Patricia Belt Conrades

September 26, 2016

Summer Science Research Symposium

Ohio Wesleyan University

NATHAN MADONICH

OWU 2016 Research Associate on NASA grant with Chris Wolverton to study the effects of zero gravity on plant roots on the International Space Station.

"My summer at OWU in SSRP provided me with the knowledge and tools to begin investigating important research questions in the field of plant biology. This included essential skills such as experimental design, common lab procedures, and keeping an up-to-date lab notebook. As my first research experience, it pointed me in the right direction and inspired me to pursue a career in plant biology."

THE PATRICIA BELT CONRADES SUMMER SCIENCE RESEARCH SYMPOSIUM

Science, mathematics, and technology continue to increase in importance as the world becomes smaller and more interdependent. Through ongoing research, scientists can help solve global problems — from eradicating infectious diseases to discovering new sources of clean, safe energy.

Now in its twenty-fourth year at Ohio Wesleyan, the Summer Science Research Program, which culminates in today's Patricia Belt Conrades Summer Science Research Symposium, encourages students to tackle tough research issues by offering an intensive 10-week opportunity to work with seasoned, accomplished mentors both on and off campus. The posters you see here today depict the research results. Please ask the students any questions you wish; they are proud and happy to tell you what they learned and why it matters.

CONTENTS

Atrium, Schimmel/Conrades Science Center

Monday, September 26, 2016, at noon

Opening remarks by President Rock Jones followed by student poster presentations

THE IMPORTANCE OF SUMMER RESEARCH ON A CAREER

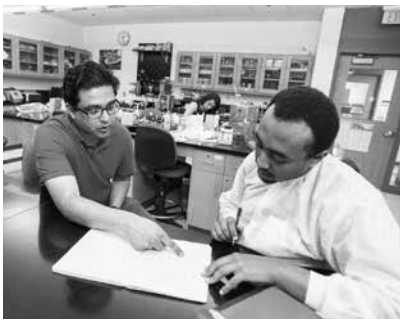
When I first came to Ohio Wesleyan as a student, I knew that I wanted to study science. Exactly which scientific discipline was going to become my career was as yet undetermined, but my mind was set on understanding why all the things in the universe did all the things that the universe does.

Following the advice of my academic adviser, I pursued a freshman research fellowship with Dr. Jed Burtt doing research on Bacillus bacteria and their ability to degrade bird feathers. I then continued to work with him and Dr. Joe Calabrese on this project over two separate summers through the next four years. Dr. Burtt and Dr. Calabrese taught me that new knowledge was earned not necessarily with brilliance, but more importantly with persistence. They taught me to not expect easy answers, but to measure carefully and to always be asking the next question. To follow an understanding of what happened with an understanding of how it happened and why it happened.

My research experience as an undergrad at OWU not only helped me get into graduate school, it helped me succeed there. I knew how to work, how to question, and how to grind through adversity. Over the course of the next eight years, I put that experience to use; assisting on a score of research projects, publishing papers in peer review journals, presenting scraps of new knowledge on how the world works at academic conferences to experts whose books I had read, and earning two advanced degrees. All this led me back to where I began, now qualified to teach here at OWU. And now when I get to consult students as they work to learn how to find answers to the right types of questions and how to share their new knowledge with others, I hope that I can impart some aspect of the grandeur of the endeavor that is scientific research. The goal is to know something that none of the more than 100 billion humans who have spent time on this Earth has ever known before. This is an amazing thing. But to be amazing, one must first be humble and patient enough to learn what those who came before you have learned. So that by standing on the shoulders of giants, you may see what lies over the new horizon.

Daniel F. Fink, Ph.D.
Ohio Wesleyan University
PT Professor of Zoology/Chemistry/Physics






THE MAKING OF A SCIENTIST

In Ohio Wesleyan's Summer Science Research Program (SSRP), students learn quickly that authentic research is quite different from classroom labs — more challenging, more creative, more frustrating, and, ultimately, more rewarding.

I have always actively involved students in my research projects during the academic year and during the summers. The most rewarding part is watching the students grow as scientists, seeing them take command of a research project, and knowing that they are gaining the confidence to speak and act as scientists. Science cannot be learned solely from a book. Science must be experienced through research, and at OWU, we encourage students to plunge in, preparing them to be successful researchers both at OWU and at other universities. Many first-year students are surprised to learn that they can contribute in substantive scientific research from the moment they arrive on campus. At Ohio Wesleyan, research is not just for the few.

During the Symposium this afternoon, you will have the opportunity to interact with 21 students who performed research at OWU mentored by OWU faculty members, 9 students from universities other than OWU who worked on campus with OWU faculty, and 9 OWU students who performed research off campus at other universities or in other countries. There is no doubt that the results presented here today are exciting and novel. However, equally exciting is the opportunity for you to speak with each of these young scientists about what discoveries they have made.

Enjoy the Symposium – and be sure to learn something new!

Laura Tuhela-Reuning
Department of Botany-Microbiology
Department of Zoology
Scanning Electron Microscopist
Summer Science Research Program Assistant Director

THE PATRICIA BELT CONRADES SUMMER SCIENCE RESEARCH SYMPOSIUM ENDOWMENT

In 2006, Dr. Nancy Reynolds Schneider '64, established an endowment to name the Summer Science Research Symposium after her good friend and fellow OWU alumna, Patricia Belt Conrades '63.

Mrs. Conrades is a volunteer registered nurse and homemaker, and a member of Ohio Wesleyan's Board of Trustees. She regularly assists in the operating room of Boston's Mount Auburn Hospital and is also a nurse with Volunteers in Medicine, assisting the poor in Stuart, Florida. Dr. Schneider is a highly regarded Professor of Pathology and Director of the Cytogenetics Laboratory on the faculty of the University of Texas Southwestern Medical Center in Dallas. She also has served on the Ohio Wesleyan Board of Trustees.

Mrs. Conrades and Dr. Schneider share a commitment to the sciences, and are both examples of individuals who have enjoyed successful careers in science. The support of Mrs. Conrades and her husband, George Conrades '61, a member of the OWU Board of Trustees, and Dr. Schneider and her husband, John Schneider, continues to strengthen the science and mathematics programs at OWU.

THE C. PATRICIA FERRY SUMMER SCIENCE RESEARCH PROGRAM ENDOWMENT

In 2008, Patricia Ferry '53 established the C. Patricia Ferry Summer Science Research Endowment in recognition of the program's value as an integral part of the liberal arts experience. The endowment that will fund the program in perpetuity follows Ms. Ferry's support of the program through gifts she has made annually for several years.

Through her contacts with SSRP participants, Ms. Ferry has observed how the program introduces students to the excitement of science and original research and provides familiarity with the many career options available in the disciplines.

Ms. Ferry's interest in the sciences is longstanding, including her years at Case Western Reserve University, where she worked in the medical school directing its medical education program. She graduated from Ohio Wesleyan with majors in psychology and sociology and as a member of Alpha Xi Delta sorority.

SPECIAL ACKNOWLEDGEMENTS

Sources of Support for the 2016 Summer Science Research Program

Harry Phillip Bahrick Summer Research Fund
Joseph H. '30 and Elizabeth Brant Collaborative Research Fund
Jack E. '52 and Joyce A. Cornett Summer Science Research Fund
Herbert L. '61 and Margaret Wright '61 DuPont Collaborative Summer Research Fund
Ferry Family Foundation
Robert V. and Alice C. Kail Summer Science Research Internship
Marcia Kunstel '69
Albert A. Mills Jr. Summer Science Research Program Fund
National Science Foundation
David H. Smith '53 Fund for the Sciences
The Student-Faculty Endowed Research Fund in Chemistry
Ohio Wesleyan University Provost and Academic Affairs Office

Support for the Patricia Belt Conrades Summer Science Research Symposium

Dr. Nancy Reynolds Schneider '64

Students conducting research on the OWU campus this summer were funded primarily through the OWU Summer Science Research Program (SSRP), but through a variety of other sources as well. Two additional funding grants for students came from the National Science Foundation-Research Experience for Undergraduates (NSF-REU) program: one to the Departments of Physics/Astronomy and Mathematics/Computer Science and a second to the Neuroscience Program. In the following pages, students listed were part of the SSRP unless otherwise noted.

Board 1

MALLORY COCHRAN[1] DEREK SHANK[1] NICK SWEENEY[2] AND OANA VESA[3]*

[1] OHIO WESLEYAN UNIVERSITY
[2] HAVERFORD COLLEGE
[3] ALBION COLLEGE
* OWU PHYSICS/ASTRONOMY AND MATH/CS REU STUDENT

Faculty Mentor: Robert Harmon
Department of Physics and Astronomy

Starspots are cooler, darker regions on stellar surfaces caused by strong magnetic fields. Our project focuses on observing the changes of the starspots over time on the star LO Pegasi, a star similar to the Sun 81 light years away that has starspots on it that are much larger than sunspots on the Sun. To do this, we are measuring the star's changes in brightness as the starspots rotate into and out of view of Earth. Studying how starspots on other stars behave will aid in better understanding sunspots on the Sun and the magnetic processes behind them.

