

## **2016 Summer Research Symposium**

Session I: Wednesday, September 28, 2016 – 12:40-2:00 p.m.

Session II: Wednesday, October 19, 2016 – 12:40-2:00 p.m.

Carver Atrium and Jordan Lecture Hall

Simpson students who conducted summer research will present their findings.

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Session I: Wednesday, September 28, 2016 – 12:40-2:00 p.m.

Oral Presentations

### **Carver 215 (Jordan Lecture Hall)**

12:40-12:45 Opening remarks

12:45-1:00 “Modeling the Spread of Palmer Amaranth Through the Corn Belt.”

Authors: Leslie Decker, Tre Loge, Maggie Long, Park Mikels, Molly Monk, Zoe Muehleip and Andrea van Wyk

Program: Palmer Amaranth Interdisciplinary Research Group, Simpson College

Abstract: Our research this summer focused on the spread of the weed Palmer amaranth across the Corn Belt. In order to demonstrate how much of a problem Palmer amaranth may be in the future, we used an agent-based simulation software called NetLogo. Starting in the counties confirmed to have Palmer amaranth, we showed how the weed spreads across the Corn Belt through machinery, wind, and places where cow manure is used, such as hog confinements. Each land unit has a field type that is used to accurately depict the spread of Palmer amaranth through wind. We will also discuss techniques on how we plan to verify our model.

1:00-1:15 “How Farmers and Other Stakeholders are Currently Coping with Herbicide Resistant Weeds.”

Authors: Leslie Decker, Tre Loge, Maggie Long, Park Mikels, Molly Monk, Zoe Muehleip, and Andrea van Wyk

Program: Palmer Amaranth Interdisciplinary Research Group, Simpson College

Abstract: This past summer our research group conducted interviews with 7 farmers and other stakeholders including a land investor, a crop insurance agent, and a crop scout. The interviews initially began to gain information and thoughts about Palmer amaranth, and they expanded to include discussions about general herbicide resistance and the culture of farming. This qualitative research allowed us to gain insight about how we can apply our quantitative research and make it useful to the stakeholders. We were funded by BASF and we are currently working on a report for them, and we will share parts of that report in this presentation.

1:15-1:30 “Optimization of Down Syndrome Specialty Care Clinic Locations using Operations Research.”

Authors: Emma Christensen, Nick Joslyn, and Maddy Kersten

Program: Bryan Summer Program in Mathematics, Simpson College

Abstract: As the field of healthcare continues to grow and evolve, specialized and coordinated care for extraordinary conditions becomes more and more necessary. Down syndrome, one of these extraordinary conditions, is a chromosomal disorder that is often accompanied by other severe medical conditions that affect an individual’s overall health. Currently, there are 71 Down syndrome specialty care clinics in 34 states in the U.S. that serve less than 10% of the eligible population. Using operations research, specifically p-median and maximal covering models, we found that the current placement of these 71 clinics adds to the problem of inaccessibility. Our research presents the optimal locations for Down syndrome specialty care clinics in the continental United States and offers potential future clinic locations given the current placement.

1:30-1:45 “Ions in the Cornell Photoinjector.”

Author: Kristina Smith

Program: Cornell Laboratory for Accelerator-Based Sciences and Education (CLASSE) Research Experience for Undergraduates (REU), Cornell University

Abstract: Excess gas in a particle accelerator beam pipe is easily ionized by collisions with an electron beam. These ions can become trapped inside the electron beam and will have an effect on the beam because the ions and electrons have opposite charge. My project uses computer simulations to determine how different distributions of ions will affect the electron beam in the Cornell Photoinjector (a type of particle accelerator).

