant demographics. This poster serves as a discussion of preliminary findings of pro-environmental behaviors of new BT volunteers. This study is part of an on-going multi-phase mixed methods evaluation of participant learning outcomes in water monitoring citizen science programs like Blue Thumb. New volunteer environmental stewardship scores will be compared to experienced volunteer scores to infer if their environmental behaviors have changed over time. Older, experienced volunteers will be asked to reflect on what specific actions they have undertaken as a result of something they learned or experienced within their Blue Thumb Participation. Results anticipated Spring 2022.

Radhika Pande, Kenneth E. Miller, and Subhas Das (Oklahoma State University Center for Health Sciences)

#### **\*\*UNDERSTANDING EPIGENETIC MECHANISM: A NOVEL WAY TO APPROACH THERAPEUTIC TARGETS FOR THE TREATMENT OF COLITIS**

Inflammatory bowel disease (IBD) is a term used to characterize the conditions like Crohn's disease and ulcerative colitis, which involve inflammation of the digestive tract. The main symptoms include repeated abdominal pain, diarrhea, fatigue, reduced appetite, and weight loss. According to CDC, approximately 3 million Americans were reportedly diagnosed with IBD. Reasons underlying IBD are still unknown, but several factors such as environmental, genetics, diet, and microbiome composition might play an essential role in disease development and the pharmacological therapies are limited. Previous studies have linked the Nerve growth factor (NGF), which plays an important role in inflammation and immune response, expression with neurogenic inflammation in various inflammatory animal models. Numerous studies have shown that epigenetic regulation, especially DNA methylation, plays an important role in inflammatory modulation. Epigenetics is the study of changes in gene expression, which occurs without any changes in the DNA sequence. The epigenetic mechanism for NGF regulation during colitis is still unexplored. Aim: In this study, we evaluated the epigenetic mechanisms which regulate the gene expression of NGF during TNBS induced colitis in rats. Method: Colitis was induced in 8-10 weeks old female Sprague-Dawley rats by infusing TNBS into the colon. The colon was collected after 24 hours of inflammation. Azacitidine (Aza) was pre- and co-administered to/with TNBS in the colon. Bisulfite converted DNA was used for Methylation-specific PCR (MSP) to analyze the DNA methylation patterns in the NGF promoter's CpG islands. RNA and protein expression of NGF was determined by qualitative, quantitative PCR, and immunoblot techniques. Results & Conclusion: Our findings show altered NGF expression in the colon during TNBS induced colitis due to hypermethylation of CpG dinucleotides in the NGF promoter. Aza treatment mitigated this hypermethylation and reduced neurogenic inflammation in these animals suggesting NGF expression can be epigenetically regulated in colon inflammation.

Sam Ray and George Wang (East Central University)

#### **\*SEASONAL VARIATION OF ARTHROPODS COLONIZING DECOMPOSING MAMMALIAN CARCASSES**

Decaying mammalian carcasses attract a variety of insect detritivores and other colonizers. The succession of insect colonizers can be used to indicate the rate of decomposition in forensics. The type and abundance of insect colonizers can be affected by season. We examined insect colonization of medium-sized mammalian carcasses between spring and summer seasons at the Botanical Outdoor Learning & Outreach Space (BOLOS) of East Central University in Ada, Oklahoma. We collected meso-mammalian (*Didelphis virginiana*, *Procyon lotor*, *Castor canadensis*, and *Dasyurus novemcinctus*) carcasses from highways and weighed them. We enclosed the specimens in metal-wire cages and placed them in a wooded area of BOLOS. We conducted the experiment twice, once in late April 2021, and then in early August 2021. During each experiment, we performed daily sampling of insects and other arthropods on all specimens for one week, and then sampled once every two days until the specimens fully decomposed. The species and densities of arthropods were recorded. The arthropod species richness is comparable for both seasons; however, the species composition differs. The densities of American carrion beetle (*Necrophila americana*) and margined carrion beetle (*Oiceoptoma noveboracense*) are higher in the spring whereas the densities of rove beetles (*Platydacus maxillosus* and *Creophilus maxillosus*) were higher in the summer. Fly larvae development period was shorter in the summer than in the spring. The mammalian carcasses decomposed faster in the summer. Our results suggest that the use of insect abundance to indicate the decomposition rate of bodies in forensics should consider the season and other environmental conditions.

Daniel Reed<sup>1,2</sup>, Toby L. Nelson<sup>1</sup>, Gabriel A. Cook<sup>1</sup>, Erika I. Lutter<sup>1</sup>, and Franklin R. Champlin<sup>2</sup> (<sup>1</sup>Oklahoma State University, <sup>2</sup>Oklahoma State University Center for Health Sciences)

