Undergraduate Research and Creativity, 2024 Fall Symposium schedule

Oral presentations:

Carver Science Building, Room 215, Jordon lecture hall

1) 12:45-1:00 p.m.

Dayton Gatewood. COX23 plays an important role in the assembly of cytochrome c oxidase in human cells. **Texas A and M University**

Mitochondria are an essential cellular organelle that harbor the enzymes for cellular respiration and ATP generation. These vital processes are linked and are carried out by the inner mitochondrial membrane localized mitochondrial electron transport chain (ETC) complexes and ATP synthase. Cytochrome c oxidase (CcO) also known as Complex IV is the terminal enzyme of the ETC that catalyzes the reduction of molecular oxygen to water by using the electrons generated by oxidation of food. In humans, CcO is composed of 14 subunits which are encoded by both mitochondrial and nuclear genomes. In addition to these subunits, CcO contains copper and heme, which are important for its redox activity and stability. The assembly of CcO is a complex process that requires approximately 30 assembly factors. COX23 is one such evolutionary conserved assembly factor that has been implicated in CcO assembly process in yeast, though its precise role in CcO biogenesis is not known. To determine the role of mammalian COX23, we used CRISPR-Cas9 to construct COX23 knockout in human embryonic kidney (HEK293T) cells. The biochemical characterization of COX23 knockout cell lines showed that in the absence of COX23 there is a decreased abundance of CcO subunit COX1, along with the reduced abundance of subunits of other ETC complexes. We used native-polyacrylamide gel electrophoresis analysis to determine the abundance of fully assembled ETC complexes and found their levels to be reduced. Together, our results suggest that COX23 is involved in ETC assembly process, and deciphering its precise molecular function needs further investigation.

2) 1:00-1:15 p.m.

Sam Derning. Quantification and Disruption of m6A Modification at the A783 Site of the Oncogenic IncRNA HOTAIR. University of Colorado, Anschutz Medical Center

HOX transcript antisense intergenic RNA (HOTAIR) is an oncogenic lncRNA that is found to be abnormally over-expressed in breast cancer, promoting a more aggressive cancer phenotype due to its ability to repress tumor suppressor genes. HOTAIR has many N6-methyladenosine sites, with the A783 site being the most consistently methylated and vital for the increased cell proliferation and migration we see in cells overexpressing HOTAIR. Previous work has shown that a mutation to this site that prevents methylation results in antitumor gene expression that is opposite to the wild-type cells overexpressing HOTAIR, switching these cells from pro-tumor mechanisms to anti-tumor effects. This opens the door to possible therapeutic potential by blocking methylation at this site using antisense oligonucleotides (ASO) to induce this antimorphic effect. However, the ability to quantify methylation at single-base resolution is needed, along with m6A standards to verify quantified methylation levels. An m6A standard was generated using DNA-splinted ligation of RNA oligonucleotides that contained a known m6A site, and denaturing polyacrylamide gels were used to verify oligonucleotide size and assess the purity of ligation. Standards were subjected to chemical treatment of glyoxal and nitrile-mediated deamination of unmethylated adenosines (GLORI) and sent off for Sanger sequencing to

assess A-to-G base conversion at single-nucleotide resolution. RNA was harvested from MDAmB-231 cells overexpressing HOTAIR that had been transfected with an ASO targeting the A783 site, along with a non-transfected control. Extracted RNA underwent polyadenylation selection and fragmentation. Poly-A RNA was combined with m6A standards, underwent GLORI conversion, and samples were prepped for library construction. Sanger sequencing assessed the conversion of the m6A standards. Our m6A standards were successfully ligated at a high degree of purity, and Sanger sequencing verified the sequence of ligated products. Additionally, sequencing results validated that GLORI was effective at converting unmethylated adenosines to guanines while leaving methylated adenosines intact. Preliminary results from our GLORI experiments with ASOs and a mix of m6A standards will allow us to evaluate the effectiveness of an ASO at blocking A783 methylation. GLORI is a reliable and effective technique for quantifying methylation at single-base resolution. In the future, Illumina sequencing will be used to provide improved sequencing results and to better quantify converted transcripts through a bioinformatic pipeline using a library of the poly-A transcriptome. This pipeline will establish baseline m6A levels of HOTAIR and allow us to measure the efficacy of ASOs at blocking A783 Methylation.