### **Carver 231**

1:00-1:15 “Comparing Methods for Controlling Invasive Woody Vegetation”

Author: Rachel Riley

Program: Simpson College Ecological Research Program

Abstract: This project focused on finding the most effective method for controlling woody vegetation out at the Riley Research Site in Marion County, Iowa. I chose four methods of control and three of the most insidious species of woody shrubs on the site. Using various tools, herbicides, and techniques for application, I observed the reactions of each species and their surrounding environment. At the end of eight weeks I compared each method, including the amounts of time, labor, and money invested as well as the overall response of the plant. Based on this, I concluded that different methods are most effective for different species. This research will be useful in determining the future of the site and its eventual prairie restoration.

1:15-1:30 “Physical and Behavioral Effects of Nitrate on the Common Freshwater Fish Genus *Lepomis* spp”

Authors: Jessie Hoffman and Adam Stewart

Program: Simpson College Ecological Research Program

Abstract: Bluegill and redear are extremely popular game fish, and are a common food item for other animals and humans. Both are also very tolerant, sturdy fish, and bluegill are nitrite (NO<sub>2</sub>) resistant. We subjected replicate fish to one of three levels of nitrate (NO<sub>3</sub>) additions: low (10-20 mg/L), medium (20-30 mg/L), high (40-50 mg/L), and a control (0-10 mg/L). The medium range was chosen based upon the readings from the three northern Iowa counties in the Des Moines Water Works lawsuit, the high range upon future

predictions with similar agricultural practices, and the low range is in line with the maximum EPA drinking water standard. Measurements of their resting location, feeding location, movement, feeding latency, and body condition were taken throughout the experimental period to determine what effects nitrate had upon the replicate fish. Statistical significance was found in the behavioral effect on resting location of the fish. Specifically, the fish were not choosing their location at random, and the low and medium level replicate fish lingered primarily at the top of the water column, where there was no cover for protection. Statistical significance was also found in the physical effect of body condition, which decreased significantly as the levels of nitrate increased, and the high level of replicate fish showed exterior body disintegration.

1:30-1:45 “Trypanosomes in Iowa Voles”

Author: Suleiman Ameh

Program: Simpson College Ecological Research Program

Abstract: Trypanosomes are flagellated parasitic unicellular protozoa that infects a number of other animals including humans, cattle, and rodents. Trypanosomiasis is a fatal disease caused by trypanosomes. Chagas disease is caused by a species of trypanosome call *Trypanosoma cruzi*. The cost of treatment of Chagas disease is estimated to be about \$900 Million in the U.S. and \$7 Billion globally annually Lee et al (2013). Research about trypanosomes are therefore important because the more we know about trypanosomes, the more likely we will be able to find more affordable solutions to the problems they pose on humans the ecosystem. To know the species of trypanosomes(s) that infect Iowa voles and compare the prevalence rate of trypanosome infections between prairie and meadow voles, and across sexes and aged groups, we captured and took three blood drops each from 26 voles – 8 males and 18 females. All were meadow voles because were unable to get samples from prairie voles due to their low population density during the field phase of this research. 50% of our capture males and 39% of females tested positive for trypanosome. The species of the trypanosomes in the infected voles is/are yet to be determined because we are yet to sequence their DNAs. We hypothesized that there will be no difference in parasitization rate between the prairie & meadow voles if they occur in sympatry because they will be exposed to the same vectors (fleas and ticks)

and that trypanosomes will be prevalent in the polygamous male meadow voles compared to their monogamous female partners and the prairie voles. We also predicted that *T. lewisi* which is the species that commonly infect rodents will be the most prevalent species of trypanosome in the infected voles. Our result support one of our hypothesis that trypanosomes will be prevalent in the polygamous male meadow voles which have larger home ranges than in their monogamous female partners. But because we were unable to get samples from the prairie voles, we were unable to compare the prevalence of trypanosomes across the species.