STARSPOTS OF LO PEGASI, 2006-2016

LO Pegasi is an ultrarotator (P = 10.1538 hr) and a young solar analog about 81 light years distant that exhibits large starspots on its surface. Starspots are regions of strong magnetic field that suppress convection on stellar surfaces. This causes the spots to be cooler and darker than their surroundings. Because starspots are darker, as the star rotates, starspots come into and out of view of Earth and vary the brightness of the star. The brightness variations of LO Pegasi were measured via differential aperture photometry, and light curves were produced through the B, V, R, and I photometric passbands using a 0.35-m Meade LX600 ACF telescope and a QSI 632wsg CCD camera. Then, an indirect photometric technique was employed to map the stellar surface. We present a study of the evolution of the starspots, including long-term changes in the size of the polar spot that we infer from year-to-year changes in the average brightness of the star.

Board 2

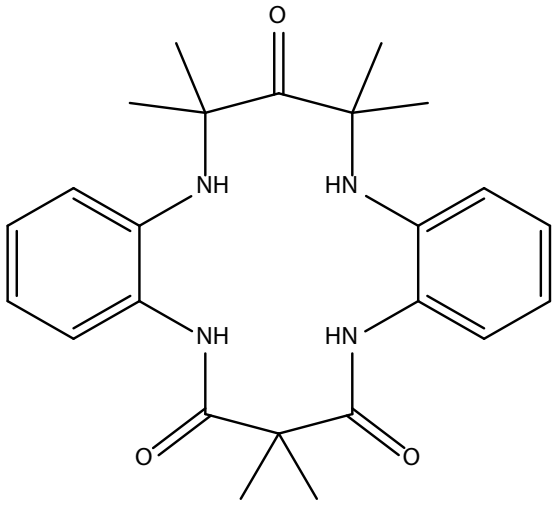
COLLEEN CHERNOWSKY

Faculty Mentor: Kim Lance
Department of Chemistry

Current chemical reactions used in water purification produce byproducts harmful to the environment and to humans. Nature can do the same thing but without the production of toxic materials by using a molecule that can carry out more efficient reactions. We are working on making a molecule similar in structure to the ones used by nature in order to apply these efficient reactions to water purification processes. This will allow us to purify water on an industrial scale without producing harmful toxins.

PREPARATION OF COMPLEXES AS ROBUST CATALYTIC OXIDANTS

Attempted synthesis of the compound described in Figure 1 was carried out by reacting BOC-protected o-phenylenediamine with 2,4-dibromo-2,4-dimethyl-3-pentanone and sodium hydride. An additional reaction of BOC-protected o-phenylenediamine with 2,4-dibromo-2,4-dimethyl-3-pentanone and silver oxide catalyst was carried out. Isolation of both products followed by NMR analysis showed the reactions to be unsuccessful. A repeat of both reactions with unprotected o-phenylenediamine also proved unsuccessful. A repeat of both reactions with 2-nitroanaline rather than o-phenylenediamine also proved unsuccessful. Synthesis of the compound described in Figure 1 was again attempted by reacting BOC-protected o-phenylenediame with dimethylmalonyl dichloride. Analysis of the product by NMR proved the reaction to be a success and demonstrated progress toward the synthesis of Figure 1.



Board 3

BRIAN JORDAN[1*]
BROOKLYN MCCUE[2*]
AUSTIN MINNICK[1] AND
CEMALIYE SEMMEDI[1]

[1] OHIO WESLEYAN UNIVERSITY
[2] COLUMBUS STATE COMMUNITY COLLEGE
[*] OWU NEUROSCIENCE REU STUDENT

Faculty Mentor: Jennifer R. Yates
Department of Psychology, Neuroscience Program




Spinal cord injuries affect thousands of people every year and available treatment therapies are insufficient. Much of the damage from spinal cord injury occurs after the initial impact in what is called the secondary injury. As an alternative to current treatments, our experiment focuses on the effects of a drug called 6-chloro-tryptophan in treating secondary injury. We found that certain doses of the drug appeared to improve recovery of injured animals over the course of one week.

EFFECTS OF 6-CHLORO-TRYPTOPHAN ON ACUTE SPINAL CORD INJURY IN GUINEA PIGS

Inflammation contributes to the secondary behavioral deficits seen in neurotraumatic injuries such as spinal cord injury (SCI). The current approved treatment for SCI primarily exists as an antioxidant that fails to reduce inflammation. Inflammation in acute SCI is associated with the production of the neurotoxin, quinolinic acid (QUIN). QUIN is produced by activated macrophages at the injury site and its accumulation is correlated with injury severity. Previous studies have shown that manipulating the tryptophan-kynurenine pathway, which leads to the production of QUIN, can attenuate QUIN accumulation and reduce secondary behavioral deficits after SCI. One way to manipulate this pathway is by administering 6-chloro-tryptophan. In the present study, the effects of 6-chloro-tryptophan on secondary behavioral deficits and QUIN accumulation were investigated in a guinea pig model of SCI. Adult female Hartley guinea pigs were injured by lateral compression of the spinal cord at the 12th thoracic segment (T12). 6-chloro-tryptophan was administered in doses of 1 mg, 5 mg, 7.5 mg, and 10 mg over a time period of either 3 or 7 days, beginning at 5 hours post injury. The severity of the behavioral deficits and the recovery rate of the subjects were quantified using several sensory and motor function tests, including *Cutaneus Trunci* muscle reflex, toe-spread, proprioceptive placing etc. Doses between 5-10 mg showed trending improvement in recovery rate. Supplementary histological analysis will be required to quantify QUIN accumulation at the injury site. In order to consider the drug viable, further experimentation will be conducted.

Board 4

KHAYYAM ZUBAIR

Faculty Mentor: Sean McCulloch
Department of Math and Computer Science

The goal of our research was to build a computer program to play a game of Modern Art. Modern Art is a modern board game that is based on auctions. We aimed to use probability based mathematics to form in game strategies for our program. A truly artificially intelligent program would play the game as well as a human being could.

ARTIFICIAL INTELLIGENCE OF MODERN BOARD GAMES

Modern Art is an auction based board game about the world of art galleries. The goal of our work was to come up with an Artificially Intelligent computer program to play a simulated version of Modern Art. Modern Art is played by 3-5 players acting as gallery owners. Each player is dealt some cash and a hand of cards, which are paintings that the players will auction to one another. Any income from selling these paintings goes to the selling player. Each painting bought during such an auction is sold at the end of a round to the bank and the buyer's compensation is based on how well the artist of the painting had performed in that round. Our work on the project focused in two directions: developing a computer simulation of the game and developing a winning strategy that a computer player could use to play the game and challenge a human competitor.

Simulating this game with code required coming up with models and simulations for cards, artists and auctions. The game logic kept track of how much money each player made and how well each artist performed. Winning in modern art hinges on bidding the right amount on a painting. A player has to decide what a painting's future worth but also the net value of their competitor after the transaction. We hypothesized that such a prediction could be made based on probability. The AI game engine was thus tasked to randomly simulate a game at the given state a number of times and then rank the performance of that artist in each of these simulations, then calculate a probable worth based on these results. We found that the program was able to read the course of a game and make reasonable bids for the paintings up for auction.

Board 5

SHANNON SCHLATER

Faculty Mentor: Amy Downing
Department of Zoology

Species can positively or negatively interact with one another, and can do so strongly or weakly. We used field data from experimental ponds of fluctuating plant (phytoplankton) and herbivore (zooplankton) populations to determine how each species interacts with one another. We were then able to show that weaker interactions tend to stabilize ecosystems.

INTEGRATING THEORETICAL AND EMPIRICAL DEFINITIONS OF ECOLOGICAL STABILITY

Researchers have found that most natural food webs consist of many weak and few strong interactions. Weak interactions are believed to be stabilizing in communities as they dampen the strength of strong interactions, ultimately, reducing the magnitude of population oscillations. Using time-series data from an aquatic mesocosm experiment consisting of zooplankton and algae, we were able to use a multivariate autoregressive modeling approach to determine community matrices composed of species' interaction strengths. Consistent with previous findings we found community matrices with many weak interactions generally exhibited stabilizing characteristics. However, we also found that weak interactions may not be an equally strong stabilizing mechanism for different measures of stability.

Board 6

JEMIL AHMED

Faculty Mentors: Laura Tuhela-Reuning and Suren Ambegaokar
Department of Botany and Microbiology

Certain bacteria have feather degrading abilities. Some of these bacteria degrade feathers faster than others. I'm studying the biochemical differences between the fast and slow degrading bacteria.

