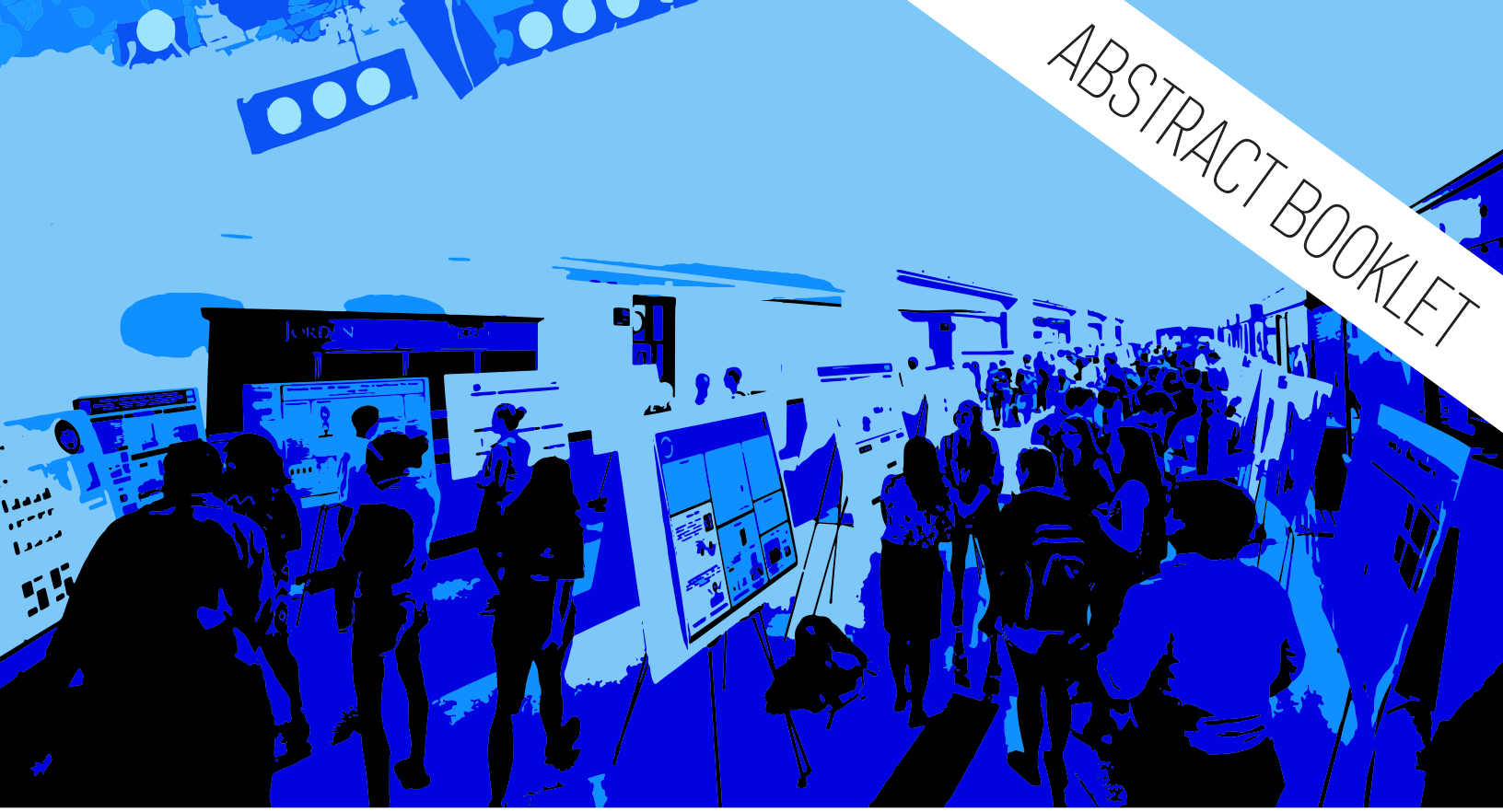

ABSTRACT BOOKLET

COS JAM 2022

COLLEGE OF SCIENCE JOINT ANNUAL MEETING

Wednesday, April 27th · 1-5 PM · JORDAN HALL GALLERIA

1:00-2:00	"The Era of Science" by Santiago Schnell, D. Phil.
2:00-3:15	Concurrent Session talks
3:30-5:00	Poster Sessions & Spirit of Science Presenters (refreshments will be provided)

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Table of Contents

COS JAM Schedule

- 1:00 pm - 2:00 pm | 105 Jordan
  "The Era of Science" by Santiago Schnell, D. Phil.
  William K. Warren Foundation Dean of the College of Science, Professor of Biological Sciences, Professor of Applied and Computational Mathematics and Statistics
- 2:00 pm - 3:15 pm Concurrent Session talks
- 3:30 pm - 5:00 pm Poster Sessions & Spirit of Science Presenters (refreshments will be provided)

Concurrent session 1:
Jordan 101
Moderator: Dr. Michelle Whaley, Teaching Professor of Biology
Co-moderator: Becca Kubick, Maeve Murdock

2:00-2:15	Examining the functional relationship between ESX-1 substrates MMAR_2894 and PPE68 in Mycobacterium marinum **Khang Chau, Emma Eckstein, Evan Peters, Meghan Fries, Elizabeth Jasek**
2:15-2:30	Elucidating the Role of Formin Proteins in Early Sensory Neural Development **Stella Cho**
2:30-2:45	Investigating Cellular Senescence as a Novel Treatment for Pediatric Glioblastoma **Regan Hines**
2:45-3:00	A Single RNA Modification Destabilizes a Pyrimidine-Motif RNA●DNA-DNA Triple Helix **Grace Schiefelbein**
3:00-3:15	Characterizing the Retinal Pigment Epithelium During Zebrafish Neuronal Regeneration **Shannon Steines**