- 3) 1:15-1:30 p.m. Jordan Bly, Eli Feekin, and Molly Lutmer. Simpson College, Econ 385 Econometrics.
- 1:30-1:45 p.m.
 Nick Warrington, Broderick Wirtz, and Zack Dueker. Simpson College, Econ 385, Econometrics.
- 1:45-2:00 p.m.
 Noah Harkness, Claire Schmitz, and Hank Gardner. Simpson College, Econ 385
 Econometrics.

Poster presentations:

12:45-2:00 p.m., Carver Science Building atrium

1) Matthew Dietrich, Caelynn Obleton, Lanie Shettlesworth, and Rachel Garcia. Is the Down syndrome birth rate in Mexico randomly distributed, and what factors influence it? Simpson College, Bryan summer research program

This project focuses on better understanding the prevalence and distribution of the Down syndrome birth rate in México. We used spatial statistics and linear regression to understand better whether Down syndrome births are geographically concentrated and what spatial processes are at play. Once we better understand where the concentration is, we can look at factors that may be influencing the spatial outputs and where the resources need to be allocated. This work is completed through the Dr. Albert H. & Greta A. Bryan Summer Research Program in Mathematics at Simpson College.

2) Kate Huisinga and Ellee Mortensen. Evaluation of Data Augmentation for Tabular Data. Simpson College, Bryan summer research program

This project aimed to determine whether current data augmentation methods effectively enhance tabular data while preserving the original patterns of the data. Data augmentation is "the process of artificially generating new data from existing data, primarily to train new machine learning (ML) models." Our project focused on the use of tabular data, which refers to data organized into rows and columns. Researchers and data scientists often use data augmentation because collecting new data is costly, timeconsuming, or simply not an option. Prior research in this field has mainly focused on the creation of methods for data augmentation, whereas we establish a framework that measures if patterns are kept throughout the data augmentation process. By maintaining data patterns, one ensures that the patterns in the augmented data are not false or misrepresented. We measured three types of relationships: feature-tolabel dependency, feature-to-feature dependency, and feature distributions. To do so, we utilized Chi-Squared tests, correlation matrices, subcategorical proportions, and the Mann-Whitney U test. For all of these tests, we used the Support Vector Machines (SVM) classifier. Our augmentation methods included modified +/- one (modPMOne), random swap (randSwap), and the histogram augmentation technique (HAT). We found that these three augmentation methods were able to sufficiently maintain patterns throughout the augmentation process, though the results varied with each test we conducted. Generally, HAT performed the best.

3) Maddy Streicher. An evolutionary investigation of human PYHIN family proteins: implications for mammalian viral immunity and placentation. University of Nebraska-Lincoln Nebraska Center for Virology

Bats are placental mammals that can asymptomatically coexist with numerous viral species, including some viruses that are lethal to other mammals. The purpose of this study was to investigate how bats have immunologically diverged from other mammals throughout evolution. PYHIN family proteins are unique intracellular DNA sensors that play a role in mammalian viral immunity. This study details a complete evolutionary history of all PYHIN proteins and establishes a complete PYHIN deletion in bat genomes. We found that PYHIN proteins are only present in placental mammals. All clades of placental mammals encode for at least one member of the PYHIN family, except bats. We conclude that the evolutionary deletion of PYHIN family proteins from the bat genome may contribute to their ability to be viral reservoirs.

4) **Jake Gioffredi.** Mapping a direct DRN-PBel connection: a central piece in the hypercapnic arousal circuit with implications in SUDEP. **University of Iowa**