COMPARING KERATINASE PRODUCTION AND ACTIVITY BETWEEN SLOW FEATHER DEGRADING BACTERIA AND FAST FEATHER-DEGRADING BACTERIA

Feathers are made up of a protein called β-keratin that can be degraded by an enzyme called keratinase. Three *Bacillus* spp. isolated from songbird plumage were selected because they degraded feathers at different rates. However, why these bacteria degrade feathers at different rates is unknown. Previous research involving differences in the keratinase amino acid sequence of fast and slow degraders did not correlate with keratin degradation rates. In addition, differences in promoter sequences of keratinase in the different strains had no impact on the rate of keratin degradation. We are investigating two hypotheses to better understand the difference in degradation rates. One hypothesis is that fast degrading strains produce more keratinase than slower degrading strains, and the expression of the keratinase gene during degradation can be quantified to determine whether this is the case. The other hypothesis is that fast degrading bacteria produce reducing agents that change the structural integrity of β-keratin making it easier for keratinase to degrade the feathers.This will be tested by examining thiol residues after reduction of disulfide bonds in keratin.

Board 7

NATE DEDEK

Faculty Mentor: Dustin Reichard
Department of Zoology

I'm studying how short-range songs and long-range songs vary geographically in Dark-eyed juncos *(Junco hyemalis)*. Moreover, I'm determining if short-range songs are more unique than long-range songs to each population of dark-eyed juncos dispersed across the western United States. If so, then it can be assumed that these short-range songs can be used as a mating barrier between the different populations. Mating barriers can eventually lead to the formation of different species which may have a major impact on the evolution of dark-eyed juncos.

UNDERSTANDING YOUR NEIGHBORS: GEOGRAPHIC VARIATION IN LRS AND SRS OF DARK-EYED JUNCOS *(JUNCO HYEMALIS)*

Nearly all species of songbird produce high-amplitude songs that can be detected over long distances, which have fittingly been classified as long-range song (LRS). These songs have been well documented in numerous species and most commonly function in mate attraction and territory defense. Recently, researchers have begun to investigate low-amplitude songs that are intended for receivers in the immediate vicinity of the signaler. This second class of song has been referred to as short-range song (SRS). Research on SRS is sparse, thus its overarching function or even how it varies between species remains poorly understood. For Dark-eyed juncos *(Junco hyemalis)* both LRS and SRS appear to be species-typical. Species-typical songs tend to vary across different geographic scales, sometimes creating dialects between different populations. These dialects have the potential to become barriers to reproduction that could in turn lead to speciation. LRS is known to vary significantly among subspecies and populations of Dark-eyed juncos but no distinct dialects exist among them. Little to no research has been conducted to assess variation in SRS within and among these populations. This raises the question as to whether or not SRS is more distinct than LRS among different populations. I will analyze multiple acoustic features to determine if SRS is more distinct than LRS between five subspecific populations of dark-eyed juncos. Given its role in close-proximity courtship interactions, I predict that SRS will be under less selective pressure for efficient transmission and greater selective pressure from female mating preferences than LRS. That is, if SRS is less constrained by sound transmission then it would be expected that SRS is more labile and will differ more significantly between populations. These results may help better our understanding of the development of SRS and its role in assortative mating.

Board 8

MEG DEETER

Faculty Mentor: Ramon Carreno
Department of Zoology

It is not uncommon for host organisms to be concurrently infected with multiple species of parasites. One example exists within the hindgut of the American giant millipede, *Narceus americanus*. The hindgut houses a microcommunity of symbionts that includes a variety of parasitic nematodes. Interestingly enough, it appears that different parasite species aggregate within the hindgut tandem to one another in predictable portions of the hindgut. This may be due to resource partitioning along the hindgut. The primary objective of our study was to quantify the diversity and distribution patterns of these parasites.

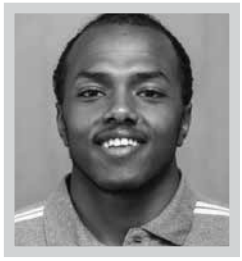
EXAMINATION OF PARASITE GUILDS IN THE HINDGUT OF THE AMERICAN GIANT MILLIPEDE, *NARCEUS AMERICANUS*

The distribution of pinworm species (Nematoda: Oxyurida) within arthropod host organisms is not well documented, particularly in those that harbor multiple parasite species concurrently. Individual American giant millipedes, *Narceus americanus*, are model organisms towards understanding parasite distribution patterns, as they simultaneously harbor 2 distinctive species of pinworm, *Aorurus agile* and *Thelastoma spp*. in their hindguts. Additionally, *N. americanus* also yields large populations of *Rhigonema spp.* (Nematoda: Rhigonematidae) in the anterior end of the hindgut. The lower intestinal tracts from N. americanus individuals (n=98) were dissected in the posterior-to-anterior direction in 5 mm increments. With each increment, the prevalence of each type of nematode was recorded. Nematodes were collected and preserved following each dissection's completion. Preliminary data show *Aorurus agile* to span the entirety of the hindgut, whereas *Thelastoma spp*. are more likely to aggregate in the medial region of the hindgut. *Rhigonema spp*. are almost exclusively found within 10 mm of the pylorus, the valve connecting the mid- and hindgut regions. Our results support the existence of realized niches for parasitic nematodes occupying *N. americanus*.

Board 9

IFA ABDULJELIL

Faculty Mentor: Kim Lance
Department of Chemistry



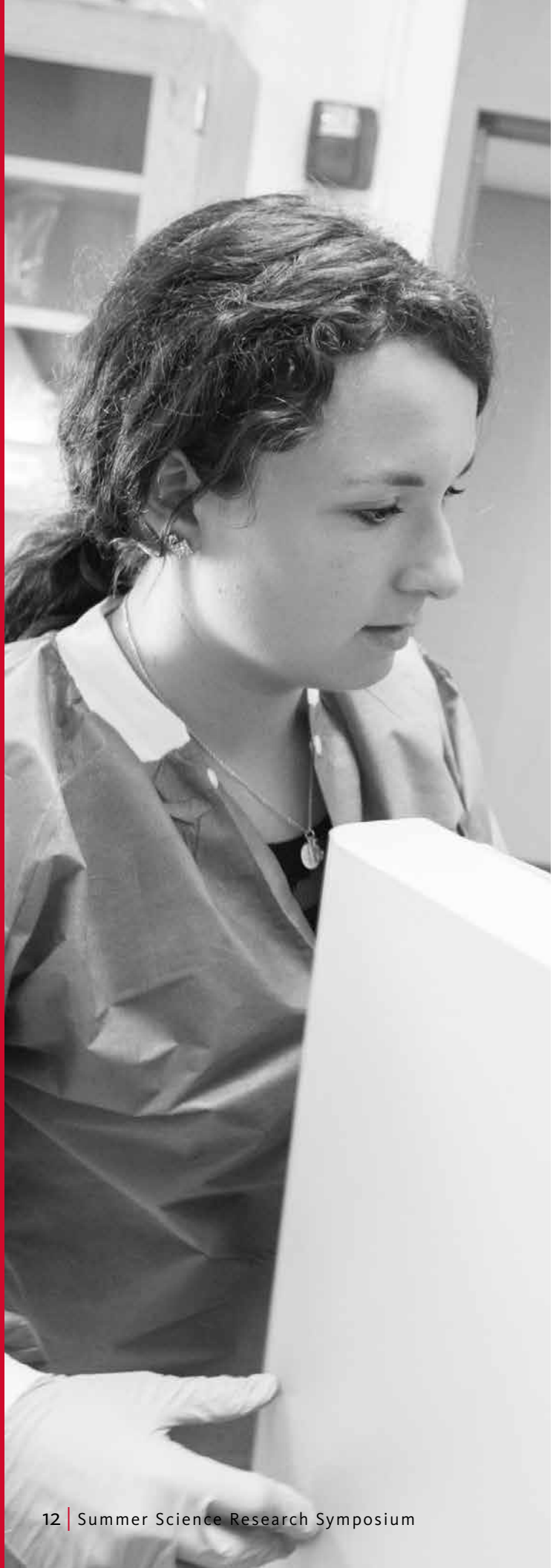
Water is accessible to human's daily life at a miniscule scale and many reactions that purify water may be harmful to the environment and may take a very long time. Nature uses a protein, cytochrome-P450, as a short cut to modify compounds to purify water efficiently. We are imitating nature's way of speeding up water purification by making and testing a molecule that mimics the structure of cytochrome-P450 to purify water rapidly.

PREPARATION OF COMPLEXES AS ROBUST CATALYTIC OXIDANTS

Fresh water accessibility for humans as a direct use is extremely difficult to attain, about 0.007% and the results of water purification today leads to toxic by-products thus a new way for purification of water is essential.[1] Through the guidelines of green chemistry by ACS, a macrocycle ligand complex of Diamide-Diamine (Da-Da) was synthesized.[2] The oxidative capability of this catalyst was to mimic the protein function of cytochrome P-450. The molecule cyclohexene was to be oxidized to form 7-oxabicyclo[4,1,0]heptane involving hydrogen peroxide as the oxidant at different conditions. A standard solution containing the internal standard and possible products of the reaction was created for comparison. The results were acquired through Gas Chromatography Mass Spectrometry (GCMS), which showed no epoxidation of cyclohexene but did show significant reduction of cyclohexene peak area, as compared to chlorobenzene, internal standard. The results showed that something was occurring through the color changing reaction conducted and some speculations have been noted, thus further investigation is needed.