**\*NOVEL MELANIN INSPIRED COMPOUND POSSESSES MEMBRANE-DIRECTED ANTIBACTERIAL MECHANISM FOR GRAM-POSITIVE BACTERIA**

Melanin-inspired compounds (EIPE) synthesized by our group possess a core that provides scaffolding for the attachment of various functional groups. The purpose of this study was to investigate the antibacterial potential of Melanin-inspired compounds EIPE-1 and EIPE-HCl which are hydrophobic and hydrophilic, respectively. Antibiotic resistance remains a threat as more pathogenic bacteria increasingly acquire resistance to clinically useful drugs. This creates a need for novel compounds to be developed to combat resilient pathogens like methicillin resistant *Staphylococcus aureus* (MRSA). A standardized disk agar diffusion bioassay was performed to qualitatively compare the susceptibility and resistance levels of 12 gram-positive and 13 gram-negative bacteria to EIPE-1 and EIPE-HCl. The hydrophobic derivative EIPE-1 exhibited a gram-positive spectrum that included two methicillin resistant *Staphylococcus aureus* (MRSA) strains, while the hydrophilic derivative EIPE-HCl possessed no antibacterial properties at the concentrations examined. Turbidimetric growth curves were constructed to investigate the EIPE-1 mechanism of action. Bacteriolysis occurred immediately upon treatment for *Staphylococcus epidermidis* SK01 and at the five-hour mark for *B. subtilis* ATCC 6633, likely resulting from dissolution of their cytoplasmic membranes. Minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) bioassays were employed to quantitatively determine EIPE-1 potency. All gram-positive bacteria tested were susceptible with MIC values ranging from 0.25 to 2.0 µg/mL, while gram-negative bacteria were resistant with MICs in excess of 128 µg/mL. MICs and MBCs for two MRSA strains and two strains of the obligate anaerobe *Clostridioides difficile* were less than 8.0 µg/mL. These data suggest that hydrophobic EIPE-1 is a novel compound that possesses a gram-positive antibacterial spectrum that involves disruption of the cytoplasmic membrane and does not involve the involvement of molecular oxygen. The intrinsic resistance of 13 disparate gram-negative bacteria is likely due to the typical impermeability properties of the gram-negative outer membrane for hydrophobic molecules.

Hallie Reed, Bobby L. Cothren, and Leah S. Dudley (East Central University)

**\*BEE POLLINATION PATTERNS WITHIN A THREE SISTERS GARDEN**

Bee pollination is an essential ecosystem service required for many plant species to set fruit. Mutualistic plant-pollinator interactions vary in efficiency, depending on the plant-pollinator species and frequency of flower visits. With the human demand for insect-pollinated crops increasing and the population of bee pollinators declining, understanding the plant-pollinator interactions of these insects are crucial. This study focused on three bee groups: the honey bee, the bumblebee, and the solitary bee and their behavior within a Three Sister (corn, bean, & squash) garden. With its open, zoophilous floral design, squash flowers may entice more visitors than the other two sisters. Here, we address the following three questions: 1) Will squash flowers receive more visitors than the other two sisters? 2) Will a squash plant receive more visitors as the number of open squash flowers increases? and 3) Do the different types of bees visit squash flowers equally? The study took place during June-July of 2021 in a Three Sister garden consisting of various Sister varieties grown in mounds in a random, full-factorial design. Plant species, number of open flowers, visitor morphospecies, visitor behavior, and number of visitors were recorded. Results show that squash flowers received the most insect visitation compared to the other two sisters. The number of open squash flowers on a single plant had no notable effect on the number of visits, and the most frequent visitor to the squash flowers were honey bees. Our results suggest that agricultural systems may benefit from planting squash to attract pollinators. By interspersing squash throughout an agricultural system, it may increase the overall pollination and yield of the entire system, not just that of squash. In addition, squash not only is used as a food source for the non-native honey bee but also is capable of supporting native bee populations.

Rakin Riza, Mehmet Aktas, and Esra Akbas (University of Central Oklahoma)

**\*HYPERGRAPH LAPLACIANS IN DIFFUSION FRAMEWORK**

Modeling diffusion on networks is an important concept in network science. It helps to understand how an idea, information, or infection, diffuses within the network. The graph Laplacian has been used to model diffusion on graphs for years. Extending graph Laplacians to hypergraphs is not an intuitive task since hyperedges can include more than two vertices, and edge incidence and vertex adjacency are set-valued in hypergraphs. To handle this issue, researchers limit their attention to specific hypergraphs, which is often not the case for real-world hypergraphs, or reduce hypergraphs to graphs, where these reductions result in information loss. In this talk, we present two new hypergraph Laplacians that can be defined on any hypergraphs. Our Laplacians take the relations between hyperedges into consideration, hence can be used to model diffusion on hypergraphs not only between vertices but also hyperedges. As an application, we study the Enron network and show the effectiveness of the proposed Laplacians in the influential node detection problem. These Laplacians can be further employed in different hypergraph mining problems, such as social contagion models on hypergraphs, influence study on hypergraphs, hypergraph classification, and hypergraph representation learning.

Robin Roberson (East Central University)

**VIRTUAL TWIN STUDY: EFFECTS ON PARENTING EFFICACY**

In this study, 235 developmental psychology students (n=169 female; n=66 male) were assigned the task of raising two virtual twins using Pearson's My Virtual Child© (n.d.). A parental locus of control pre/post survey was used to determine if students improved in their understanding of parental influence on child/adolescent development. Significant changes were seen overall, as well as when disaggregated by student classification, ethnicity, and course delivery mode. Results suggest using My Virtual Child© (n.d.) as a twin study improves student understanding of parental influence on human development.

