2024 FULL STEAM AHEAD EDUCATOR SYMPOSIUM

Poster Session
8:00am – 3:30pm

Atrium, Anderson Choral Building

"Empowering Education: AI at the Heart of Learning"
Jacob Hesselschwardt
Bossier Parish Schools & Louisiana State University in Shreveport (LSUS)

Explore the dynamic intersection of Artificial Intelligence and Education. This visually compelling exhibit demonstrates the transformative role of AI in shaping the future of education.

"Moon Trees: A Multi-"Branched" Collaborative Project"
Katie Chirhart and her students
Shreve Island Elementary School

NASA's most current Moon Tree Project allowed educational institutions to apply to receive and plant a Moon Tree on their campus. A Moon Tree is a seedling that has grown from a seed that has orbited the moon! To complete the application (we still don't know if we will receive one) and to spark interest in the students, I planned a series of collaborative lessons revolving around these special trees. All students in grades second through fifth took part in researching the necessary requirements of these trees.

"The Effects of Sulfide-Releasing Pharmaceutical Drugs on Xanthine Oxidase Dependent Nitrite Reduction to Nitric Oxide"
Caymen Hawkins, Class of 2024 - Biology & Neuroscience Double-Major (Pre-Med)
Centenary College of Louisiana

Xanthine oxidase (XO) is an enzyme that helps to mediate the process of reduction of nitrite (NO_2^-) to nitric oxide (NO) in hypoxic conditions. NO, in turn, is used in vasodilation and vascular remodeling in endothelial cells, leading to effects on blood flow in the cardiovascular system. Sulfide and other sulfide-releasing products in the past have been shown to induce the XO-mediated of NO_2^- reduction to NO in hypoxia. Being that patients of cardiovascular diseases are often in a state of ischemia (and therefore hypoxia) and lack sufficient levels of NO_2^-, NO, and sulfide, a potential treatment that would increase sulfide levels would lead to NO being produced – and as a result, blood flow improving.

This project looked to see if sulfide pro-drugs – including, both, FDA-approved and experimental – would release sulfide and mediate XO-induced NO_2^- reduction to NO. This was done using 4 models: cell-free chemiluminescent models NO release, with experiments preformed in the sparger detection system; cell culture chemiluminescent models testing NO release using mouse endothelial cells, including trials with inhibitors of the different components of NO_2^- reduction to NO; mice models testing the drug's sulfide release; and immunofluorescence models, in which

MAECs cultures were stained for detection of sulfide levels. The samples used to test these models were sodium sulfide and diallyl sulfide (DATS) as controls, and an FDA approved drug and two experimental compounds – one being sulfide releasing and the other, not. From the results of these experiments, it was seen that there wasn't any data to support the release of NO by the drugs according to the chemiluminescent models; however, the FDA-approved drug saw sulfide release in both cell culture and mice models.

"Functional Characterization of Novel lncRNA in *Arabidopsis thaliana*"

Tarif Islam, Rebecca Murphy, Daryl Morishige, Andrew Nelson
Centenary College of Louisiana

Long non-coding RNA (lncRNA) are composed of 200 or more nucleotides, and unlike mRNA, they do not translate proteins. Instead, they have other ways to regulate gene expression including being a transcriptional enhancer or repressor, forming a scaffold, and splicing. This project served to explore the role that lncRNA may play in regulating protein coding genes by characterizing the phenotypes of *Arabidopsis thaliana* with mutations in a set of high confidence lncRNA identified as antisense or adjacent to the protein coding gene through previous transcriptome analyses.

"Genetic Alteration of Rab 7 in Radishes When Introduced to *Ustilago maydis*"

Sarah Murphy, Class of 2024 Biology and Neuroscience Double Major, Chemistry Minor and Shelby Roy, Class of 2024 Biology Major
Centenary College of Louisiana

Ustilago maydis is a member of the smut fungi family and belongs to the phylum Basidiomycota. It is referred to as "corn smut" because it most commonly infects corn, but it can also infect radishes, asparagus, and other crop plants. This is a plant pathogen that has a narrow host range, is biotrophic, and spreads through small spores that are airborne. Once infected, it takes approximately 10 days for galls or tumors to appear on the crop.

The first layer of protection in plants' immune system is known as PTI or PAMP-triggered immunity. PTI signaling components are targeted by various effector molecules which infiltrate the system, diminishing the plants defense system and increasing bacterial virulence. *Ustilago maydis* secretes effector molecules that are able to infiltrate the PAMP-triggered immunity system. Once it is infected, the fungi works to change the metabolic pathways of the plant to use it for its own benefit.

Our experiment will focus on *Ustilago maydis* infection in radishes. *Ustilago maydis* alters gene expression in corn, we will be testing to see if that is a universal truth by experimenting with radishes. We will be strengthening the immunity of the plant with mycorrhizae and a fungicide to see if we can protect the plant from infection and gene alterations. We will be looking at Rab GTPase, specifically Rab7, because it is a common target of bacterial effector molecules. We hypothesize that the infected radishes with no mycorrhizae or antifungal will produce an altered gene expression in comparison to our control when run through a PCR test. The radishes infected and treated with mycorrhizae and an antifungal will not produce an altered gene expression.

"The Role of STAT1 in HCMV Persistence"

Melissa Krzywanski, Class of 2024 Biology and Neuroscience Double Major
Centenary College of Louisiana

Human cytomegalovirus (HCMV) is a beta herpes virus which establishes persistent infections in humans. HCMV contributes to life-long diseases such as cancer and cardiovascular diseases and is a leading cause of morbidity in congenitally infected neonates, even though infection in the immuno-competent is usually asymptomatic. HCMV establishes a latent infection in CD34+ hematopoietic progenitor cells (HPCs) in the bone marrow as well as in peripheral blood monocytes. Following infection of monocytes, HCMV reprograms the infected cells to promote their differentiation into macrophages. Virus replication in these cell types relies on the differentiation of latently infected cells to express viral genes and cause disease in affected individuals. Even though the differentiation program is initiated early on following the infection of monocyte, it remained unclear why viral gene expression and virus replication occurs later on, for example, 2-3 weeks in in vitro cultured monocytes. Previous studies from our laboratory show that the signaling molecule and transcription factor, STAT1, was linked with monocyte-to-macrophage differentiation following a primary HCMV infection. We next investigated STAT1's involvement in HCMV's viral gene expression and replication during virus latency and reactivation from latency. Our data supports an antagonistic role of STAT1 activation to viral gene expression and implicates type I interferon signaling in the activation of STAT1 leading to HCMV latency. We anticipate that interferon-stimulated genes (ISGs) induced following STAT1 activation are responsible for suppressing viral gene expression leading to virus latency. We intend to identify these candidate ISGs in our future studies.