1: "The World's Water." *Where Is Earth's Water? USGS Water-Science School*. U.S. Geological Survey's Water Science School, 02 May 2016. Web. 29 July 2016.

2: Sheldon, Roger A. "Green Chemistry Principle #9 - American Chemical Society." *American Chemical Society*. N.p., 2016. Web. 27 July 2016.



Board 10

RICKY HE

Faculty Mentor: Pamela B. Pyzza
Department of Mathematics and
Computer Science

The study of the human brain has become increasingly popular in contemporary science and yet the dynamics of neuronal networks within the brain are not well understood. We investigate the dynamics of an idealized neuronal network in the hippocampus, which comprises three types of integrate-and-fire model neurons that interact with each other based on their unique properties. Our model balances some loss of detail for the individual neurons with computational efficiency to investigate the behavior of the entire network. Given various parameter values and connectivity structures, we hope to gain a better understanding of how these properties impact the network dynamics.

DYNAMICS OF INTEGRATE-AND-FIRE MODEL OF HIPPOCAMPAL CIRCUIT

The behavior of neuronal networks in the hippocampus is the topic of many experimental and modeling studies, and yet much of these networks' structures and functionalities in this part of the brain are not well understood. We can use computational models to reproduce some of the hippocampal behavior seen experimentally and begin to investigate possible underlying mechanisms for the network activity. A common computational neuron model used for modeling such networks is the Hodgkin-Huxley (HH) neuron, which can describe the spiking behavior of a single neuron very well. However, the complexity of this model, compounded by network properties makes network simulations with HH computationally expensive. In this work, we will focus on the network dynamics, rather than individual neuron properties and consider a simpler, more computationally efficient model called the integrate-and-fire (I&F) neuron. Motivated by experimental work, we consider a network of three types of neurons: fast excitatory neurons (decay rate ~2-5 ms), fast inhibitory interneurons (decay rate ~4-10ms), and a slow inhibitory neuron based on the oriens lacunosum-moleculare (O-LM) cell whose interactions are believed to be responsible for network oscillations measured in the characteristic gamma (30-90 Hz) and theta (4-12 Hz) frequency bands. We investigate parameter regimes for the coupling coefficients, external spike input, and other parameters, in which our model can qualitatively reproduce the behavior seen in other computational models, as described in Kopell et al. (2010), which employ the HH model. We further consider network dynamics created by various network architectures including all-to-all coupled and sparse network connectivity to begin to make links between network properties and network behavior.

Board 11

KYLE DAVIS

Faculty Mentor: Dustin Reichard
Department of Zoology

We are looking to see what kind of microorganisms reside on the chicks, parents, and nests of local nest box species. I am then looking to see if there are any patterns in the types of microorganisms based on habitat, time of year, species, and the direction the nest box is facing.

POSSIBLE DIFFERENCE IN MICROBIAL COLONIES FOUND IN AVIAN CAVITY NESTING SPECIES

While there are reports of the microbial content of single species of birds in nest boxes there are few reports that compare microbial content between different species and explore whether outside factors affect these differences. We compared microbial loads on the parents, the nests, and the nestlings, of the Eastern Bluebird (*Sialia sialis*), Tree Swallow (*Tachycineta bicolor*), House Wren (*Troglodytes aedon*), and House Sparrow (*Passer domesticus*) that occupy local bird boxes. We looked for correlations between weather, location, and box orientation to see if they have an effect on bacterial load.

Board 12

SEAN MCCARTT[1*] KEVIN ROSSI[1] AND BROOKE MARTINEAU[2*]

[1] OHIO WESLEYAN UNIVERSITY
[2] BAY PATH UNIVERSITY
[*] OWU NEUROSCIENCE REU STUDENT

Faculty Mentor: Kira Bailey
Department of Psychology,
Neuroscience Program

Our research looks at how video games may affect daily life. Specifically, we are looking at the effects of playing video games on the brain's ability to maintain goals. Action video game players are potentially less likely than strategy game players to actively focus on the task at hand.

THE EFFECT OF VIDEO GAME TRAINING ON THE NEURAL CORRELATES OF COGNITION

Improvements in visuospatial processing have been shown following as little as 10 hours of playing action video games (AVGs; Green & Bavelier, 2003); however, other work suggests these same games may have a negative impact on cognitive control, the ability to flexibly adapt behavior to meet task demands (Bailey, West, & Anderson, 2010). Few studies have examined the impact of other genres of video games on cognitive control. The goal of the current study was to replicate and extend previous work examining the effects of action video games on cognitive control, and to examine the effects of a previously unstudied genre, real-time strategy (RTS) video games. Neural (event-related brain potentials) and behavioral (response time and accuracy) correlates of cognitive control were measured before and after 10 hours of training on either an AVG (Unreal Tournament 3) or an RTS (League of Legends). Data collection is ongoing, but at this time there are minimal differences pre and post-training in both the AVG and RTS groups.

Board 13

VIESULAS SLIUPAS

Faculty Mentor: Christian Fink
Department of Physics and Astronomy

In order to better understand how epilepsy spreads from one area of the brain to another, we used a computational model which simulates epileptic seizures in a chunk of the brain. We then took a network of the connections in the macaque brain between fairly large chunks, and ran our model in each part. The seizure spread from one area of the brain to the rest of it, and we tried to find if there was any connection we could remove which would prevent it from spreading. We found such a connection, removed it, and as a result the seizure only happened in one small region of the brain.

NETWORKING EPILEPSY

Current clinical practices for treating epilepsy are fairly crude and unrefined, including the use of vaguely-targeted incisions intended to prevent the seizure from spreading. In order to work towards developing finer and more precise tools for impeding the spread of seizures, we simulated seizures in a network model of the brain. Using the "Epileptor" dynamical model (developed via a phenomenological analysis of voltage traces, V.K. Jirsa et al 2014), we modelled a seizure event on the coarse connectome of a macaque brain in which the seizure generalized.l We were able to show that the seizure was prevented from spreading with minimal damageto neuronal connections by removing a single connection. This provides further proof to our hypothesis that we might be able to use this to develop targeted tools to prevent epilepsy from spreading in a real brain.

Board 14

ALLYSON WOJNOSKY MEKA GEORGE AND RACHAEL QUICK

NASA STUDENT ASSOCIATES

Faculty Mentor: Chris Wolverton
Department of Botany and Microbiology

Data will be collected as a control and used as a "1g" comparison for data to be collected aboard the International Space Station at fractional gravity. Differences in gravity responses were observed via the analysis of timelapse photography of wild type Arabidopsis thaliana, a Eurasian weed, and starchless mutant Arabidopsis thaliana plants.

COLLECTION OF 1G REFERENCE DATA FOR ISS EXPERIMENTS

Plants grow and develop through an adaptive process by which numerous inputs from the environment are detected and acted upon to determine the final shape of the plant body. Upon displacement from vertical, primary roots respond to gravity at a rate that varies depending on the angle of stimulation, a process which relies on the sedimentation of starch-filled plastids called statoliths. We have previously shown that roots lacking statoliths show reduced gravitropic response and rates of differential growth that do not vary with the angle of stimulation. These results suggest an alternate mechanism of gravity perception not involving plastid sedimentation. We are planning to probe this alternate mechanism by applying fractional g treatments to wild type and starchless mutants using centrifugation in the EMCS facility aboard the ISS.

As part of Flight Definition, we have investigated a number of parameters in order to optimize seedling growth in flight hardware. All of our previous work on root gravitropism has been carried out with primary roots between 4 and 5 d old growing on agar-based nutrient media containing 1% sucrose. Agar-based substrates differ significantly from the growth environment in the Seed Cassettes designed for the EMCS, in which seedlings grow along the surface of a polyethersulfone (PES) membrane. One objective here was to compare growth and gravity response of roots growing along the surface of membranes with those of roots on agar. Results thus far suggest that roots growing on membranes elongate and respond to gravity consistently and at a lower rate than in previous experiments on agar media. These data will be used to develop a model of gravitropic response rates for use in interpreting the fractional g flight treatments. Supported by NASA grant NNX15AG55G.

Board 15

NADYA SOTNYCHUK
LARYNN CUTSHAW

Faculty Mentor: Laura Tuhela-Reuning
Departments of Zoology, Botany and Microbiolgy

We travelled to Victoria, Australia in the summer of 2015 to collect bacterial and feather samples from 26 species and 279 individual birds. We were looking for *Bacillus spp*. which are a bacterial group capable of degrading feathers. We found that all 26 species captured and 87.46% individuals sampled had at least one colony of *Bacillus*. This research is the first report of *Bacillus* on living Australian bird plumage in the wild.