Sudden unexpected death in epilepsy (SUDEP) is the leading cause of death in refractory epilepsy. SUDEP usually occurs at night and in the prone position and studies indicate that is due to faulty arousal and ventilatory responses to hypercapnia after a seizure that leads into respiratory then cardiac failure. Serotonergic neurons of the dorsal raphe nucleus (DRN) are intrinsically chemosensitive to CO2, and have been implicated in epilepsy and arousal, but the exact arousal circuit that it participates in has not been identified. A potential downstream target, the external lateral parabrachial nucleus (PBel) is investigated in the present study. The PBel is a sensory relay station and innervates several arousal structures in the forebrain. The present study injected 9 Pet1-Cre mice with AAV5-mCherry into the DRN and conducted immunohistochemistry on brain slices to determine the effectiveness of methods used and to tag the nuclei for further in-depth analyses. Stained slices revealed mixed success in both injection and immunohistochemistry methods. Roughly half of injections, as well as staining for TPH2 and CGRP were successful, but less success was found in staining for VGLUT2 and VGAT. Interestingly, coexpression of mCherry with TPH2, VGAT, or VGLUT2 were found in areas lateral and dorsal to the DRN. The successful results allow for a preliminary examination of the DRN and PBel populations, and the unsuccessful results point to a consideration of methods - both of which are useful for future studies.

Future studies in the topic will attempt to provide direct evidence for a link between the DRN and the PBel mediated by serotonergic transmission.

5) Paul Llamas. The effect of doxycycline on the intestine's morphology and behavior of stressed mice. Stowers Institute for Medical Research, Kanasas City

Doxycycline is a broad-spectrum antibiotic that inhibits bacterial protein synthesis. It is known that microbes engage in symbiotic activity with their host organism. In the Yu Lab, we have seen that chronic exposure to doxycycline alters gut morphology. However, little is known about how fast these changes occur. In this project, mice were given food with doxycycline for several weeks. The gut and behavioral test samples were done every week for the mice selected for that week. The behavioral results of the project were that mice that ingested doxycycline seemed to have lower levels of anxiety and depression; the morphological results of the project were that the doxycycline feed mice appeared to have a heavier cecum, an increase in colon crypt density, a decrease in goblet cell diameter, and no difference in oxidative damage and proliferation.

6) Kayla Jensen and Illiana Murphy. I-RAISE. Simpson College/Iowa State University

In a broad stroke, the I-RAISE internship program aims to create a new pipeline of young workers in the field of grant-writing and research administration. Research Administration (RA) is the process of managing and supporting academic/scientific projects, focusing on funding acquisition, proposal development, compliance, budgeting, and project oversight to ensure successful outcomes. Interns will **not** conduct research themselves during this internship. Interns spent 10 weeks at ISU, 2 in bootcamp and 8 with mentors, followed by an academic year at their home institution.

7) **Breana Hinson.** Using T7 Endonuclease I to identify mutations in the maize CenH3 gene. Corteva Agriscience

The mutation in the CenH3 gene in maize would allow for the production of haploids which helps create new plant varieties. The goal of this study is to use T7 endonuclease I (T7EI) to develop a protocol for and to locate a mutation in the CenH3 gene of maize. To develop the protocol we compared the A63 and EDH5G lines of maize, they have a two base pair difference in the CenH3 gene. We determined the ideal concentration of T7EI and plant DNA adequate for pooling and locating a mutation. Using radiation treated seed from the desired maize line, we harvested DNA and used the developed protocol to locate a mutation. Due to time constraints the mutation in the desired maize line was not located, but with the protocol developed future studies can work to locate the mutation more effectively.

8) Maddie Allen. Assessing the turtle population at Nahant marsh. Eastern Iowa Community College

This study is an overview of the turtle population at Nahant Marsh Education Center, a nonprofit dedicated to protecting and restoring local marshes through education, research, and conservation. The survey contributes valuable data on turtle species diversity, aiding ongoing conservation efforts.

9) Madison Harvey. Tactile Art Barricade. Simpson College

My project presents an innovative U-shaped barrier designed to enhance the viewing experience of art installations while promoting tactile engagement for children. This barrier stands 38 inches tall and spans 5 feet wide. The barrier serves as a noticeable and inviting boundary that helps guide young visitors away

from the artworks while encouraging exploration. Constructed with various tactile elements, including pom poms, sticky dots, and beads, the barrier provides an interactive surface that invites touch, fostering sensory engagement and curiosity. This approach not only protects the integrity of the artworks as a barrier for the artworks but also supports the developmental needs of children by allowing them to interact with the barrier itself. This barrier was presented in the Simpson Gallery of Art and Designs next to artwork created by Professor Rachel Terlop, the barrier also has gained the interest of Art Farm Iowa located in Northwood, IA. The barrier aims to create a more accessible and enriching environment in galleries and museums, balancing the need for preservation with the importance of hands-on learning experiences.