Concurrent session 2:
Jordan 105
Moderator: Dr. Benedicte Fustec

2:00-2:15	Effect of Temperature on Infection of Biomphalaria glabrata by Schistosoma mansoni: An Assessment of the effects of Climate Change on Transmission Risk of Human Schistosomiasis **Caroline Bice**
2:15-2:30	Estimating risk of emerging infectious diseases: a review of tick-borne pathogens in Kenya, Belize, and Florida, USA. **Margaret Elliott**
2:30-2:45	Survey of human pathogens from tick samples collected in Corozal and Orange Walk Districts, Belize, Central America **Caroline Pitts**
2:45-3:00	The Challenges of Zoonotic Disease Spillover Surveillance: Learning from a Literature Review and an Experience in Florida **Brooke Rodriguez**
3:00-3:15	Wait, Should I Even Have Kids? — Redefining “Your 20s” in the Daunting Anthropocene **Caroline Zlaket**

Concurrent session 3:
Jordan Reading Room
Moderator: Dr. Manoel Couder, Associate Professor of Physics

2:00-2:15	Cleaning up RIBs with TriSol **Sydney Coil**
2:15-2:30	Radio Frequency Quadrupoles Studies and Design for St. Benedict **Jamie Harkin**
2:30-2:45	Commissioning of the St. Benedict Radiofrequency Carpet **Carrie Davis**
2:45-3:00	Development of Beam Profile Analysis Application: Design and Implementation **Joseph Henning**
3:00-3:15	Measurement of PFAS in Chicken Egg Yolk and Development of Standards using Ion-Beam Analysis **William Kacey**

Poster session abstracts

College of Science, Department of Biological Sciences

Name	Abstract Title
Acevedo Amanda	Influence of Host Diet and the Environment on the Gut Mycobiome of Long-Tailed Macaques (Macaca fascicularis) in Southeast Asia
Anthuvan Jacob	Analysis of Membrane Vesicle Production by Mycobacterium Avium in Biofilm Settings
Bali Adviti	Efficacy of rAAV9 Gene Therapy in treated mice with attenuated Non-Ketotic Hyperglycinemia
Bice Caroline	Effect of Temperature on Infection of Biomphalaria glabrata by Schistosoma mansoni: An Assessment of the effects of Climate Change on Transmission Risk of Human Schistosomiasis
Bosio Sam	Ecological Linkages Between Amphibians and Wetland Vegetation in the Upper Midwestern USA
Brennan Livia	Investigating expression of PYGO2 as a potential prognostic marker in pan-cancer and specific cancer analyses through bioinformatic techniques
Curtis Erik	Periodical cicadas and leaf litter as allochthonous resource subsidies in nutrient-limited experimental streams
Chau Khang	Examining the functional relationship between ESX-1 substrates MMAR_2894 and PPE68 in Mycobacterium marinum
Hammond Catherine (group)	Analyzing phenotypic effects of current norpA mutants and genotype effects of novel norpA mutants in Aedes aegypti
Hines Regan	Investigating Cellular Senescence as a Novel Treatment for Pediatric Glioblastoma
Heston Emma	Long term impact on Juday Creek invertebrate populations from the 1997 restoration for construction of the University of Notre Dame Warren Golf Course, St. Joseph Co., Indiana
Hlavin, John (group)	Investigation of Aaop1 Cycling in Aedes aegypti and Aedes albopictus

Kerner Elizabeth	Unlocking Climate Science Literacy Through Art
Khouzam Nadim (group)	Processing and Analyzing data in order to establish trends in the unpredictability of Respiratory Syncytial Virus (RSV)
Kortick Genesee	An Assessment of the Herbicide Fluridone as an Invasive Aquatic Plant Treatment Option in Alaska (USA) Wetlands
Kowalkowski Hannah	Number of daily load cycles positively affects Haversian remodeling in the rabbit mandible
Mignondje Kossivi	Characterizing ESX-1-responsive proteins in Mycobacterium marinum
Nguyen Kayla	E. faecalis requires fibrinogen in re-catheterization in CAUTIs
Smith Carson	Medicinal plants in the diet of Macaca fascicularis may mediate microbiome variation associated with Plasmodium infection
Steines Shannon	Characterizing the Retinal Pigment Epithelium During Zebrafish Neuronal Regeneration
Sun Seunghoon	Senescence-associated secretory phenotype induces non-apoptotic cell death in normal mammary epithelial cells
Chou Brandon (group)	Transcriptomic Analysis of the Defensive Response to Emerald Ash Borer in Fraxinus pennsylvanica (green ash)

College of Science, Physics

Name	**Abstract Title**
Barbera Thomas	Development of Hodoscope for High-Energy Particle Detection: Precision Timing, Radiation-hard, Electromagnetic Calorimetry
Henning Joseph	Development of Beam Profile Analysis Application: Design and Implementation
Komater Dante	Dynamically Tagged Groups of Metal-Poor Stars from The Radial Velocity Experiment Data Release 6
Mikol Grace	Impact of Sustainable Announcements on Company Performance and Perception

College of Science, Department of Chemistry and Biochemistry

Name	**Abstract Title**
Bohling Sarah	Investigating the cellular functions and evolutionary history of cytoskeletal components in Porphyra umbilicalis and Rhodelphis
Chang Lucia	An Investigation of CRISPR Cas12a's potential as a Homing Guide System
Cheong William	1,3,5 Trithiane as a Sulfur Source in Metal Sulfide Nanoparticle Synthesis
Connelly Lauren	An Investigation of the Localization of *rhoV* mRNA in *Xenopus laevis* Oocytes and Potential Mechanisms of Animal-Hemisphere Localization
Fletcher David	Conformational Study of Apicularen A
Fulkerson Daniel	Impact of Targeted Mutations on Aquaporin-7 Structure and Breast Cancer Progression
Kautzky Jenna	Generation of a Collection of N-Heterocyclic Small Molecule Inhibitors of Protein-Protein Interactions Between DYRK1A and DCAF7
Weiss Laura	Investigating the structural properties of peptide-MHC complexes that contribute to immunogenicity