UNDERSTANDING THE PREVALENCE OF PLUMAGE MICROBES IN AUSTRALIA

The microbial ecosystem in plumage includes bacteria that degrade keratin in feathers. The prevalence and diversity of these microbes vary geographically and by foraging type in the United States. However, little is known about plumage microbes of Australian birds. To investigate keratinolytic bacteria outside the U.S., feathers were sampled from 279 birds of 26 species in 10 different locations within a 170 km radius of Deakin University (Geelong Waurn Ponds Campus) in Victoria, Australia. Birds were sampled using contact plates of Tryptic Soy Agar, Mannitol Salt Agar, Eosin Methylene Blue Agar, and Yeast Mold Agar. Following inoculation, colonies were counted and classified by morphology with special attention given to those that appeared to be *Bacillus licheniformis, Bacillus cereus, Bacillus subtilis,* and *Staphylococcus,* as these are potential keratinolytic species. Presumed *Bacillus spp*. were identified on all 26 species captured and 87.46% individuals sampled. Bacillus was found on all sixteen of the White-browed Scrubwrens *(Sericornis frontalis)*, a forest floor dweller, sampled. These findings are consistent with previous studies that found ground and arboreal foragers had higher loads of *Bacillus* than aerial foragers due to the soil dwelling nature of *Bacillus* spp. This research is the first report of *Bacillus* on Australian bird plumage in vivo.

Board 16

LARYNN CUTSHAW
NADYA SOTNYCHUK

Faculty Mentor: Laura Tuhela-Reuning
Departments of Zoology, Botany and Microbiology

Bird plumage is an ecosystem of microbes within the avian host, most of which are soil-dwelling organisms. We questioned how method of capture influences the microbial loads in plumage. Understanding the effect trap types have on microbe abundances can help us better refine methodologies in avian microbiology studies.

THE EFFECT OF CAPTURE METHOD ON MICROBIAL ABUNDANCE IN PLUMAGE OF EASTERN YELLOW ROBINS *(EOPSALTRIA AUSTRALIS)*

Bird plumage is an ecosystem of microbes within the avian host. Most of these organisms are soil-dwelling bacilli so birds with more soil contact tend to have higher microbial loads. While investigating whether bacillus species are present in plumage of Australian birds, we questioned if trapping method influenced microbial loads. We expected microbial abundance on birds caught with mist nets, a device used on birds in flight, would be of a lower abundance than those captured with snap traps, a tool which restrains the bird in the soil. The abundance of microbes on Eastern Yellow Robins *(Eopsaltria australis)* captured in both trap types was compared by sampling each bird with Tryptic Soy Agar contact plates at the back, tail, and venter. After statistical analyses using t-Tests in SPSS, the data were significant overall ($p = 0.004$), but when comparing data from specific parts of the bird, capture method was only a significant factor on the back ($p = 0.039$; $p = 0.055$ and 0.125 on tail and venter, respectively). We assume that our methodologies have created a detection limit in our data, leaving our results inconclusive to whether or not method of capture is a factor in microbial abundance.

Board 17

AAINA GUPTA

Faculty Mentors: Ali Dhinojwala, Gaurav Amarpuri, and Dharamdeep Jain
Department of Department is the Department of Polymer Science, University of Akron

Many commercial glues that are used today become less sticky under high humidities. We are studying spider glue, which is known to become stickier as the humidity increases, so ultimately a commercial glue can be produced. To study only the glue properties, an apparatus was used to transfer the glue to a substrate. This was done to study the surface energy and other properties of the spider glue.

CHARACTERIZING SPIDER GLUE PROPERTIES BY MANIPULATION OF LARGE GLUE VOLUMES

Many commercial glues that have been developed have a one thing in common: the reduction of adherence under high humidity environment. However, spider species catch insects using glue even under humid conditions. We studied Larinioides cornutus, an orb spider. Throughout the different sectors of the web, there are glue droplets that are very similar in size and evenly spaced. It is important to study the properties of the glue because it will allow us to develop a commercial glue with similar properties. Spider glue consists of both low molecular weight molecules, proteins, and water. The glue on the underlying flagelliform can be described as a bead on a string and both are made up of different proteins, which makes it difficult to analyze the properties of the glue alone. My project this summer sought out the problem of transferring the glue to a substrate to collect the glue in bulk quantities, something that has not been reported in literature before, for analysis without the flagelliform transferring. From recent studies, it was found that at high humidity the fluidity of the glue increases and allows the glue to properly adhere to different surfaces. Through many modifications, I was able to make an apparatus that allowed for the glue transfer at high humidity. By comparing the control (untouched) slide with glue slide, it was concluded that the glue had transferred successfully to the substrate. This was able to occur because the glue has a property known as cohesive failure. This means that at high humidity some portions of the glue would transfer to the substrate, while some would stay on the spider silk (more than 50% would transfer). With the success of the transfer, we had the ability to analyze the properties of the glue further. Through the help of other colleagues in the lab, we can further test the surface energy of the glue through JKR and quantify the viscoelasticity of the glue through particles transfer.

Board 18

DANIEL DELATTE

Faculty Mentor: Leila Pinchot
Forest Service Northern Research Lab

Total Leaf Area increases with light while Specific Leaf Area decreases with light. This study aimed to observe the structure of leaves as they grew positioned differently on different trees where some were shaded more than others in order to see if they would build up more of a tolerance to the Dutch Elm Disease. We believed the trees with smaller leaf sizes spent more of their energy into producing a defense system strong enough to combat the disease making it tolerant. We also wanted to create a formula from the information gathered in the process to be able to in the future gather leaf mass in a non-destructive manner after gathering the midrib length of a leaf.

ELM MORPHOLOGY

Dutch Elm Disease (DED; *Ophiostoma novo-ulmi)* is an invasive fungus that attacks several species of elm *(Ulmus sp.)* native to the United States and Canada, including American elm *(Ulmus americana)*. To examine the potential trade-off between growth and DED-tolerance, we evaluated leaf morphology 1. between American elms tolerant and susceptible to DED, and 2. among three tree canopy positions: high, intermediate, and low. We hypothesized that elms with tolerance to DED would allocate less energy to leaf growth, which we assessed using leaf area, dry mass, and specific leaf area (SLA). Leaf area and dry weight were greater in the high canopy than low canopy position in the DED-tolerant cultivars, but not for the susceptible cultivar. Differences in dry mass and leaf area between tolerant- and susceptible elm- may be explained by tree form of the cultivars rather than tolerance. Across cultivars, SLA of low-canopy leaves was 20% greater than that of high-canopy leaves. In our study American elm, a fast-growing species, allocates more energy to upper canopy than lower canopy leaves, suggesting that elm has a flexible growth strategy. This study will inform future studies evaluating trade-offs between growth and DED-tolerance.

Board 19

YUXIAO TAN

Faculty Mentor: Jin-Xiong She
Department of Genomic Medicine,
Augusta University, Augusta, GA

Cancer cells derive from cells with multiple gene mutations and end up with infinite life span. Some mutations lead to anti-cancer drug resistance or increased level of expression of other genes, such as *SLC7A11*. In this project, the expression level of *SLC7A11* was decreased using siRNA. We found that cancer cells with decreased expression level of *SLC7A11* have lower survival rate under anti-cancer drugs treatment.

KNOCKDOWN OF GENE *SLC7A11* IN OVCAR8 CELLS INCREASES SUSCEPTIBILITY OF CELLS TO ANTI-CANCER DRUGS

Multiple genes have increased expression level in cancer cells, some of which correlate with resistance to anti-cancer drugs and poorer patient survival rates. *SLC7A11* is a gene that codes for the membrane protein xCT, a member of a heterodimeric Na^+ independent anionic amino acid transport system that highly specific for cystine and glutamate. Downstream to the transportation pathway, cystine is rapidly reduced to cysteine, which is a precursor of synthesis of Glutathione (GSH). Production of GSH limits over accumulation of reactive oxygen species (ROS) and prevents ferroptosis, a non-apoptotic form of cell death. *SLC7A11* has been shown with increased expression level in majority types of vivo cancer cells. Limiting GSH synthesis by decreasing *SLC7A11* expression becomes a potential pathway of killing cancer cells. In this project, siRNA screening tested six different siRNA sequences, and knockdown efficiency was determined using RT-qPCR. OVCAR8 cell viability test after drug screening indicated that treatment with selected *SLC7A11* sense siRNA had markedly decreased survival rate in combination with drugs than either drugs or knockdown alone. Based on the results of drug screening, a synergic effect was demonstrated between *SLC7A11* knockdown and drug treatment. Thus, we concluded that knockdown of *SLC7A11* could increase the susceptibility of OVCAR8 cells to anti-cancer drugs and promote drug efficiency.

Board 20

JUDE FAHOUM

Faculty Mentor: Herbert DuPont-OWU Class of '61
Center for Infectious Diseases at the University of Texas School of Public Health

The unnecessary overuse of antibiotics has set obstacles in the progressive pathway such wonder drugs paved for medicine. One example can be seen through the increase in healthcare-associated bacterial infections mainly caused by *Clostridium difficile*. The most effective treatment for *Clostridium difficile* infections (CDI) is Fecal Microbiota Transplantation (FMT) in which stool from healthy donors is administered to patients with CDI through enema or pills. This study aimed to find a biomarker that can serve as a predictor for success/failure of FMT in the tens of thousands of patients seen each year with this complication.