1:45-2:00 “Single-cell mRNA Sequencing Identifies BASC-like Cells as Progenitors for K-ras Driven Lung Tumors”

Author: Alec McIntosh

Program: Summer Program for Undergraduate Research (SPUR), Medical College of Wisconsin in Milwaukee

Abstract: Lung cancer is the leading cause of cancer-related mortality in the world. Around 85% of these cases are non-small cell lung carcinomas (NSCLC); a majority of which are adenocarcinomas. NSCLCs provide challenges for clinical oncologist because adenocarcinomas in particular tend to form metastases at earlier stages than other malignancy subtypes. Despite decades of lung cancer research, patient outcomes have not significantly improved. A reason for this lack of progress may be due to the high heterogeneity of adenocarcinomas. This high heterogeneity has created a challenge for cancer researchers because the use of bulk mRNA sequencing (RNASeq) methods to determine treatment efficacy and condition initiation is limited. In fact, there is much debate amongst the scientific community as to which cell type is responsible for lung tumorigenesis. In this present study, single-cell RNASeq is utilized to eliminate the limitations that high tumor heterogeneity places upon bulk RNASeq methods in order to elucidate cell type(s) responsible for the initiation of K-ras driven lung tumors in mice. The identification of such cell type(s) could have quintessential implications in the chemotherapeutic prevention and treatment of the overall condition. The results of this study implicate a cell type, with expression patterns aligned with that of bronchioalveolar stem cells (BASCs), whose variable expression profiles between its subtypes are indicative of a transition highly reminiscent of tumorigenesis. Our findings are supported by bulk RNASeq fractionation,

Differential gene expression analysis, and tumor marker indicators of cancer progression. These data can potentially have a high translational impact in improving modern chemotherapy and other treatment methods of NSCLCs.

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Session II: Wednesday, October 19, 2016 – 12:40-2:00 p.m.  
Poster Presentations

“Adjuvant Pharmacological Ascorbate Sensitizes Cancer Cells to Radiation and Chemotherapy”

Author: Megan Bradley

Program: Free Radical and Radiation Biology Department, University of Iowa

*Abstract: Pending*

“Numerical Modeling, Simulation, and Parameter Estimation with Water Quality Data”

Author: Allison Frideres

Program: LAKES REU, University of Wisconsin-Stout

Abstract: Tainter Lake is a reservoir located in Northern Dunn County, Wisconsin, and has had numerous problems in regards to cyanobacteria blooms. A mathematical model was desired that could be used to test the feasibility and effectiveness of potential solution to the algae problem. Previously collected REU and DNR data was examined in conjunction with local weather and flow data. We found that Tainter Lake has features similar to previously modeled lakes but it also differs significantly. In order to account for these differences, a statistical model had to be created to specifically account for the conditions of Tainter Lake. The statistical model yields parameter estimates for a mathematical model created to forecast bloom conditions and severity.

“Localization of the Corticospinal and Rubrospinal Tracts within the Porcine Spinal Cord”

Author: Blake Brown

Program: Summer in Biomedical Science (SIBS), University of Alabama at Birmingham.

Abstract: Although spinal cord injuries (SCI) are a devastating clinical problem, there continues to be failure in translation of research. Rodents continue to be the main and most well established model for traumatic spinal cord injury research. However, motor tract anatomy differs between humans and rodents. Because of this, some research groups are turning to the pig as an intermediate model due to their extensive anatomical and physiological similarities to humans. However, the neural anatomy and localization of major spinal tracts of the pig spinal cord has not yet been described. The goal of this study is to localize the major motor tracts, the corticospinal tract (CST) and the rubrospinal tract (RST), within the pig spinal cord. Mature female domestic pigs received injections of fluorescent dextran tracers into the primary motor cortex and the red nucleus using StealthStation® image guided navigation. 5-6 weeks post injections, the pigs were euthanized and their brain tissue and spinal cord were collected. The tissue was serially sectioned and examined using confocal microscopy to observe to location of the CST and RST. The results demonstrated that the CST in pigs is laterally located in the white matter, very similar to that of humans. However, the CST does not appear to descend past the cervical regions. The exact location of the RST cannot be determined at this time, but preliminary results also point to a lateral location within the white matter throughout the entire length of the neural axis. The location of the CST and RST in the porcine model are anatomically similar to humans. Further work needs to be done to pinpoint the exact location of the RST, however, these results point to the porcine model as a valuable pre-clinical tool to improve translation of promising SCI treatments.