Department of Applied and Computational Mathematics

Name	Abstract Title
Lee John	Multi-fidelity Data Augmentation for U-Net Retinal Vessel Segmentation
Ruelle Julia	Assessing Exposure of Urban Air Pollution with Citizen Science Data

MD Anderson Cancer Center

Name	Abstract Title
Dineen Brian	Rimiducid's Effect on T Cell Development and Differentiation
Hollmer Lauren	Mathematical Modeling of the CA19-9 Response to chemotherapy in patients with pancreatic cancer
Robinson Kathryn	Anti-B7H3 Monoclonal Antibodies Induce Natural Killer Cell-Mediated Apoptosis In Triple Negative Breast Cancer
Wernecke Elena	Clinical characteristics may predict lymph node burden in hormone receptor-positive (HR+), human epidermal growth factor receptor 2-negative (HER2-) breast cancer patients

Neuroscience & Behavior

Name	Abstract Title
Aiello Christopher (group)	Evaluation of the Biological Activities of Echeveria fimbriata, Tradescantia pendula, and Sedum morganianum

Science Business

Name	Abstract Title
Chen Emily	Coping with stress on a college campus during COVID-19: cortisol, individual disposition, social support, and mental well-being among undergraduates

Marketing

Name	Abstract Title
Nunez Zoe	Getting Student Athletes Outside

Abstracts for all presenters

Acevedo Amanda (Poster #1)

Influence of Host Diet and the Environment on the Gut Mycobiome of Long-Tailed Macaques (*Macaca fascicularis*) in Southeast Asia

Amanda Acevedo
Majors: Biological Sciences and Anthropology
Advisor: Dr. Hope Hollocher, Department of Biological Sciences, University of Notre Dame
Co-Authors: Benjamin Gombash, Chissa Rivaldi, Carson Smith, and Hope Hollocher

Most studies concerning the microbiome have focused on bacteria. However, gut fungi (termed "mycobiome") remain relatively uncharacterized. Previous research attributes mycobiome variation to host diet variation. Although diet is implicated, the environment is rarely taken into account. To investigate the influence of diet and environment on the mycobiome, fecal samples were collected from long-tailed macaques (*Macaca fascicularis*) on Singapore and Bali, Indonesia. The diet and mycobiome were assessed by amplifying the V9 hypervariable region of the 18S ssu rRNA. Dietary and fungal taxa were categorized into groups (e.g., for diet: crop plants; for fungi: animal pathogens). Principal component analyses (PCA) were performed to identify groupings of environmental factors for each island. The PCA sorted the factors into "anthropogenic" or "physical" or a "mixture" of the two categories. After defining the taxonomic and environmental groupings, Multiple Factor Analysis (MFA) was used to search for interactions between diet, fungi, and environment. On Bali, MFA suggests that "anthropogenic" and "mixed" environmental groups more strongly influence the diet than the mycobiome, which is instead more strongly associated with the "physical" environment. Linear regressions showed that elevation is significantly related to core fungal richness, a direct relationship between the environment and fungi that is not tied to diet. However, diet may still act as an intermediary between fungi and "anthropogenic" and "mixed" environmental groups. Singapore's MFA suggests a more direct relationship between diet and fungi, and linear regressions revealed no environmental factors with a direct relationship to core fungal richness. Regressions show that diet richness is significantly related to fungal richness on both islands. These results confirm that the diet and mycobiome do interact in long-tailed macaques, but these interactions are not uniform between different populations of the same host organism and elevation plays a greater, more direct role in some contexts relative to others.

Aiello Christopher & Brown Melissa (Poster # 2)

Evaluation of the Biological Activities of *Echeveria fimbriata, Tradescantia pendula,* and *Sedum morganianum*

Christopher Aiello & Melissa Brown

Herbal medicine has a rich history but has been rejected in most parts of the world in favor of synthetic drugs and antibiotics. The implementation of herbal medicine in combination with modern medicine could provide solutions to the problem of antibiotic resistance that affects medicine today (Cunha 2000). *Echeveria fimbriata, Tradescantia pendula, and Sedum morganianum,* three plants endemic to Mexico, were identified for their applications in the medical industry based on previous findings from plants of their genera that indicated beneficial properties (Martínez et al. 2013, Tan & Kwan 2020, Zhu et al. 2009). These properties included treatment of intestinal infections, inflammation, fever, and potentially tumors. This study attempts to measure the feasibility of using *E. fimbriata, T. pendula and S. morganianum* in human medical contexts by evaluating toxicity, as well as testing antioxidant properties as a preliminary evaluation of one medical application. To measure antioxidant properties of the plants we used a DPPH radical model assay (Kedare and Singh 2011), and toxicity to human cells was estimated using a brine shrimp model (Sarah 2017). It was hypothesized that all plants would show low levels of toxicity and some level of antioxidant activity. The findings of this study partially supported this hypothesis with particularly promising results in the antioxidant activity of *E. fimbriata*. These results serve as a preliminary indication of medical applications of this plant species and call for further research on its beneficial properties.