November Sankey and Avishek Mitra (Oklahoma State University)

**\*HOW DOES *MYCOBACTERIUM TUBERCULOSIS* ACQUIRE HEME IRON?**

Before the SARS-CoV-2 pandemic, *Mycobacterium tuberculosis* (Mtb) was the leading cause of death worldwide by an infectious disease resulting in 1.4 million deaths annually. Mtb is transmitted through aerosols that enter the host alveolar passages, where it proliferates by efficiently inhibiting the phagolysosome. An essential aspect of Mtb survival and virulence is the acquisition of iron within the macrophage. Even though iron is abundant in the human host it is sequestered within proteins such as transferrin (Tf), lactoferrin (Lf) or ferritin (F) or stored within heme (Hm). Mtb secretes siderophores to extract iron from host Tf, Lf or F, but siderophores cannot extract the iron from Hm. Our goals involve understanding the mechanisms that are employed by Mtb to acquire iron from Hm, which stores >80% of the host iron. In previous experiments we observed that in the presence of Hm Mtb upregulates genes that encode the components of the ESX-4 type 7 secretion system. In this study we explored the hypothesis that ESX-4 is required for Hm iron acquisition by Mtb. We constructed a Mtb ESX-4 mutant and then determined that the mutant has a growth defect specifically in the presence of Hm as the sole iron source. Then we tested the hypothesis that the ESX-4 mutant is required for secretion of specific proteins that is required for transporting Hm into the cell. We used mass spectrometry to analyze the culture filtrate proteins from WT Mtb and ESX-4 mutant strains and identified heme utilization specific proteins (HUSPs) whose secretion is dependent on the ESX-4 system. In conclusion, we have identified that the ESX-4 secretion system is required for efficient Hm utilization by Mtb and identified proteins that are specifically secreted by ESX-4 for Hm utilization.

Andrew Seeberger, Ethan Strickler, and Bryhan Douglas (East Central University)

**\*AN ANALYSIS OF 400-450NM COMPONENTS OF SEMICONDUCTOR AND UV ILLUMINATION**

Traditional lighting was based on either incandescent filaments with their poor efficiency or mercury vapor fluorescent lamps with a somewhat elevated UV component and unnaturally blue spectral output. More recent lighting innovations have included both compact fluorescent ("CF") lamps which can have a lower color temperature than earlier industrial fluorescent lamps and semiconductor ("LED") lighting in a variety of color temperatures. However there have been 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 varying 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.

Austin Segrest, Cade Huston, Chanock Lee, Gang Xu, and Melville Vaughan (University of Central Oklahoma)

**\*PHENOTYPICAL ANALYSIS OF OLD AND YOUNG DUPUYTREN'S DISEASE CELLS**

Dupuytren's disease is a fibrotic disease in the hand that reduces motility. An antibody stain for focal adhesions was conducted on old and young cells that were treated with and without TGF- $\beta$ . Both old groups had a higher average area of focal adhesion and grayscale intensity. After 24 hours the old TGF- $\beta$  group had the highest compactional ability with young TGF- $\beta$  slightly surpassing after 24 hours. These results indicate a switch in specialization based on age to a more stationary phenotype that exerts more force. Further research is needed to quantify the effect proliferation has on the compactional ability following the 24 hours.

Jeevotham Senthil Kumar (Oklahoma State University)

**\*\*FUNCTIONAL STUDY OF C1Q/TNF-RELATED PROTEIN 6 (CTRP6) IN OBESITY AND DIABETES**

The prevalent pathophysiologies associated with obesity like insulin resistance are caused by a chronic unresolved low-grade inflammation in the adipose tissue. This heterogeneous tissue is highly populated by macrophages, activated to their inflammatory phenotype, M1. Although the macrophage M1 phenotype explains pathological inflammation, the mechanistic details behind the induction of M1 during obesity remain unclear. In previous studies, C1q/TNF-related protein 6 (CTRP6) has been correlated with clinical indicators of obesity and diabetes. It is also correlated with the accumulation of inflammatory macrophages in the adipose tissue. In this study, we investigate the effects of CTRP6, which is secreted mainly by macrophages, on the polarization of macrophages into their inflammatory M1 phenotype in an autocrine manner. Overexpressing CTRP6 in murine macrophages induced genes specific to the M1 phenotype like Cd11c and iNOS but inhibited the expression of M2 marker genes like Cd206 and IL-10. The effect of CTRP6 on Cd206 persisted even when the macrophages were treated with IL-4, a stimulant of the M2 phenotype. Hence, our findings indicate that CTRP6 helps promote the M1 inflammatory phenotype primarily by inhibiting the Cd206. Further studies will help establish CTRP6 as a mechanistic target for therapeutic regimens against obesity and its related pathologies.

Andrew J. Sims and Megan E. Runion (Oklahoma Christian University)

**\*MARTY MCFLY: A GENE ANNOTATION STORY**

The insulin/TOR pathway is a regulator of cell and organism growth in metazoans with evolutionary conservation being observed and assessed within the *Drosophila* species. The ideal examination for research was on Dsor1 and ImpL2 genes. To determine the level of conservation, the annotation of the Dsor1 and ImpL2 genes in species similarly related to and evolutionarily diverged from *Drosophila melanogaster* were compared to the original transcript in *D. melanogaster*. The hypothesis was that Dsor1 would show greater genetic conservation compared to ImpL2 due to its greater connectivity within the insulin/TOR (IT) pathway. The results showed higher conservation of Dsor1 when compared to ImpL2 in the annotated species of *Drosophila*. Research showed that the number of connections a gene holds is related to the degree of conservation within the pathway. Overall, genes interactions and genetic conservation is an exceptionally complex process that shows the specificity in the evolutionary processes. In future directions, measuring other genomic model findings from gene annotations can provide understanding on the accuracy of computer-generated modeling. A higher amount of focus can be attributed into examining the genes that remain conserved or continue to diverge. Examination on the role of mutations in these genes can also be researched in the future to

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observe the influence of conservation in the insulin/TOR pathway. There can be more development in generating new hypotheses that can further contribute with results concluded in this project.