“*Trichomonas vaginalis* Glycogen Synthase Can Functionally Complement the Respective Yeast Mutants”

Author: Galen Gist

Program: Des Moines University Undergraduate Research Program

Abstract: *Trichomonas vaginalis* is a protozoan parasite responsible for the widespread sexually transmitted disease trichomoniasis. Like many cells, *Trichomonas vaginalis* uses glycogen as a storage form of carbon and energy, possessing enzymes such as glycogen synthase to properly

polymerize glucose into glycogen. A glycogen synthase candidate in *Trichomonas vaginalis* is encoded by the TVAG\_258220 open reading frame. Specifically, the C-terminal third of the predicted protein is similar to plant starch synthases and bacterial glycogen synthases. The N-terminal two-thirds of the protein is not homologous to any known protein and its function is unknown. We have previously shown that full length TVAG\_258220 is functional as a glycogen synthase by complementation of yeast glycogen synthase mutants and through in vitro studies using recombinant protein produced in an E. coli expression system. However, we were wondering if expressing only the C-terminal third of the TVAG\_258220 protein would be sufficient to function as a glycogen synthase. In order to answer this question, we constructed plasmids expressing this domain and transformed them in to strains of yeast and E. coli cells. We found that glycogen synthase deficient yeast strains as well as E. coli strains gained an ability to express glycogen synthase activity and make glycogen when complemented with the *Trichomonas vaginalis* C-terminal glycogen synthase domain. Thus we theorize that this specific domain of the TVAG\_258220 protein is a functional glycogen synthase.

“Batch Active Search”

Author: Geoff Converse

Program: Machine Learning, NSF Grant 1560191, Washington University

Abstract: There exists a database which has information on millions of different chemical compounds. A very small percentage of these compounds have potential use for humans and could be useful pharmaceuticals. There are techniques which we can test each compound in order to determine its usefulness, but it is very expensive (time, money, manpower). Our project goal was to develop effective algorithms to search through massive databases and select the most promising chemicals for testing. The machine learning technique we used, Active Search, is transferable to many other applications and other data sets.

“Ternary Complexes of the Voltage-Gated Sodium Channel Nav1.2: Allosteric Interactions of Fibroblast Growth Factor 12A and Calmodulin?”

Author: Matt Hayden

Program: Biochemistry Summer Undergraduate Research Fellowship (BSURF), University of Iowa



Abstract: Voltage gated sodium channels (Navs) are the primary transmembrane proteins responsible for the propagation of action potentials. Calmodulin (CaM), the a calcium sensor in eukaryotes, as well as fibroblast growth factors (FGFs), regulate these channels. Perturbations in both Ca<sup>2+</sup>-mediated regulation and FGFs have been associated with neurodegenerative diseases. Understanding these diseases has been impeded by the absence of a well characterized structural mechanism by which these proteins interact. Currently, it is known that the C-domain of CaM binds to the C-domain of Nav1.2 in a region known as the IQ motif. FGFs bind to Navs at the EF like hand domain, which is upstream of the IQ motif. Past studies have utilized truncated versions of FGF at the N-domain, however recent evidence has suggested that the N-domain may act as a deactivator of Nav1.2. The purpose of this study is to determine if the N-domain of FGF12A interacts with N-domain of CaM to form a ternary complex with Nav1.2. Protein overexpression in E. coli BL21 (DE3) was used to produce GST tagged FGF12A, GST tagged FGF12A-CaM, and GST tagged FGF12A-CaM-Nav1.2 (1777-1937). Protein purification was performed using a Glutathione Sepharose column. Structural data of the FGF12A-CaM-Nav1.2 (1777-1937) complex was gathered on a Bruker 500 MHz Spectrometer. The binding of FGF12A with CaM was explored through fluorescence spectra and SDS-PAGE gel analysis. Currently, attempts are being made to increase the solubility of FGF12A. Preliminary fluorescence spectra and SDS-PAGE gel analysis suggest an interaction between FGF12A and CaM. A greater structural understanding of the interactions of CaM, FGFs, and Navs will hopefully provide insights to treating neurodegenerative diseases associated with these proteins. Supported by N1H R01 GM157001 & BSURF.