BIOMARKERS EVALUATED AS PREDICTORS OF SUCCESS OR FAILURE OF FECAL MICROBIOTA TRANSPLANTATION (FMT) IN PATIENTS WITH MULTIPLE (≥3) BOUTS OF *CLOSTRIDIUM DIFFICILE* INFECTION (CDI)

Clostridium difficile infection (CDI) is the most common hospital-associated infection resulting in 70% of all fatalities from diarrhea-causing pathogens in the U.S. It develops in people with depleted gastrointestinal microbiota and recurs in 25% of patients (RCDI). The treatment of choice for RCDI is microbial restoration through a process called fecal transplantation using healthy donor bacteria which cures ~90% of patients after a single transplantation. There is currently no biomarker to see which patients with CDI should receive FMT and nor is there one to predict the success/failure of FMT in the hundreds of thousands of patients seen each year in the United States with this complication.

The goal of this study was to find biomarkers predictive of success/failure of FMT. Fifty-one subjects with ≥ 3 CDI bouts undergoing FMT at University of Texas Program for Restoration of Intestinal Microbiota and providing stool samples at days 0 (pre-FMT) and days 7, 14 and 30 (post FMT) were enrolled. The stool samples were assayed for inflammation biomarkers, calprotectin and lactoferrin, and markers of *C. difficile* (CD), CD antigen (GDH) and CD toxins A/B by commercial immunoassay, using positive and negative controls and standard curves. FMT recipients were grouped into successful or unsuccessful based on cure or recurrent CDI during the 2 months after FMT. Subjects becoming ill requiring anti-CD therapy before they could provide the four stools were excluded from the study.

51 subjects undergoing FMT for RCDI provided four stool samples. The small quantity of stool available did not allow all studies to be performed at all time points for some subjects, explaining different assay numbers. Median fecal lactoferrin concentrations at four respective time points showed non-significant increases in the groups failing treatment (n=16): 2,114 ng/ml; 5,882 ng/ml; 4,764 ng/ml and 2,025 ng/ml versus those cured (n=35): 735 ng/ml; 1,812 ng/ml; 1,072 ng/ml; and 882 ng/ml (P=0.1738). The median calprotectin concentrations in the respective stools from 16 subjects failing FMT were: 0 µg/g; 7,493 µg/g; 1,670 µg/g and 0 µg/g versus 0 µg/g for each of the four samples provided by the 34 subjects cured (P = 0.001). Presence of fecal GDH in the four respective stools in the 15 subjects failing FMT were more often positive: 1 (6.7%); 11 (73.3%); 8 (53.3%); and 8 (53.3%) versus the samples provided by the 34 subjects with cures: 1 (2.9%); 4 (11.8%); 7 (20.6%) and 7 (20.6%) (P=0.001). Presence of fecal CD toxins occurred in a greater frequency in the 16 subjects studied failing FMT: 2 (13%); 12 (75%); 8 (50%); 4 (25%) versus the 35 cured subjects: 2 (5.7%); 0 (0%); 0 (0%) and 0 (0%) (P<0.0001).

The study identified fecal markers predictive of success or failure of FMT in the management of multiple recurrent CDI. All values were similar comparing pre-FMT samples in the subjects who failed treatment or were cured. On day 7 after FMT a divergence became obvious. Presence of fecal calprotectin, CD antigen (GDH) and CD toxin(s) at that point after FMT were highly predictive of clinical failure of the microbial restoration treatment. Limitations of the study include a subset of subjects failing FMT before 30 days being excluded from the study, minimizing the number of failures in the study. Also, fecal samples were insufficient in quantity to perform all assays in given subjects. This study identified three strong fecal marker predictors of success in FMT: calprotectin, GDH and CD toxins. The findings have therapeutic and prognostic implications for treatment of this important chronic disorder seen in subjects receiving antibiotics or being confined in hospitals.

Board 21

XI PENG

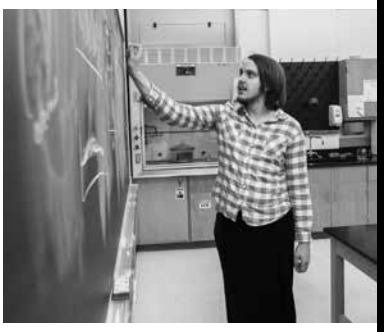
Faculty Mentor: Daniel Lacorazza
Department of Pathology, Baylor College of Medicine & Texas Children's Hospital Feigin Center

Acute myeloid leukemia (AML) is a malignant disease of the bone marrow, in which the bone marrow starts to make blasts that have not completely matured. The mechanism of the developmental arrest in AML is under study, but previous studies have shown that the expression of Krüppel-like factor 4, a transcription factor, is repressed in AML cell lines and patient samples. We are studying whether overexpressing KLF4 has any effects on cell growth rate, cell cycle, cell differentiation, and apoptosis in the AML cell lines that previously do not have KLF4 expression. Understanding the role of KLF4 in AML will lead to a better understanding of the disease on the molecular level, and may lead to more effective treatments.

EFFECTS OF KRÜPPEL-LIKE FACTOR 4 OVEREXPRESSION ON CELL GROWTH RATE, CELL CYCLE, CELL DIFFERENTIATION, AND APOPTOSIS IN ACUTE MYELOID LEUKEMIA CELL LINES

Acute myeloid leukemia (AML) is a malignant disease of the bone marrow, in which hematopoietic precursors are arrested in an early stage of development. The mechanism of the developmental arrest in AML is unclear, but previous studies have shown that the Krüppel-like factor 4 (KLF4), a transcription factor that regulates proliferation, differentiation, apoptosis and somatic cell reprogramming, is repressed in AML cell lines and patient samples. The restoration of expression is expected to inhibit cell growth and promote differentiation. The hypothesis is that KLF4 acts as a tumor suppressor in AML by regulating monocyte differentiation and cell cycle progression. KLF4 overexpression in two AML cell lines (NB-4 and MM6) was induced via retroviral transduction with the retroviral supernatant produced by calcium phosphate transfection of 293T cells. The NB-4 or the MM6 cells were transduced with either the empty vector MIGR1 (LTR-iRES-GFP-LTR), or MIGR1-KLF4 (LTR-KLF4-iRES-GFP-LTR). The transduced NB-4 cells were sorted using the flow cytometer, and the live cells with high GFP+ expression were collected for cell growth rate monitoring, cell cycle analysis, Annexin V apoptosis detection, and cell differentiation analysis via surface markers detection (CD14, CD16, CCR2, CD33, and CD66b). The results suggested that KLF4 overexpression repressed the cell growth rate significantly, increased the cell population in the SubG1 phase, and decreased the cell population in the S phase in the NB-4 cell line. The surface markers detection showed that KLF4 overexpression increased CD14 expression in both cell lines suggesting differentiation, and resulted in a significant larger apoptotic population in the NB-4 cell line. The observations suggested that KLF4 overexpression could contributes to the cell cycle arrest and apoptosis in AML cell lines, which was consistent with the initial hypothesis.



Board 22

JORDAN BROWN

Faculty Mentor: Daniel Amador-Noguez
Department of Bacteriology, University of Wisconsin-Madison

4 strains of the biofuel producing bacteria, *C. thermocellum*, were engineered with differing pathways for the conversion of phosphoenolpyruvate (PEP) to pyruvate. The strains were analyzed from an integrated metabolomics and thermodynamic point-of-view. Finding the optimal pathway for this conversion is a step towards optimizing the bacteria as a whole to more effectively produce ethanol from cellulosic biomass.

METABOLIC AND THERMODYNAMIC ANALYSIS OF *C. THERMOCELLUM* STRAINS ENGINEERED FOR HIGH ETHANOL PRODUCTION

Ethanol is a carbon neutral fuel that can be produced from the microbial conversion of cellulosic biomass. One microorganism that is being engineered to perform this conversion is the aerobic thermophillic bacteria, *Clostridium thermocellum*. Past efforts that focused solely on metabolomic analyses have been able to increase ethanol production, but only up to a certain amount. Studies show that the overall pathway of this conversion is not as energetically favorable as in other biofuel producing strains. This causes the conversion of cellulose to ethanol to proceed slowly and, in some cases, allows for reactions in the pathway to proceed in reverse. By making the change in free energy (ΔG) more negative at key steps in the reaction, the overall reaction will become more spontaneous and proceed at a faster rate. This would increase ethanol production, and drive down the price, allowing ethanol-based biofuels to better compete with fossil fuels at the pump.

One key step in the pathway to be optimized is the conversion of phosphoenolpyruvate (PEP) to pyruvate. *C. thermocellum* utilizes the Emben-Meyerhof-Parnas (EMP) pathway, but unlike other bacteria that use this pathway it does not have the enzyme pyruvate kinase (PYK), which catalyzes the direct conversion of PEP to pyruvate. Instead it utilizes two different pathways. One is the direct conversion of PEP to pyruvate by a different enzyme, pyruvate phosphate dikinase (PPDK). This pathway has been experimentally shown not to be able to be the sole pathway in PEP to pyruvate conversion. The other pathway is the malate shunt, which uses PEP carboxylase (PEPCK), malate dihydrogenase (MDH) and malic enzyme (ME)[1]. This pathway has been shown to be able to be the sole PEP to pyruvate pathway.