Anastasia Smith and William Ranahan (Oral Roberts University)

**\*ANALYSIS OF EFFECTS OF CANNABINOIDS ON GENE EXPRESSIONS IN TRIPLE NEGATIVE BREAST CANCER**

Contemporary cancer treatments such as radiation, chemotherapy, and surgery have negative off-target effects in nontumorigenic tissue. Alternative remedies may offer treatment with little to no side effects. Medicinal plants have been used worldwide as adjuvant therapy and treatment for cancer. Given that initial in vitro and animal model studies investigating the effect of cannabinoids on tumors show promising results, the authors proposed to investigate a full spectrum extraction of cannabinoids from hemp. It is hypothesized that this extraction will negatively affect the viability of cancer cells and alter gene expression. Cannabinoids from a hemp extract were analyzed using high pressure. The cancer cell line MDA-MB-468 is a triple negative breast cancer (ER-/PR-/Her2-). Full cannabinoid extractions tested on MDA-MB-468's decreased cell viability when applied in amounts of four and eight  $\mu$ l in 100  $\mu$ l of total suspension. The extractions were again tested on MDA-MB-468's, but in a six cm petri dish, and successful results were used to obtain RNA. cDNA was made from RNA samples and added in a primePCR assay. The primePCR assay well's contained preloaded primers for 91 genes and four controls. Of these genes, the gene expression of three were examined: HMOX1, IL6, and VIM. Future studies will aim to examine other genes analyzed in the primePCR assay, test isolated cannabinoids, and examine the effects of full hemp extracts on different cell types.

C. Claire Smith, Francisca M. Mendez-Harclerode, Gloria M. Caddell, Chad B. King, and Michelle L. Haynie (University of Central Oklahoma)

**\*PRELIMINARY TRENDS IN SMALL MAMMAL POPULATIONS AFTER THREE YEARS OF MARK-RECAPTURE RESEARCH IN THE GYPSUM HILLS OF WESTERN OKLAHOMA**

The purpose of this project is to monitor changes in small mammal populations and communities over multiple generations to determine what factors affect how the populations and communities change over time. In March of 2018, a permanent trapping web was established at the University of Central Oklahoma's Selman Living Lab (SLL). Two additional permanent webs were established in June of 2018. The SLL is located in the gypsum hills of Woodward County in western Oklahoma. Surveys of the 3 webs are conducted for 3 nights, 4 times a year, and include collection of mammalian and vegetation data. Climate data also is obtained for each day of the trip; monthly and yearly climate data also will be assessed. To date, 13 mammalian and vegetation surveys have been conducted. Based on preliminary data, seasonal and habitat trends have been detected in mammalian populations, with the lowest capture numbers occurring in the summer and reaching peak numbers in the spring. The trapping web located on mixed, slightly disturbed habitat has the most diverse community and the most number of captures/recaptures. In the future, the animal, climate, and vegetation data will be used to build mathematical models that can be used to determine which factors have the largest impact on population and community persistence. Additionally, changes in the genomic make-up of the populations over time will be assessed.

Reagan Stephens<sup>1</sup>, Jacob Knox<sup>1</sup>, Lindsey Long<sup>1</sup>, and Laura Reed<sup>2</sup> (<sup>1</sup>Oklahoma Christian University, <sup>2</sup>Genomics Education Partnership (GEP) University of Alabama)

**\*COMPARING DIVERGENCE AND CONSERVATION IN THE SLMB GENE BASED ON GENOMIC NEIGHBORHOODS**

The insulin and target of rapamycin (TOR) pathway serves to regulate glucose metabolism and contributes to an organism's survival. This project represents the examination of conservation of genes along the insulin/TOR pathway among *Drosophila* species through the Genomics Education Partnership (GEP). Examination and annotation of the slmb gene in the pathway was carried out for six *Drosophila* species that were compared against *Drosophila melanogaster*. The conservation of the gene was assessed through the genomic neighborhood and the score from a divergence scoring system. The species *D. virilis* and *D. willistoni* were the only species with genomic neighborhoods that differed from *D. melanogaster*, with two of the four surrounding genes being different. The slmb gene was determined to be very well-conserved due to consistent similarity of genomic neighborhood and divergent scoring.

Ethan Strickler, Andrew Seeberger, and Bryhan Douglas (East Central University)

**\*AN ANALYSIS OF 400-450NM COMPONENTS OF SEMICONDUCTOR AND UV ILLUMINATION**

Traditional lighting was based on either incandescent filaments with their poor efficiency or mercury vapor fluorescents with a somewhat elevated UV component and unnaturally blue spectral output. More recent lighting innovations have included both compact fluorescent ("CF") lamps which can have a lower color temperature than earlier industrial fluorescent lamps and semiconductor ("LED") lighting in a variety of color temperatures. However, there have been claims that 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 varying 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.