Anthuvan Jacob (Poster # 3)

Analysis of Membrane Vesicle Production by Mycobacterium Avium in Biofilm Settings

Jacob Anthuvan

Non-tuberculosis mycobacteria (NTM) are environmental pathogens that are increasingly becoming a cause of infections in the United States, and are particularly dangerous in immunocompromised individuals. The American Lung Association reports that 86,000 individuals are currently living with NTM infections. *Mycobacterium avium* is the NTM that causes most of these infections in the United States. *M. avium* is present in various environmental locations including showerheads and soil and is known to form biofilms in these environments. Bacterial biofilms are compact communities of microbial cells which adhere to living or inert surfaces and encase themselves in secreted polymers. For my studies I evaluated some of the physical properties of the *M. avium* biofilms as well as evaluated their secretion of extracellular vesicles. I analyzed the integrity of *M. avium* biofilms following treatment with various enzymes to gain insight into the composition of the biofilm matrix. Membrane Vesicle (MV) release has been described for bacteria previously, but relatively little of this research has been done on biofilms. Biofilms require communication to foster their formation and degradation and MV release could potentially be mediating this communication. To begin dissecting MVs potential role in biofilm formation/degradation, I analyzed MV production by M. Avium grown in both liquid culture and within biofilms. The concentration and size of the MVs was defined using a NanoSight instrument. This instrument uses lasers to track MVs in solution to define concentration and speed of MV movement in solution to infer sizing of these particles. Initial results show that mycobacteria in biofilm and liquid culture produce similar amounts of MVs although average size may differ under the different experimental settings.

Bali, Adviti (Poster # 4)

Efficacy of rAAV9 Gene Therapy in treated mice with attenuated Non-Ketotic Hyperglycinemia

Adviti Bali, Caroline Bickerton, Shaun Calhoun, Prasad Padmanabhan, Alejandro Lopez Ramirez, Suhail Alam, Kasturi Haldar

Advisor: Kasturi Haldar, Center for Rare and Neglected Diseases, Dept. of Biological Sciences, University of Notre Dame

Non-Ketotic Hyperglycinemia (NKH) is a rare, neurometabolic disease characterized by a mutation in the *Gldc* gene. The *Gldc* gene codes for the enzyme Glycine decarboxylase (GLDC) or P-protein, a component of the Glycine Cleavage System (GCS). The lack of functional GLDC protein prevents glycine breakdown and leads to its accumulation in the blood and cerebrospinal fluid. High glycine levels lead to symptoms such as epileptic seizures, hypotonia, and severe developmental delays. Current treatment for NKH is directed towards symptom management and does not address the mutation causing the disease. Gene Therapy is a potential molecular treatment to address the lack of functional GLDC protein. The Haldar Lab designed a novel AAV9 viral vector recombinant with a copy of wild-type *Gldc*, prepared by Penn Vector Core (University of Pennsylvania). The virus enters cells via endocytosis and is expressed as an episome in the nucleus. In the nucleus, it can be transcribed and translated to produce functional GLDC protein. To test this hypothesis, homozygous mutant mice with the attenuated form of NKH were injected with rAAV9 virus particles either post-weaning or pre-weaning, and the dose was optimized. Injected mice were assessed for plasma glycine, survival, and neurological outcomes. Preliminary data suggest improvements in plasma glycine levels, neurological conditions, and animal survival. This experiment demonstrates the efficacy of rAAV9 gene therapy in treating the metabolic defect caused by *Gldc* mutations in mice with attenuated NKH.

Barbera Thomas (Poster # 5)

Development of Hodoscope for High-Energy Particle Detection: Precision Timing, Radiation-hard, Electromagnetic Calorimetry

Thomas Barbera

The European Center for Nuclear Research (CERN) will be increasing its luminosity tenfold by 2027 in order to expand its search for new particles. Due to this increase in luminosity, there is a demand for novel detectors that are able to detect particles more precisely at higher energies and in intense radiation fields.

The goal of this research is to develop an effective method to collect data from higher energy particles, which can then be used as detectors of electrons, positrons and photons in these future colliders. This is mainly done with capillary tubes containing a wave shifting fluid, which sense the light created by charged particles passing through scintillator plates. The wave shifter emits specific intensities of light depending on the energy of the particles and the efficiency of the wave-shifting fluid. These emissions are then measured by detectors and analyzed for their significance.

The current focus is on a visualization system to be placed within a detector apparatus in order to visualize the particle beam and its interaction with the capillaries. The initial design of the so-called “Hodoscope” was created using Micro-Channel Plates, Image Intensifiers, and pinhole optics, and uses a camcorder to capture video of the interactions of the beam which is then projected onto a monitor. The capillary tubes and Hodoscope were tested at Fermilab National Laboratory, and the capillaries accurately detected the contents of the particle beams. The visualization system was also effective in locating the position of the beam relative to the apparatus and visualized the difference in energy between each test. The following experiment, which will be conducted in June at Fermilab, will consist of a hexagonal array of capillary tubes (rather than a circular array) to provide equidistant spacing between each capillary and a shape more attuned to the beam.

Bice Caroline (Oral Presentation & Poster # 6)

Effect of Temperature on Infection of *Biomphalaria glabrata* by *Schistosoma mansoni*: An Assessment of the effects of Climate Change on Transmission Risk of Human Schistosomiasis

Caroline Bice

In order to predict how climate change will affect the ecology-level dynamics of infectious diseases, it is imperative to study how climate change will affect individual-level physiology. Many studies have demonstrated nonlinear responses for life-history traits to temperature. Human schistosomiasis, which is caused by the parasite *Schistosoma mansoni*, affects more than 200 million people globally, and it is predicted to be affected by global climate change (Blum and Hotez 2018, Bruun and Aagaard-Hansen 2008, King and Dangerfield-Cha 2008).