Board 23

LIZ URBANSKI

Faculty Mentor: Graydon Gonsalvez
Department of Cellular Biology and Anatomy,
Augusta University

A patient's undiagnosed disease has similar characteristics to the ciliopathies Lowe Syndrome and Dent Disease. A mutation in the patient's FAM109 gene was found, and may be causative of the disease. Since very little is known about FAM109, studying its localization, function, and relationship to other genes associated with Lowe Syndrome and Dent Disease is necessary to understand the role of this gene in the patient's undiagnosed disease.

EXAMINING THE ROLE OF FAM109 IN AN UNDIAGNOSED DISEASE

The National Institutes of Health Undiagnosed Disease Program identified a de novo arginine to cysteine mutation in a patient's FAM109A gene (R6C). The human genome contains two FAM109 genes, FAM109A and FAM109B. The patient presents with disease characteristics reminiscent of a ciliopathy, a type of disease that results from mutations in OCRL, an interacting partner of FAM109. The aim of our project was to identify the functions and localizations of the FAM109 paralogs and determine if the R6C mutation is causative of the patient's disease. HeLa cells were treated with antibodies against various cellular components to determine the localization of FAM109A and FAM109B. Immunofluorescence showed co-localization between FAM109A and the midbody marker MKLP1, as well as with the Golgi marker 58K. OCRL was found to co-localize with FAM109A and MKLP1 at the midbody. GFP-tagged wildtype and mutant constructs of FAM109A were transfected into HeLa cells and the phenotype of these cells was analyzed by immunofluorescence. Transfected mutant isoforms of FAM109A did not affect the ability of FAM109A to localize to the midbody. Immunofluorescence with FAM109B showed localization with the mitochondrial marker Cox IV, and transfection with FAM109B siRNA led to cell death. We hypothesize that the cell death is occurring via apoptosis. Our findings reveal that FAM109A localizes to both the Golgi and the midbody, while FAM109B localizes to the mitochondria. Mutant isoforms of FAM109A localize to the midbody in an identical manner to the wild type, and co-localization at the midbody with OCRL has been validated. The specific functions of the FAM109 paralogs remain largely unknown and will be the topic of future studies.

Board 24

ERIC BAUGHMAN

Faculty Mentor: Frank Secreto
Department of Molecular Pharmacology and Experimental Therapeutics, Mayo Clinic

Hypoplastic Left Heart Syndrome is a congenital heart defect in which the left side of the heart fails to develop and function properly. Specific and definitive causes are yet to be identified with the disease, but studies of certain families, such as the 2H and 14H families, can provide insights into these relations. In the 14H family, the mother has a mutation in the gene for NOTCH1, which is vital during heart development, and she passed this mutation on to her child. Through the use of patient derived stem cells, called human induced pluipontent stem cells, we differentiated the cells into beating heart muscle under different conditions to test the influence of this specific mutation, and thus the overall gene, to the development of HLHS.

CHARACTERIZATION OF CARDIOMYOCYTE DIFFERENTIATION INVOLVING HLHS HIPS CELLS HARBORING A MUTATION IN THE PROMOTER REGION OF NOTCH1

Hypoplastic Left Heart Syndrome (HLHS) is a congenital heart defect in which associated genetic mutations have yet to be established. The 14H family is of particular interest due to the afflicted child (proband) having inherited a single base pair mutation in the promoter region of NOTCH1. Notch/Activin/NO signaling is critical for cardiac development, and studying the potential dysregulation may provide an underlying mechanism explaining the development of HLHS. Previous studies conducted in the Nelson lab on 2H family indicated that human induced pluripotent stem cells (hiPSCs) carrying a mutation in the ORF of NOTCH1 failed to differentiate into cardiomyocytes without NO supplementation. Based off this study design, we differentiated 14H family hiPSCs using spermine NONOate, an NO donor, and sildenafil, a protector of Notch/Activin/NO signaling. Beating activity was unaffected by the drugs in any of the clones. However, no beating activity was recorded in the absence of Wnt modulation. Expression of genetic marker expression by RT-qPCR supported these conclusions, specifically that modulation of Wnt signaling enhanced cardiomyocyte differentiation. Immunoblotting assays targeting NOTCH1 and the downstream Notch/Activin/NO pathway components Akt and eNOS showed no proband-specific differences compared to hiPSCs and hiPSC derived cardiomyocytes. Overall, this pilot study demonstrated that the mutation present was insufficient to affect NOTCH1 protein or RNA expression as well as beating activity. However, before a conclusion can be made regarding this mutation's potential effect on cardiomyocyte and HLHS development, a broader study needs to be undertaken.

Board 25

HOLLY LATTEMAN

Faculty Mentors: Emily Kuzmick and Frank Lopez
Ohio Department of Natural Resources/Ohio Division of Wildlife

Citizen Science is the incorporation of the public, with proper training, in ongoing or beginning research questions. I worked with Bald Eagle nesting data to form predictions as to the cause of recent nest failure. I created the Avian Monitoring Program at Old Woman Creek National Estuary Research Reserve/Ohio Division of Wildlife, in order to better understand the species present as well as how species are affected by climate.

OBSERVING SPECIES PHENOLOGY THROUGH CITIZEN SCIENCE

Citizen Science programs are created with the idea of achieving public support for growing and monitoring initiatives of various native species. The species or area of study is usually of particular concern or interest. Initiatives are used as a teaching tool for the public and help to encourage the use of nature preservation systems. My research was performed through the Ohio Division of Wildlife/National Estuary Research Reserve System of Old Woman Creek in Huron, Ohio. The research aimed to address the importance of the reserve to the species that inhabit it, while also addressing concerns and issues seen in previous years. For the first part of my research, I analyzed Bald Eagle *(Haliaeetus leucocephalus)* nesting data and developed hypotheses about the recent abandonment of nests in previous years. Several hypotheses regarding the reasoning behind abandoned nests were made based on behavioral changes in the parents. For the second part of my research, I created a method of monitoring avian species in the reserve. The reserve is located on Lake Erie and is a major stopover point for migrating avian species. This is an ongoing project with interspecies comparisons of phenological, spatial, and temporal data. The data collected thus far have revealed intriguing findings as to the amount of species present, temperature dependency, and habitat overlap at the reserve. This research also aims to analyze the importance of the reserve for spring and fall migration routes of avian species.

The NSF-funded REU (Research Experience for Undergraduates) program at Ohio Wesleyan makes it possible for students from universities across the country to do research in the fields of astronomy, computer science, mathematics, and physics on the OWU campus.




Board 26

ELIZABETH SARKEL

WAKE FOREST UNIVERSITY
NASA STUDENT ASSOCIATE

Faculty Mentor: Chris Wolverton
Department of Botany and Microbiology

Plant roots need to grow vertically into the ground so they can reach water and nutrients. When roots are disturbed from growing vertically, they release a series of signaling molecules that allow them to bend while growing so they can resume vertical growth. This research project evaluates the roles of two types of signaling molecules that counteract each other, flavonols and reactive oxygen species, in initiating the growth responses that allow roots to resume vertical growth.

REACTIVE OXYGEN SPECIES (ROS) AND FLAVONOLS MODULATE THE ROOT GRAVITROPIC RESPONSE

During the gravitropic response, a root disturbed from its vertical orientation will grow asymmetrically so that it returns to the vertical orientation. We are testing the roles of reactive oxygen species (ROS) and flavonols, which are plant metabolites that scavenge ROS, as signals that control *Arabidopsis* root gravitropism. The *tt4* mutant, which makes no flavonols, has delayed gravity response, but treatment with the flavonol precursor naringenin restores wild-type gravitropic response. When wild type seedlings are treated with naringenin, root gravitropism shows an initial delay, but overall is enhanced and continues past vertical. Higher levels of ROS were visualized by confocal microscopy in *tt4* using the ROS sensor DCF, consistent with flavonols as ROS scavengers. *Treatment* with 3-aminotriazole (3AT), which inhibits catalase, an enzyme that degrades hydrogen peroxide, inhibited gravity response, consistent with elevated ROS interfering with root gravitropism. Additionally, experiments are being performed to quantify the gravitropism of the *respiratory burst oxidase (rboh)* mutant family, which have defects in signaling induced ROS synthesis. We have also examined the distribution of ROS and flavonols across roots reoriented 90 degrees relative to gravity. *Arabidopsis* seedlings expressing *pCHS*:CHS:GFP, a reporter that visualizes the site of expression of chalcone synthase, the first enzyme of flavonoid biosynthesis, show elevated GFP signal on the lower side of the root where auxin accumulation inhibits growth. Current experiments seek to resolve the timing and location of flavonol synthesis, ROS accumulation, and auxin accumulation using mutants, inhibitors, reporter constructs, and the feedback response system ROTATO, which continuously gravistimulates the root by holding it at a constant angle. These experiments will provide insight into the auxin and ROS signals that control root gravitropic response. (Supported by an ASPB SURF to ERS)

Board 27

KSENIA KLUE[1*] AND MIHAELA PAULA SUCIU[2*]

[1] **COLLEGE OF WOOSTER**
[2] **GEORGE MASON UNIVERSITY**
[*] **OWU NEUROSCIENCE REU STUDENT**

Faculty Mentor: Surendra Ambegaokar
Department Botany and Microbiology, Neuroscience Program

The gene microRNA-7 is thought to have a role in brain development and several disorders including Alzheimer's disease, the sixth-leading cause of death in the United States. Studying how levels of microRNA-7 expression changes in brain cells as they grow and mature will allow better understanding of how microRNA-7 functions in healthy neurons, and what might be going wrong in diseases. Such knowledge could contribute to new therapies for Alzheimer's disease, improving the lives of many.