Benjamin O. Tayo<sup>1</sup> and Sanjiv K. Jha<sup>2</sup> (<sup>1</sup>University of Central Oklahoma, <sup>2</sup>East Central University)

**SINGLE-MOLECULE ANALYSIS OF DNA NUCLEOBASES USING VAN DER WAALS HETEROSTRUCTURES: A COMPUTATIONAL STUDY**

Electronic DNA sequencing using two-dimensional (2D) materials such as graphene has recently emerged as the fourth-generation of DNA sequencing technology. Owing to its commercial availability and remarkable physical and conductive properties, graphene remains the most widely investigated material for DNA sequencing by both theoretical and experimental groups. One of the major issues with graphene is its lack of a band gap. Furthermore, the hydrophobic nature of its surface causes

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DNA bases to stick to its surface, slowing down translocation speed and increasing sequencing error rates. As part of the materials research project, our goal is to extend these studies to several 2D materials beyond graphene, including van der Waals heterostructures. In this talk, we discuss recent accomplishments and future perspectives.

Genesis Terrazas Valero and Avishek Mitra (Oklahoma State University)

#### \*PURIFICATION AND CHARACTERIZATION OF TWO HEME INDUCED GENES IN *MYCOBACTERIUM TUBERCULOSIS*

*Mycobacterium tuberculosis* (Mtb), the causative agent of human tuberculosis (TB), is transmitted through aerosols and successfully replicates within alveolar macrophages by inhibiting macrophage maturation. Before the SARS-CoV-2 pandemic, Mtb had surpassed HIV/AIDS to become the leading cause of death worldwide from a single infectious agent. In 2019, 11 million people were infected with Mtb resulting in 1.3 million deaths<sup>1</sup>. The WHO estimates that globally 3.3% of new cases and 18% of previously treated cases were multidrug resistant TB (MDR-TB) in 2019<sup>1</sup>. Thus, there is an imminent need to develop chemotherapeutic strategies to prevent TB disease progression. Mtb is completely dependent on iron acquisition to successfully colonize the human host. Greater than 75% of host iron is stored in the form of heme, which makes it the major source of iron for Mtb in the human host. An overarching goal of our lab is to identify novel components of Mtb that are required for Hm iron acquisition so that we can develop novel strategies to block heme iron acquisition and starve this pathogen of an essential nutrient. Previous transcriptomic studies had identified that expression of ppe64 and rv0125 are significantly increased by Mtb in response to heme iron in growth medium. The first specific goal of this project was to clone these genes and attempt to purify encoded recombinant proteins from *E. coli*. The second goal was to characterize these proteins through various biochemical experiments.

Darcy Tessman and Robin Roberson (East Central University)

#### FIRST-GENERATION STUDENT NEEDS IN STEM "WEED-OUT" COURSES

In Oklahoma, more than 50% of students taking the ACT are classified as first-generation college students [FGCS] (ACT, 2019) and these students demonstrate college STEM readiness benchmark scores of 9.6% compared to 31.3% of students whose parents hold degrees. Many FGCS enter college with lower GPAs and ACT/SAT scores, which translates to only about 50% obtaining a college degree compared to 64% of non-FGCS low-income students (Plaskett et al., 2018). Of ECU's entering 2018 fall freshmen class, 73% scored a composite of 20 or below on their ACT test, 36% scored 17 or below on English, and 38% scored 17 or below on Math. This lack of preparation also is demonstrated in ECU's 2012-2018, six-year graduation rate of 39% (ECU OIE 2018-19). Many FGCS lack academic efficacy, or confidence in their ability to successfully complete college, due to their lack of academic preparation in high school. While 31.9% of ECU undergraduates (4-year mean, Fall 2017-Fall 2020) majored in STEM related fields, only 7.5% of FGCS did so, indicating that ECU's FGCS likely do not see STEM-related careers as attainable goals due to their lack academic efficacy in STEM. FGCS also face many other social barriers prior to and upon college entry that detract further from their academic efficacy. FGCS often feel alienated in their struggle to find venues for academic and social involvement as they navigate campus and are reluctant to ask for help (Solanki et al., 2019). Since FGCS are less likely to interact with faculty or contribute in class discussions (Soria & Stebleton, 2012), they lack the social integration and faculty interaction, which are strong predictors of STEM degree attainment.

Kaylee Thoma (East Central University)

#### \*THE NEAR SIGNIFICANCE OF THE RELATIONSHIP AMONG CHILDHOOD TRAUMA, ATTACHMENT STYLE, AND RELATIONSHIP SATISFACTION

This study was conducted to find any relationships among Adverse Childhood Experiences (ACEs), attachment style, and relationship satisfaction. It was anticipated that attachment style would act as a mediator between ACE score and relationship satisfaction, and that people who are more securely attached would have higher relationship satisfaction and lower ACE scores than those who are not securely attached. Participants were 130 and individuals within the Amazon MTurk panel who indicated being in a relationship for 3 months or longer within the past month. Three valid and reliable scales were used to measure Relationship Satisfaction (CSI), Adult Attachment Style (RSQ), and Childhood Trauma (ACE questionnaire). The sample of 130 individuals reached near significance, leading to further research of people with 3 or more ACEs, those results will not be discussed in this presentation.