“Cyber Operations Analysis and Research”

Author: Audrey LoVan

Program: DHS-HS Stem Summer Internship Program, Argonne National Laboratory

Abstract: Cyber Operations Analysis and Research (COAR) is a division at Argonne National Laboratory that specializes in researching new cybersecurity technologies and applications that help protect from cyber-attacks. A current application being researched is Moving Target Defense (MTD), a method for defending client/server applications. MTD works

toward abstracting some portion of how a system works in order to make it more difficult for an attacker to successfully gain access into the system. There are three different models of MTD, these include: Multiple Operating System Rotational Environment (MORE) [1], Dynamic Application Rotation Environment (DARE), and Stream Splitting (SS) [2]. COAR also works with the Department of Homeland Security to help research Emerging Technologies as well as creating reports and infographics to send out to the general public. Some areas include Intelligent Transportation Systems (ITS), Smart Grids, and Healthcare technologies. Cybersecurity is a most important field that is always changing, researchers needs to be constantly innovating new ideas in order to keep up with the fast pace environment of technology and the Internet of Things.

[1] MORE MTD has a current patent

[2] SS-MTD is patent pending

“The Effect of Increased Water Intake on Food Consumption”

Author: Briana McCloskey

Program: Institute for the Strategic Enhancement of Educational Diversity (iSEED), The University at Buffalo

Abstract: With the obesity epidemic on the rise, people are looking into diets to help reduce their weight. One newfound method for weight loss is increasing water intake; however, research on this topic is limited. Previous studies have been conducted on this topic but the results have been equivocal. This study examines the effects of hydration on energy intake at lunch and the remainder of the day. This study will help to determine the level of hydration needed to reduce energy intake in order to serve as a significant dietary tool. Male and female subjects drank either 1, 3, or 4 bottles (500 ml) of water throughout the morning before being given access to a lunch buffet. Furthermore, during the course of the visit, participants rated how hungry they were on a visual analog scale (VAS) at three different time points before the lunch buffet and once after. Participants also provided urine samples to check hydration levels before and after lunch. Following the visit, participants kept a dietary log of food and beverage intake. Results showed that there was an effect of hydration status on energy intake post visit. When males were in the hydrated condition there was a significant increase in the amount of energy consumed during the rest of the day after their laboratory

visit compared to when they were in the control group ( $p=0.027$ ).

Additionally the results also found an effect of hydration status on daily energy intake. Even when energy intake at lunch was taken into account, males ate significantly more in the hydrated group than when they were in the control group ( $p=0.024$ ). Consequently increased hydration may have adverse effects on energy intake dependent on the timing of water consumption.

“Towards the Purification of MxiK, an Essential Component of the Shigella Type III Secretion System”

Author: Ryan Skaar

Program: University of Kansas Pharmaceutical Sciences

Abstract: Bacterial infections caused by Shigella, called shigellosis, result in diarrhea and in some cases dysentery. There are approximately 164.7 million cases of shigellosis each year worldwide annually and 163.2 million of these cases occur in developing countries. Children under the age of 5 account for 69% of all cases and 61% of the 2.6 million deaths that occur annually (2). Shigella are Gram-negative bacteria that invade the epithelial cell lining of the colon via a Type 3 Secretion System (T3SS). The T3SS is essential for invasion by Shigella and it delivers virulence proteins through an apparatus that consists of external needle and tip complex, a basal body and a cytoplasmic sorting platform that energizes and controls secretion (1). The objective of this project is to examine what role MxiK plays in the sorting platform and how it might interact with MxiN, Spa33, and/or MxiG within the sorting platform. MxiK and its homologs in other T3SS bacteria are essential for T3SS activity. The sorting platform in MxiK null mutants is lost from the basal body which results in complete loss of virulence. This effect on the apparatus is also apparent in a Spa33 null mutant strain which suggests that Spa33 and MxiK may be interacting within the apparatus. To date, there have been no reports describing the purification of MxiK (or its homologs), an outcome likely hindered by insoluble expression in E. coli cloning strains. The goal of this project is to overcome this limitation and obtain refolded MxiK for biophysical analyses and protein-protein interaction studies.