My study seeks to explore how increasing temperature due to global climate change may affect the various population dynamics and physiological processes involved in the spread of human schistosomiasis. I conducted a 16-week long study with four 17-L mesocosm tanks, each maintained at their respective temperature treatments of 18, 21, 25, 29, 33, or 37°C. I studied the *Biomphalaria glabrata* population dynamics of each mesocosm, the transmission of *S. mansoni* to snails the *S. mansoni* (parasite) production from snails, and periphyton growth (independent from snail herbivory) across temperatures (18, 21, 25, 29, 33, 37°C).

The focal analysis will be to test how temperature affects the production of schistosoma cercariae because this is the lifestage of the parasite that infects humans. Through statistical analyses conducted in R, I found that the snail population growth, egg laying, survival, and schistosome cercarial production all exhibited a hump-shaped relationship with temperature peaking between 21 and 25 degrees C.

This study is essential in understanding how global climate change will affect parasitic disease dynamics at an ecological level. By measuring the effects of changing temperature on key life-history traits, my results will help the formulation of predictions and modeling for future disease dynamics. The data collected in this study will add to the growing body of knowledge on the complexity of host-parasite dynamics under climate change.

Bohling Sarah (Poster # 7)

Investigating the cellular functions and evolutionary history of cytoskeletal components in *Porphyra umbilicalis* and *Rhodelphis*

Advisor: Dr. Holly Goodson, Dept. of Chemistry and Biochemistry, University of Notre Dame
Sarah Bohling

Abstract:
The last eukaryotic common ancestor (LECA) is shared between all eukaryotic organisms. The cytoskeleton is essential for key cellular functions including cell division and intracellular transport. Therefore, learning more about the cytoskeleton of divergent organisms could provide insight into the basic biology of LECA and the function of cytoskeletal proteins in eukaryotes. Red algae diverged from the lineage leading to green plants more than 1 billion years ago. Thus, we are studying the cytoskeletons of the red alga *P. umbilicalis* and a predatory (phagotrophic) red algal relative *Rhodelphis* to gain an understanding of the functions and history of cytoskeletal components.

We are using both experimental and bioinformatic approaches to address these questions. Experimentally, *P. umbilicalis* spores were allowed to extend rhizoids, long root-like structures in which membrane transport can be imaged. My goal was to image intracellular transport in this organism using generic membrane dyes (e.g., DiI, DiO) and a lysosomal dye (lysotracker). These efforts were unsuccessful, but experiments with a mitochondria dye (mitotracker), completed by collaborators, showed that mitochondria in *P. umbilicalis* move in a directed manner and that mitochondrial motion slowed in response to actin inhibitors (this was surprising because *P. umbilicalis* lacks myosin). Bioinformatics studies into actin and actin-related proteins (Arps) confirmed the presence of the nuclear proteins Arp4 and Arp5 in *P. umbilicalis* and identified potential Arp1-8 and Arp10 in *Rhodelphis* (which was surprising because the dynactin complex component ARP10 was considered specific to the fungi/animal lineage). Two cytoplasmic dyneins were identified in two relatives of *P. umbilicalis*, confirming that dynein fragments recently identified in the *Porphyra* genome may be real (previous papers had reported that red algae lack dynein). Several additional components of the dynactin complex were also identified in *Rhodelphis*, indicating that LECA may have had a complete or near-complete dynactin complex.

Bosio Sam (Poster # 8)

Ecological Linkages Between Amphibians and Wetland Vegetation in the Upper Midwestern USA

Sam Bosio

Global environmental change has resulted in a variety of negative impacts on wetlands of the Midwestern United States. Amphibians play a critical role in the proper functioning of these wetlands and the ecosystem services they provide, but are experiencing unprecedented declines globally. As further amphibian loss is likely despite conservation actions, I sought to understand the ecological services that will be lost with them. The effects of amphibian predation on community diversity and abundance of organisms occupying lower trophic levels are in particular need of direct study, especially in wetlands of the upper Midwest region. I addressed this knowledge gap by conducting enclosure experiments to measure the impact of amphibians on insect abundance and behavior around vernal pools in the upper Midwest, as well as indirect amphibian impacts on plant communities at the habitat scale. Insect herbivory was on average 26±13% lower in treatment plots with enhanced amphibians than control enclosures with ambient amphibians, and the members of the herbivorous insect order Hemiptera were observed less frequently in treatment enclosures. However, impacts of amphibians on lower trophic levels were not observed in the larger habitat-scale study. Amphibians may provide localized protection to terrestrial plants by consuming herbivores, but additional research is needed to understand relationships between vegetation and amphibian communities.

Brennan, Livia (Poster # 9)

Investigating expression of PYGO2 as a potential prognostic marker in pan-cancer and specific cancer analyses through bioinformatic techniques

Advisor: Xuemin (Sheryl) Lu, Department of Biological Sciences, University of Notre Dame
Livia Brennan

PYGO2 is a protein coding gene predicted to perform multiple functions, in particular chromatin binding, histone acetyltransferase activity, and histone binding activity. This gene is involved in the WNT signaling pathway, and predicted to take part upstream in many processes such as cell differentiation. PYGO2 has recently been identified as a possible point of investigation in cancer development; PYGO2 expression is potentially a prognostic marker for a multitude of cancer types. A variety of data sets have an abundance of data on PYGO2 expression, and the primary goal of this research was to decipher from this data an association of PYGO2 with specific cancer and cell types. These data sets include the Human Protein Atlas, CCLE, TISCH, and others. To identify the cancers closely related to PYGO2, the top 5 expressing cancers were chosen from any one data source. Breast, prostate, liver, urothelial, and skin cancer had consistently high PYGO2 expression across our resources. In order to gain a more detailed understanding of where PYGO2 is affecting outcomes in these cancers, single cell analysis was performed. The top 5 cell lines with highest PYGO2 expression among all available cancer datasets and our specified cancers were chosen. The highest expression of PYGO2 was depicted in several types of immune cells. PYGO2 was also investigated as a prognostic marker for pan-cancers; PYGO2 was identified to have a significant association with poor prognosis in LHC, LGG, and ACC, as well as improved prognosis for BRCA and HNSC. To understand PYGO2 influence in addition to expression, the top 25 associated genes with PYGO2 were identified from different sequencing types, and those with WNT pathway roles or immune influences were identified as potential comarkers. Overall, this preliminary data depicts PYGO2 as a potentially influential and informative prognostic marker for multiple cancers and cell lines.