Simon A.M. Underhill (Oklahoma State University)

#### BIOFILM SIGNALING BY GLYCEROL IN *PSEUDOMONAS AERUGINOSA*

Biofilm formation in *Pseudomonas aeruginosa* is dependent on diverse signal inputs. The carbon source an organism utilizes is a critical factor in many of its behaviors, including the expression of polysaccharides and proteins involved in generating a biofilm. The effect of carbohydrate source on the biofilm development process has not been extensively studied in *P. aeruginosa*. Glucose has been found to stimulate the process in strain PAO1 through flagellar formation; succinate and glutamate encourage dispersion of established biofilms. However, our results in strain PA14 indicate that this strain forms thick biofilms only when grown on glycerol, making this carbon source unique. We show that glycerol acts by raising production of c-di-GMP, the second messenger molecule which positively signals for biofilm behaviors. We then query the importance of the Nitro-PTS in this process, a phosphotransfer system (also called PtsNtr) consisting of PtsO, PtsP, and the terminal acceptor PtsN. This was implicated in biofilm formation on glycerol-supplemented medium, with ptsP and ptsO mutants producing about 2-fold less Pel exopolysaccharide than wild-type PA14 colonies. Subsequent deletion of ptsN rescues Pel output to wild type levels, suggesting that unphosphorylated PtsN represses biofilm formation. We show that while phosphorylation of PtsN is slightly sensitive to carbohydrate source, that sensitivity does not within current models explain why glycerol leads to higher Pel output. Finally, we demonstrate that PtsO enhances the efficiency of but is not required for PtsN phosphorylation, while PtsP is essential for this

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process. The GAF domain in PtsP also enhances PtsP-PtsO-PtsN phosphotransfer but does not affect the bypass of PtsO, indicating that there may be another phosphate carrier that is phosphorylated by PtsP independent of this domain. Our findings begin to unravel the mechanisms of the Nitro-PTS while showing that it is not responsible for the special influence of glycerol on biofilm behavior.

Forrest Valkai (University of Tulsa)

#### **\*\*THE POTENTIAL FOR USING CERVIDS AS PROXIES FOR PALEOECOLOGICAL RECONSTRUCTION THROUGH STABLE ISOTOPE ANALYSIS: IMPLICATIONS FOR OUT OF AFRICA I**

Approximately 1.8 million years ago, *Homo erectus* moved through the Levantine corridor to spread throughout Europe and Asia. 'Ubeidiya, a 1.5-million-year-old archaeological site in Israel, provides some of the earliest evidence of this dispersal. The details of the environment of the region at the time would provide a great deal of insight into the lives of our ancestors but is largely unknown. The analysis of the differential fractionation of stable isotopes is a powerful tool for paleoecological and paleoclimate reconstruction. The usefulness of cervids as proxies for this kind of reconstruction, however, is debated due to their foraging habits as variable browsers and grazers. In this study, I first develop a modern model to test if stable isotopes can distinguish between deer populations. I sample the tooth enamel from the M3 of different modern cervid populations to test for the  $\delta^{13}\text{C}$  and  $\delta^{18}\text{O}$  content of the tooth enamel. These data, when combined with data from GIS, will allow me to build an isotopic map of different cervid environments which can then be compared to samples taken from fossil cervids excavated from 'Ubeidiya. This preliminary study will provide support for using cervids as a robust paleoecological proxy and could be a large step along the way to reconstructing the environment in which our ancestors lived and gaining a better understanding of *Homo erectus*'s movement out of Africa.

Shelbie Weaver, Jessica Neuzil, and David Bass (University of Central Oklahoma)

#### **\*\*INVESTIGATION OF THE ECOLOGY OF HARRIS MUD CRAB IN LAKE TEXOMA**

Harris mud crab (*Rhithropanopeus harrisi*) was first reported in Lake Texoma in 2008 and its distribution was documented. Since that time, very little research regarding this population has been conducted. Purposes of this investigation are 1) document current distribution, 2) estimate population size, 3) record sex and individual measurements, 4) determine reproductive periods, and 5) note microhabitat preferences and any other pertinent ecological information. Six sampling stations were established on the Oklahoma side of Lake Texoma in a transect from the OU Biological Station to near the Denison Dam. Sites were sampled from August 2019 to August 2021. Average density of crabs at each site ranged from 0.0 crabs/m<sup>2</sup> to 159 crabs/m<sup>2</sup>. More crabs were found during the warmer months than the cooler months. Larvae were present in plankton samples from June to October, indicating reproduction occurs during the warmer months. Of the crabs returned to the laboratory, 464 were females, 596 were males, and 264 were too immature to determine sex. Measurements include carapace width (0.90-17.85 mm), carapace length (0.60-12.60 mm), chela width (0.25-10.2 mm), chela length (0.2-13.6 mm), and dominant claw were recorded. Results from an independent study indicated 94% selected rock as a microhabitat over plants and sediments, confirming what was observed in the field.

Andrew Wells (East Central University)

#### **CLASSIFYING NBA PLAYER POSITION FROM BOXSCORE STATISTICS**

The five different positions in basketball have somewhat different responsibilities. Many attempts to measure player value rely in part on comparing to other players with the same position. Those positions are not clearly based on anything except what the team or player decide. An automatic method of position assignment could remove that uncertainty from player performance models. Some work using regressions has been done in a variety of settings, but here we look at a k-nearest neighbors approach.