THE ROLE OF *miR-7* IN NEURONAL DIFFERENTIATION

MicroRNAs (miRNAs) are negative regulators of gene expression. Previous research has found microRNA-7 *(miR-7)* expression may be altered in neurobehavioral disorders, such as schizophrenia or Alzheimer's disease; however research is inconclusive as to its role. Previous data have also found expression in developing brains of animals, but there are uncertainties as to whether *miR-7* promotes or inhibits neuronal differentiation, or if *miR-7* expression has any effect at all on neuronal differentiation. Our research uses SH-SY5Y cells, which are human glioblastoma cells that have neuronal progenitor-like properties, in that they can be induced to differentiate into neuron-like cells when treated with retinoic acid (RA). We examined if *miR-7* expression changes during the course of differentiation. We also examined if overexpressing *miR-7* was sufficient to induce neuronal differentiation, as measured by morphology and expression of neuronal-specific genes. We found *miR-7* expression goes down during differentiation. In support of this, *miR-7* overexpression was not sufficient to induce differentiation; however expression of some neuronal markers increased, which suggests *miR-7* may have a partial and more complex role in differentiation. This research will better inform our understanding of microRNA function, and the potential use of miRNAs as therapeutic targets in neurobehavioral disorders.

CLAIRE PLUNKETT

CASE WESTERN RESERVE UNIVERSITY

OWU PHYSICS/ASTRONOMY AND MATH/CS REU STUDENT

Faculty Mentor: Craig Jackson
Department of Mathematics and Computer Science

Due to changing climates and habitat destruction, better understanding what influences the stability of ecosystems is increasingly important. Using data previously collected on plankton population sizes, we investigated how different definitions of stability relate by using a mathematical model to calculate stability in various ways. Additionally, we explored how the presence of weak links in a food web is related to stability.

INTEGRATING THEORETICAL AND EMPIRICAL DEFINITIONS OF ECOLOGICAL STABILITY: ARE THEY MEASURING THE SAME THING?

In ecology, the topic of stability has been studied from both empirical and theoretical perspectives, leading to potentially conflicting definitions of stability. Theoretical stability depends on the community matrix of interaction strengths while empirical stability is often calculated as temporal variability of individual species and community populations. While studies have shown that measures of empirical stability are often related and measures of theoretical stability are often related, the connections between theoretical and empirical stability have yet to be sufficiently investigated.

In this study, we investigate the connection between different measures of theoretical and empirical stability using data from a freshwater plankton mesocosm experiment. Further, we explore whether stability is related to the presence of weak interactions, which are often thought to be stabilizing. We find that stability is correlated with interaction strength in 13 of 21 comparisons. Also, we find 2 significant relationships between empirical stability and interaction strength out of 21 comparisons, but we do not find any significant correlations between theoretical and empirical stability measures. This suggests that empirical and theoretical stability are measuring different attributes.

KENDRICK HARDISON

FRANCIS MARION UNIVERSITY

OWU PHYSICS/ASTRONOMY AND MATH/CS NSF-REU STUDENT

Faculty Mentor: Scott Linder
Department of Mathematics and Computer Science

Clinicians search for presence of a disease by examining a handful of particular gene locations known to be closely associated with it. When measurements are taken at these gene locations, they are compared to similar measurements taken on a large number of controls. Here we examine the sampling distribution of a rank sum statistic obtained by comparing measures of the case to corresponding measures of the control. We derive the exact distribution, compare it to an approximate distribution proposed in the literature, and then demonstrate that use of the approximate distribution leads to an overstatement of the test's power and an understatement of Type 1 error risk.

A RANK-SUM TEST FOR SIGNIFICANCE OF DIFFERENCE IN COPY VARIATION

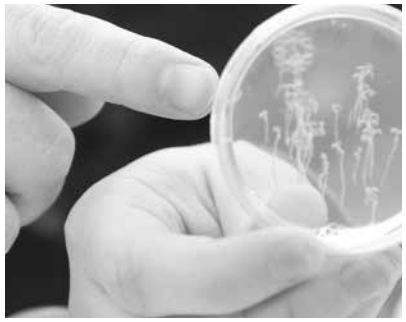
Copy number variation (CNV) results from duplications and deletions of genomic DNA, and is known to correlate with a number of genetic diseases. Typically, a subject being screened for a particular disease will have measurements from k sections of DNA, and these measurements are compared to those from a collection of N controls. Here we describe a rank sum statistic useful for determining whether the subject is at risk for disease.

We derive the exact distribution of this statistic and compare the exact distribution to an approximate distribution proposed in the literature. We demonstrate that use of the approximate distribution of the rank sum statistic results in higher than nominal Type 1 error rate and an exaggeration of power.


Leica 200M 2000

Graduation with Honors in Scholarship requires an independent project, an oral exam on the project, and a comprehensive exam in the student's major department during the senior year. The program is open to students who have attained cumulative grade point averages of 3.5 in their majors after fall semester of the junior year, as well as overall grade point averages of 3.0 or the support of their academic major departments, and have successfully petitioned the Ohio Wesleyan Academic Policy Committee.

Student Name	Supervising Professor	Title
Morgan Christie	Sarah Bunnell	Conversations About Race: Parent-child Conversations About Race and Implications for Adolescent Coping and Color-blindness
Jessica Harpel	Vicki DiLillo	Motivational Strategies Encouraging Influenza Prevention Behaviors Using the Health Action Process Approach
Khanh Le	Craig Jackson	Specializations of the Lawrence Representations of the Braid Groups at Roots of Unity
Khanh Le	Barbara Andereck	Approximation Methods for the On-Dimensional Time-Independent Schrödinger Equation
Sarah Lucas	Mark Gingerich	With Brave Wings She Flies: Recovering the Stories of Women Pilots in World War II
Onyinye Okoli	Mary Anne Lewis	The Persistence of Scientific Racism in Azouz Begag's Béni Ou Le Paradis Privé
Selena Ross	Lee Fratantuono	Tenui Auro: A Look at Spinning and Weaving in 'Golden Age' Rome
Nam Tran Hoang	Craig Jackson	A Recursive Formulation for the Rank-Sum Statistic used to detect Genomic Copy Number Variation
Tyler Wake	Julide Yazar	Misperception of Probabilities and All Pay Auctions: Evidence from Behavior in an Equivalent Lottery
Emily Webb	Shala Hankison	Birds and Blooms: Understanding Avian Florivory Through Chemical Analysis

HERE ARE SOME OF THE THINGS PAST SSRP PARTICIPANTS ARE DOING NOW.

Eric Baughman, ’17
Mayo Clinic, Rochester, Minnesota, working on regenerative health, specifically having to do with the heart and diseases in the heart that currently have no cure, returning to OWU for senior year in the fall.

Alex Landgraf, ’16
Attend the University of Toledo for a Ph.D. program in chemistry and biochemistry.

Luke Steffen, ’16
Summer of 2016: Philmont Scout Ranch, the largest scout camp/cattle ranch/wilderness reservation combination (214 square miles) near Cimarron, NM as a historical interpreter/reenactor.
Fall of 2016: National Geospatial Intelligence Agency (NGA) — cartography/GIS and human geography research to assist with the missions of the US military and the Federal Government in Springfield, VA, or St. Louis, MO.

Meghan Schulze, ’16
This summer – studying for the MCAT and applying for medical school.

Maddie Vroom, ’16
Starting graduate school Ph.D. program at University of Florida, Department of Microbiology and Cell Science.

Jess Gooden, ’16
Applying to Physical Therapy school this fall.

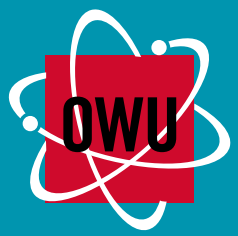
Elizabeth Kurowski, ’16
Attending University of Connecticut Health Center, Ph.D. program in Biomedical Sciences: Genetics and Development.

Campus and Off-Campus Researchers

NSF-REU Researchers

Special Thanks

Rock Jones
Charles L. Stinemetz
Karen McNeal
Laurie Patton
Dale Swartzentruber
Ohio Wesleyan University Buildings and Grounds Staff
OWU/Aramark Housekeeping staff
Chartwells Dining Services
Office of University Communications
Faculty supervisors and student volunteers
Parents and guardians of student researchers



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