Carmody, Matthew (Poster # 10)

Great Lakes Taxonomy and Barcodes to Support Early Detection Monitoring

Matthew Carmody

The analysis of environmental DNA (eDNA) is an important tool for the detection of invasive species and generating estimates of biodiversity in a specific region. The effective use of eDNA relies on a library of diagnostic genetic markers ("barcodes") that are representative of the taxonomic diversity sampled. However, many invertebrate taxa lack this essential genetic information. Our goals in this project were to: Procure specimens of Great Lakes invertebrate species that lacked relevant barcode data, generate diagnostic barcodes, create a Great Lakes DNA barcode reference library, and create a Great Lakes species list. In this assay 759 samples were collected in multiple locations across the Great Lakes. The samples were filtered for invertebrate aquatic taxa and sorted into taxonomic groups. These samples were then identified by experts and photographed to create vouchers specimens. Then the DNA from 387 of these samples was extracted, PCR amplified, purified, and Sanger sequenced to create barcode sequences. For the barcode regions we used a Cytochrome c oxidase I gene (COI) sequence specific to individual species which enhanced the existing library of DNA signatures. Many Great Lakes zooplankton lacked barcodes previously. In the process of this project, we identified a new species of copepod present in the Great lakes *Cyclops divergens*. We also found that harpacticoid copepods are now dominated by nonnative species in Lake Ontario. These sequences were made publicly available through the Barcode of Life Database (BOLD). A validated barcode reference library must be linked to specimens identified by a taxonomic expert, so by creating barcode sequences from identified samples we significantly expanded the existing library.

Chang Lucia (Poster # 11)

An Investigation of CRISPR Cas12a's potential as a Homing Guide System

Lucia Chang

Previous studies have used the CRISPR-Cas9 homing gRNA system to generate generational random genetic mutations in living cells which could be used for wide range barcoding applications. However, because the PAM sequence of the Cas9 system is located very close to the cutting site for the Cas9 enzyme and often gets removed after rounds of cutting, this study proposes that utilizing Cas12a enzyme may be a better alternative to increase long lasting genetic editing efficiency. Thus, this study aims to design a homing guide RNA (hgRNA) system for CRISPR-Cas12a to assess the *in vivo* editing efficiency of Cas12a proteins. This was accomplished by infecting and transfecting murine breast cancer cell e0771 with the cloned vector containing the hgRNA with PAM sequence and CRISPR Cas12a protein. The efficiency of the genetic mutation was assessed by extracting DNA from the cell and conducting Illumina Sequencing. However, the results show that there were no significant amounts of genetic mutation as the study hoped to achieve. This is most likely due to the stringent demands of the gRNA hairpin structure and specific PAM recognition sequence unique to Cas12a that hindered Cas12a from allowing the placement of PAM sequence in the stem loop. As a result, this experiment demonstrated that without modifying the interactions at the binding pocket between Cas12a enzyme and the gRNA hairpin stem, it would be a difficult endeavor to design a homing guide RNA for the current Cas12a system.

Chau Khang, Emma Eckstein, Evan Peters, Meghan Fries, Elizabeth Jasek (Oral Presentation & Poster # 12)

Examining the functional relationship between ESX-1 substrates MMAR_2894 and PPE68 in *Mycobacterium marinum*

Khang Chau, Emma Eckstein, Evan Peters, Meghan Fries, Elizabeth Jasek

The ESX-1 (ESAT-6 system 1) secretion system is essential to the virulence of *Mycobacterium tuberculosis*, the causative agent of human tuberculosis. ESX-1 secretes protein substrates that enable the mycobacteria to escape the phagosome and continue infection. However, the functional roles of the substrates remain largely unknown. *M. marinum*, an established model of *M. tuberculosis*, is being used to characterize their contribution to virulence and secretion. We will study the relationship between the MMAR_2894 and PPE68 substrates. These two PE/PPE family proteins are proposed to be the first of the 12 known *M. marinum* substrates to be secreted and may form the base of the extra-cytoplasmic ESX-1 secretion machinery. Using secretion assays and western blotting, we will determine if, like other ESX-1 substrate pairs, PPE68 and MMAR-2894 are dependent on each other for secretion. If co-dependent, we predict that loss of both substrates would result in attenuation of *M. marinum*. We will examine this through macrophage infection by a *Δppe68Δ2894* double deletion strain. Macrophage lysis levels will be compared to those of *Δppe68* and *Δ2894* single deletion strains, which have unexpectedly been measured as only slightly reduced from wild-type. Additionally, we will begin to test a current hierarchical model of ESX-1 substrate secretion through examining potential interactions between the MMAR_2894 and PPE68 proteins. A LexA-Bacterial-Two Hybrid experiment will indicate if there is direct protein-protein interaction between the two substrates, which would support the model. Together, our results will provide a base for further examination of substrate contribution to ESX-1 secretion.