“Ions in the Cornell Photoinjector”

Author: Kristina Smith

Program: Cornell Laboratory for Accelerator-Based Sciences and Education

(CLASSE) Research Experience for Undergraduates (REU), Cornell University

Abstract: Excess gas in a particle accelerator beam pipe is easily ionized by collisions with an electron beam. These ions can become trapped inside the electron beam and will have an effect on the beam because the ions and electrons have opposite charge. My project uses computer simulations to determine how different distributions of ions will affect the electron beam in the Cornell Photoinjector (a type of particle accelerator).

“Spontaneous Mouse Model of Prostate Cancer”

Author: Karli Wittorf

Program: Summer Undergraduate Research Program (SURP) with the Biochemistry Department at the University of Nebraska Medical Center (UNMC)

Abstract: Prostate cancer is one of the most common cancers in males and one of the most frequent causes of male cancer-related death. Prostate cancer can develop in two forms; the most common is fairly slow growing (indolent) and the uncommon form is more aggressive, growing rapidly. However, it is difficult to know whether a patient’s prostate cancer will be indolent or aggressive which makes deciding the proper treatment for a patient challenging. Learning the exact mechanisms of prostate cancer would allow for the finding of an effective treatment. One way to better understand prostate cancer’s mechanisms have been by generating genetically engineered mouse models. The overall goal of these models is to accurately mimic all of the stages found in human prostate cancer. Our study focused on generating the  $PTEN^{loxp/loxp}; Trp53^{R172H/+}; ROSA26; Hi-C-Myc; PB-Cre4$  mouse model, which would allow us to detect tumor progression non-invasively in mice. Through sequential breeding, DNA isolation, and genotyping, we were able to observe that we had generated two composite strains of mice models. Strain 1 contained  $PTEN^{loxp/+}$  and  $Hi-C-Myc$ , and Strain 2 contained  $PTEN^{loxp/loxp}$ ,  $Trp53^{R172H/+}$ , and  $ROSA26$ . Breeding of the 2 composite mice strains should be continued until obtaining the final cross of  $PTEN^{loxp/loxp}; Trp53^{R172H/+}; ROSA26; Hi-C-Myc; PB-Cre4$ . Obtaining this model would allow us to use it for studies related to prostate tumor latency, prostate histology, and incidences of prostate metastasis. This model would also

enable us to produce a generation of mouse syngeneic cell line that can that be used for therapeutic studies.

“A Mathematical Evaluation of Ionic Equilibria”

Author: Ben Rajewski

Program: University of Kansas Pharmaceutical Chemistry Department

Abstract: Equilibrium occurs when the reactants and products of a system are unchanged and independent of the initial point of the reaction coordinate, meaning concentrations of species in solution remain constant. Ionic equilibria are more complex because of the need to estimate multiple species of ions at equilibrium, taking into account ionic interactions in solution. In order to understand these systems, mathematical methods are used to estimate the composition of a solution at equilibrium. Important to these models are equilibrium constants and their origin. Highlighted is the general approach to solving ionic equilibria problems, including pH calculation and determination of species concentration. Newton approximation is a helpful tool used to determine the roots of a high order polynomial, which is often seen in these types of problems. It is imperative to understand this quantitative approach to ionic equilibrium as it provides vital information about a system and its contents, allowing scientists to accurately make solutions for example.

Jason Kiehne. Title and abstract pending