Sarah Woller, B. Okda, M. Anderson, and S. Das-Bradoo (Northeastern State University and Oklahoma State University Center for Health Sciences)

#### **\*\*CO-LOCALIZATION STUDIES REVEAL DISTINCT PATTERNS OF POLE: MCM10 ASSOCIATION DURING CELL CYCLE IN HUMAN CELLS**

In eukaryotic DNA replication, Polymerase epsilon (POLE) is responsible for synthesizing the leading strand of DNA. POLE is known to have roles in the activation of the DNA damage response pathway and is believed to have roles in cell cycle control. Unfortunately, the distinct roles of POLE are not well understood and heavily debated. However, mutations in POLE have been known for tumor predispositions in several types of cancer. Our laboratory has shown that Minichromosome maintenance protein 10 (MCM10) plays a vital role in the functionality of POLE through studies in budding yeast. MCM10 is essential for DNA replication and, its interactions are highly regulated by the cell cycle. Genetic amplification and/or over expression of MCM10 has been observed in colon, breast and prostate cancer. Therefore it is imperative to determine if the POLE: MCM10 interaction is conserved in human cells and if the interaction is regulated by the cell cycle. To achieve our goal we cloned POLE and MCM10 into RFP and GFP vectors, respectively. The vectors were transfected into HEK293T cells and visualized by fluorescence microscopy as well as confocal microscopy. Interestingly we observed interactions between POLE and MCM10 in human cells using co-localization fluorescence studies. To understand the dynamics of POLE and MCM10 throughout the cell cycle, cells were synchronized in G0 phase by serum starvation and interaction was studied by fluorescence and confocal microscopy. We were able to identify localization patterns of MCM10 and POLE in the nucleus throughout the S phase. Interestingly, MCM10 and POLE interaction is only seen in the mid to late S phase even though both proteins are present throughout the S phase. Our data suggest that both POLE: MCM10 interact in human cells to carry out specific functions during DNA replication.



Taje' Woods, Emma Davison, and Lindsey J. Long (Oklahoma Christian University)

#### \*3H04 KINETIC ANALYSIS

Proteins are in all living organisms. The protein that is being discussed in this study is 3H04. The protein sample had to be transformed and purified through the formation of *Escherichia coli* (*E. coli*) strain BL21(DE3) cells so that we can have a pure substance of 3H04, with no imperfections. Protein samples can also be described as enzymes. Enzymes are proteins and have four different levels of functional structures that determine the enzyme's purpose. All enzymes are made up of at least three structural levels. Those three levels are primary, secondary, and tertiary structures. For a protein to function correctly, it needs to have a three-dimensional shape. A protein structure determines the type of function it will have, and the type of ligands that will bind and react with the protein. Bioinformatic analysis and modeling can provide evidence to support or disagree with the classification of an enzyme of a certain enzyme class (EC), and provide information regarding the location of an enzyme's active sites and what type of amino acid residues are likely to bind to those sites. This information is vital data that can also determine the function of an enzyme. By using bioinformatics analysis, it can also determine how likely an enzyme will catalyze and bind with a ligand. After an analysis, it concluded that the 3H04 enzyme is a part of EC 3 which means that the enzyme is a hydrolase, and its function is to catalyze chemical bonds by using water to break them down off a particular substrate. This study supported the claim that not only is the 3H04 enzyme a hydrolase, but also gave examples of what a common hydrolase consists of. More analysis was performed by Pfam and BLAST also supporting that 3H04 was part of the alpha/beta hydrolase (abhydrolase) 3 superfamily.

Joseph Zajac (Oklahoma Christian University)

#### \*EVALUATION OF SLMB AND ROC1A CONSERVATION WITHIN THE E3 UBIQUITINATION LIGASE OF THE INSULIN/TOR PATHWAY

In this presentation, the evolutionary conservation of the insulin/TOR pathway within *Drosophila* was examined. The focus was on slmb and Roc1a for our species. The hypothesis was that these genes would show similar conservation due to them both being key components of the E3 ubiquitination ligase of the insulin/TOR pathway. To test this, resources such as Gene Record Finder, Flybase, NCBI BLAST, and GEP Genome Browser were used to be able to make reliable gene models that could be analyzed. Verified gene models were then scaled on a divergence scoring system to grade their degree of evolutionary conservation when compared to *D. melanogaster*. The results showed that slmb had a higher level of conservation than Roc1a due to its involvement within the insulin/TOR pathway. This followed the hypothesis that they would have similar conservation and demonstrated that there are many contributing factors within gene conservation. The one that this research showed was that the number of involvements/connections a gene has is directly related to its degree of conservation. In the end, genes and gene conservation is a highly complex process that reflects the intricacies of the evolutionary process. Going forward, more focus could be on examining genes that are on the edge of divergence and examine what sort of connections need to be made for it to fully diverge or remain conserved. Along with this, looking at what sort of roles slmb and Roc1a play within the insulin/TOR pathway and what their deletions might do could help shine light as to how crucial their divergence is. And lastly, studies could be looking at how mutations within the insulin pathway might influence the conservation of Roc1a and slmb.

Check out the Callixylon tree when walking between PES and CBCC Foundation Hall. The Callixylon tree is a 250,000,000 year old petrified tree stump discovered by John Fitts in a field in 1913. This stump is reputed to be the largest stump of Callixylon in the world. See the Campus Map on the back of this program for location details.