Chen Emily (Poster # 13)

Coping with stress on a college campus during COVID-19: cortisol, individual disposition, social support, and mental well-being among undergraduates

Emily Chen

COVID-19 has significantly impacted college students' educational experience. As institutions transitioned to remote learning or adopted "hybrid learning", students navigated an unpredictable educational and social atmosphere, which posed challenges to personal health. Individual differences in personality dimensions, internal resources, and social support systems may interrelate with the way young adults responded to the pandemic in a university setting. Studying undergraduate students at the University of Notre Dame (n=41) during an in-person semester in Spring 2021, we assessed individual neuroticism, fear of COVID-19, self-compassion (via mindfulness), psychosocial stress, perceived social support and loneliness, and satisfaction with Notre Dame's COVID-19 response program "HERE". Undergraduates who scored higher for mindfulness reported lower levels of psychosocial stress and neuroticism (r's = -0.43, -0.59; p's < 0.05). Students experiencing greater psychosocial stress reported more loneliness and lower perceived social support (r's = 0.31, -0.37; p's < 0.05). Fear of COVID-19 was not meaningfully correlated with any measures. Individuals who were more capable of practicing mindfulness and had more social support had higher cortisol (r's = -0.28, -0.20, p's > 0.09, 0.2). Individuals who held a greater sense of school membership with Notre Dame also had higher cortisol levels (r = -0.23, p > 0.2). Finally, higher cortisol was associated with greater neuroticism and psychosocial stress (r's = 0.31, 0.18; p's > 0.06, 0.3). These cross-sectional results suggest that social support and individual disposition are important correlates of undergraduate mental well-being during the pandemic in this setting. An understanding of these factors may assist educational institutions in addressing social and personal needs of students during times of unpredictable stress.

Cheong William (Poster # 14)

1,3,5 Trithiane as a Sulfur Source in Metal Sulfide Nanoparticle Synthesis

William Cheong, Jonathan Stoffel, and Emily Tsui
Department of Chemistry and Biochemistry, University of Notre Dame

Metal sulfide nanoparticles are of great interest due to their photo- and electrochemical properties. Although there are many methods to synthesize metal sulfide nanoparticles, there is a lack of comprehensive understanding on the reaction mechanisms. For example, the use of thiols or organic disulfide compounds requires the cleavage of C−S bonds. Comparison of different organic sulfur precursors may elucidate the high temperature nanoparticle formation mechanism. The synthesis of Fe_xS_y and CdS nanoparticles using different sulfur precursors, including the thioformaldehyde equivalent 1,3,5-trithiane, was studied to characterize the influence of the C−S bond strength in these reactions. Molecular studies of 1,3,5 trithiane and other sulfur sources were performed to identify reactive species formed *in situ*. Further experiments were performed to study the release of H_2S gas from 1,3,5 trithiane and other sulfur sources, in an effort the find a causal relationship between C−S bond strength and H_2S release. Understanding the mechanism of how 1,3,5-trithiane interacts with solvents at high temperatures to form metal sulfides may lead to the development of improved and more selective synthetic procedures.

Cho Stella (Oral Presentation)

Elucidating the Role of Formin Proteins in Early Sensory Neural Development

Stella Cho

Dorsal root ganglia (DRG) axon navigation and entry are key components of sensory neural development. By utilizing drug-induced and CRISPR-induced inhibition of formin proteins, single-cell RNA sequencing analyses, and confocal microscope time-lapse imaging, we demonstrate a role for Daam1a in DRG neuron entry into the spinal cord. Using a cell-specific genetic approach, we identify that Daam1a acts within the neuronal cell population to result in failure of DRG axon entry. Time-lapse imaging examines how formin protein inhibition disrupts actin organization and causes a failure of invadopodia formation in the axonal growth cone. Animal behavioral analyses in response to noxious cold stimuli further confirm our findings that formin inhibition disrupts DRG axon entry. Together, our data demonstrate a key role for Daam1a and other FH2 domain-containing formin proteins in DRG axon entry during early sensory neural development.

Coil Sydney (Oral Presentation)

Cleaning up RIBs with TriSol

Sydney Coil

The University of Notre Dame has been at the forefront of Radioactive Isotope Beam (or RIBs) research. This is a result of the *TWIN-SOL* system. This system has undergone an upgrade through the addition of a third solenoid and thus has become the *TRI-SOL* system. The capabilities of TRI-SOL include increased beam focus and better beam purification, leading to more precise analysis and better results. In the past year, TRI-SOL has been installed and tuned. This tuning process has included tuning each individual component of the line with an alpha source (^{228}Th) as well as various types of beam.

Connelly Lauren (Poster # 15)

An Investigation of the Localization of *rhoV* mRNA in *Xenopus laevis* Oocytes and Potential Mechanisms of Animal-Hemisphere Localization

Lauren Connelly

Localization of cytoplasmic mRNA to either the animal or vegetal hemisphere of the developing oocyte is a key regulatory mechanism which controls proper cell determination and embryonic development. The mRNAs transported to the vegetal and animal hemispheres of *Xenopus laevis* oocytes bind to many of the same proteins, which leaves open the question of which factor(s) determine the final destination of any given mRNA. Vg1 mRNA, which localizes to the vegetal hemisphere, is found in a biocondensate ("liquid droplet") that forms as the mRNA emerges from the nucleus. This biocondensate contains approximately 70 proteins and more than a hundred different RNAs. Unexpectedly, mRNAs that ultimately localize to the animal hemisphere are present in this complex, suggesting that sorting of RNAs destined for the vegetal or animal hemisphere does not occur immediately upon entering the cytoplasm. *In situ* hybridization was used in order to confirm that *Ythdf2* and *rhoV*, two of the most abundant mRNAs in the biocondensate, in fact, localize to the animal hemisphere in the mature oocyte. This data supports the current hypothesis that some mRNAs destined for the animal hemisphere are first transported to the vegetal hemisphere and, only after breakdown of the biocondensate, accumulate in the animal hemisphere, likely as a result of cytoplasmic streaming. These results suggest that sorting is the result of capture of vegetal mRNAs as they arrive at the oocyte cortex, while accumulation of mRNAs in the animal hemisphere is a passive process.