## OKLAHOMA ACADEMY OF SCIENCE

Established in 1909

**“The purpose of the Academy shall be to stimulate scientific research; to promote fraternal relationship among those engaged in scientific work in Oklahoma; to diffuse among the citizens of the State a knowledge of the various disciplines of science; and to investigate and publicize the human, natural and educational resources of the State.”**

**(Article 1, Section 2 OAS Constitution)**

### Activities of the Academy

- **Publishes the Proceedings of the Oklahoma Academy of Science, Annals of the Oklahoma Academy of Science and Transactions of the Oklahoma Junior Academy of Science.**
- **Hosts the Annual Technical Meeting for the presentation of scientific papers by both professional and collegiate scientists.**
- **Sponsors symposia on selected topics of timely and vital interest to the State and Nation.**
- **Arranges fall field meetings in different biogeographic regions of the State.**
- **Coordinates and promotes the activities of the Oklahoma Junior Academy of Science.**
- **Supervises the activities of the Oklahoma Collegiate Academy of Science.**
- **Provides research grants and scholarship awards to outstanding proposals submitted by secondary school and undergraduate college students.**
- **Provides scientific consultation services to governmental and private agencies throughout the State.**

### Land Acknowledgement Statement

As we come together upon this land to learn, we first want to acknowledge the original inhabitants of these lands and this region. We honor and extend our respect to the Kitikiti'sh (Wichita), Hasinai (Caddo), Na i sha and Ndee (Apache), Numunuu (Comanche) and Cáuigù (Kiowa) peoples and their eventual successors, the Chikashsha (Chickasaw Nation), who have since made various contributions to the success and development of East Central University (ECU) and the larger community. ECU exists because of the foresight of community leaders and the generosity of Chickasaw citizen Daniel Hays. East Central University would like to acknowledge the history of the land and the people that inhabited this place before us.

To express our appreciation and gratitude to the peoples that inhabited and cared for these lands before us and to honor their memory, East Central University acknowledges and respects the diverse historical contributions made by various Indigenous groups to these lands. ECU is fully committed to recognizing and supporting the sovereignty of the 39 tribal nations residing in the state of Oklahoma. This land acknowledgement statement is an extension of ECU's mission statement and core values to foster a learning environment that prepares students for life in a rapidly changing and culturally diverse world. As an institution founded upon the generosity of Chickasaw citizen Daniel Hays, ECU honors and respects the diverse groups of people and their cultures that form our Tiger community.

## OKLAHOMA ACADEMY OF SCIENCE PRESIDENTS

1910	H. L. Lane, OU	1969	L. V. Scott, OUHSC
1911	D. W. Othern, Okla. City	1970	C. C. Carpenter, OU
1912	S. W. Reaves, OU	1971	P. Buck, TU
1913	C. W. Shannon, OU	1972	W. A. Carter, ECSU
1914	No meeting	1973	C. J. Mankin, OU
1915	C. W. Shannon, OU	1974	N. N. Durham, OSU
1916	C. N. Gould, OU	1975	B. Shirley, TU
1917	L. C. Raiford, ISU	1976	G. W. Todd, OSU
1918	No meeting	1977	D. E. Kizer, Noble Fdn
1919	No meeting	1978	G. Odell, OSU
1920	M. M. Wickham, Norman	1979	R. Couch, ORU
1921	A. F. Reiter, PU	1980	G. Wolgamott, SWOSU
1922	J. B. Thoburn, Okla. City	1981	E. Rice, OU
1923	R. O. Whitenton, OAMC	1982	E. Grigsby, NSU
1924	S. Weidman, OU	1983	J. Sokatch, OUHSC
1925	(spring) C. E. Sanborn	1984	M. Whitmore, OU
1925	(fall) H. L. Dodge, OU	1985	J. Black, OBU
1926	J. H. Could, OAMC	1986	J. Wilhm, OSU
1927	C. N. Gould, OU	1987	M. K. Patterson, Noble Fdn
1928	O. M. Smith, OAMC	1988	M. P. Carpenter, OU
1929	A. Richards, OU	1989	K. E. Conway, OSU
1930	L. Long, Okla. City	1991	J. K. McPherson, OSU
1931	A. O. Weese, OU	1993	J. R. Estes, OU
1932	H. Patterson, OAMC	1994	J. D. Tyler, CU
1933	J. E. Knowles, PU	1996	C. Taylor, SEOSU
1934	F. G. Brooks, OCU	1998	R. J. Tyrl, OSU
1935	C. E. Decker, OU	2000	D. Bass, UCO
1936	H. J. Harper, OAMC	2002	C. Clifford, NSU
1937	B. D. Barclay, TU	2004	S. Young, SNU
1938	C. M. Perry, OU	2006	S. Barber, OCU
1939	H. D. Chase, TU	2008	U. Melcher, OSU
1940	G. L. Cross, OU	2010	K. R. Hobson, OU
1941	R. W. Jones, OAMC	2012	C. Clifford, NSU
1942	H. I. Featherly, OAMC	2014	S. Rice, SEOSU
1943	O. F. Evans, OU	2016	T. Conley, CU
1944	V. G. Heller, OAMC	2018	A.K. Ryburn, OCU
1945	J. R. Nielsen, OU	2020	R. Mather, UCO
1946	O. C. Dermer, OAMC		
1947	J. T. Self, OU		
1948	L. S. McLeod, TU		
1949	J. C. Shirley, PU		
1950	H. Taylor, OCW		
1951	H. W. Larsh, OU		
1952	V. B. Monnett, OAMC		
1953	S. P. Massie, LU		
1954	A. N. Murray, TU		
1955	R. E. Olson, OU		
1956	A. M. Stebler, OAMC		
1957	D. E. Howell, OAMC		
1958	G. J. Goodman, OU		
1959	E. Lucas, OU		
1960	P. E. Smith, OUMS		
1961	E. M. Hodnett, OSU		
1962	H. G. Barclay, TU		
1963	G. A. Moore, OSU		
1964	A. D. Buck, NOJC		
1965	J. E. Webster, OSU		
1966	C. R. Williams, PU		
1967	C. D. Riggs, OU		
1968	E. A. Reynolds, SWSC		