Curtis Erik (Poster # 16)

Periodical cicadas and leaf litter as allochthonous resource subsidies in nutrient-limited experimental streams

E.M. Curtis, A.N Pruitt, J.L. Tank, E.D. Snyder, A.E.S. Vincent, E.M. Thrift

Irregular resource pulses to aquatic ecosystems, such as the addition of cicada carcasses as a result of brood emergence and subsequent die-off, cause significant changes in community respiration and primary productivity. More regular resource pulses, such as those provided by the annual senescence of leaves, can also affect these parameters, especially in small streams. To date, no controlled experiments have been performed comparing how these resource subsidies influence stream ecosystem function. In Summer and Fall 2021, we quantified the effects of both leaf litter and cicada resource pulses in low-nutrient experimental streams at the Notre Dame Linked Experimental Ecosystem Facility (ND-LEEF). During the summer, we added known weights of dead cicadas in litter bags to two experimental streams at both a high (47 g dry mass/m^2) and low (23 g dry mass/m^2) biomass. A third stream containing empty bags served as a control treatment. In the fall, we performed an analogous study in the same streams, substituting cicadas for senesced maple leaves. During each study, we monitored ecosystem functional metrics, including water-column nutrients, ash-free dry mass (AFDM), fine benthic organic matter (FBOM), and algal chlorophyll-a, and we estimated reach-scale metabolism using dissolved oxygen sensors. The cicada addition had an immediate, but brief effect on heterotrophic respiration, with an increase on Day 3 post-addition, but by Day 20, we saw no differences in response metrics. For the leaf litter addition, we observed a slower but more prolonged effect on heterotrophic respiration, which was significantly higher for the low-density treatment on day 20. On day 29, chlorophyll-a was significantly higher than the control for both litter and cicada additions for either biomass. These results suggest that decomposing leaves and cicadas differ in their impact on stream ecosystem function due to differences in both composition and the temporal dynamics of decomposition dynamics.

Davis Carrie (Oral Presentation)

Commissioning of the St. Benedict Radiofrequency Carpet

Carrie Davis

The Standard Model (SM) describes fundamental building blocks and interactions in our universe. The Superallowed Transition BEta NEutrino Decay Ion Coincidence Trap (St. Benedict) at Notre Dame will conduct precision tests of the SM by allowing for a determination of the V_{ud} element of the Cabibbo-Kobayashi-Maskawa matrix for many mirror transitions for the first time, which will require slow radioactive ion beams (RIB). Because the RIB at TwinSol is produced "in-flight," it needs to be stopped in a large volume gas cell before being formed into a slow beam. This process requires pressures on the order of 100 mbar, while a pressure of 10^{-7} mbar or lower is required for transport at low energy along the beam line. To allow for these pressures, several differential pumping regions located after the gas cell and before the Paul trap where the measurement will occur are necessary.

St. Benedict's differentially pumped extraction system will include a section housing a radio frequency (RF) carpet at a pressure of around 3 mbar, followed by a section housing a radio frequency quadrupole ion guide at 2×10^{-3} mbar, pressures which were calculated and then confirmed in an experimental setup. Transport efficiency of potassium ions using the RF carpet in static gas was determined to be above 90% using the ion surfing method after optimizing the potentials applied to various electrodes. Transport efficiency of potassium ions using the RF carpet in the presence of gas flow was determined to be near 100%.

Dineen Brian (Poster # 17)

Rimiducid's Effect on T Cell Development and Differentiation

Brian Dineen, Dan Li, Qing Ma

Chimeric antigen receptor modified T cells (CAR-T cells) have been found to be effective antitumor agents when treating chronic lymphocytic leukemia and acute lymphoblastic leukemia. However, attempts to treat other types of leukemia, as well as solid tumors, with CAR-T cells have been less successful. One of the major barriers to widespread use of CAR-T cells is the toxicity of these cells. CAR-T cells cause cytokine release syndrome, on-target off-tumor toxicity and neurological toxicities. Several deaths in clinical trials have been attributed to these.

The addition of a "suicide gene" encoding the caspase-9 protein to CAR-T cells has been proposed as a method to decrease their toxicity. This strategy uses rimiducid (AP1903), a drug that causes dimerization of the caspase-9 protein. Dimerization of caspase-9 domains leads to CAR-T cell death and thereby prevents inflammation and off-tumor toxicity. Rimiducid's effect on the development and differentiation of native T cell populations has not yet been studied.

Human peripheral blood mononuclear cells (PBMCs) were isolated from buffy coat by layering with HISTOPAQUE-1077 and centrifugation. PBMCs were divided into three time points (days three, five, and seven) and three treatments. The control group was not treated. The stimulation group was treated with CD3 and CD28. The rimiducid group was treated with CD3 and CD28 as well as either 20µL or 80µL of 10µM rimiducid. Cells were mixed with antibodies for various markers of T cell development and differentiation and were analyzed using flow cytometry.

Treatment with rimiducid increases the prevalence of helper T cells (CD4) in vitro. It also increases the prevalence of naive helper T cells while decreasing the prevalence of central memory and terminally differentiated helper T cells.
Rimiducid does not appear to affect the prevalence of cytotoxic (CD8) T cells or the differentiation of these cells in vitro.

Elliott Margaret (Oral Presentation)

Estimating risk of emerging infectious diseases: a review of tick-borne pathogens in Kenya, Belize, and Florida, USA.

Margaret Elliott
Department of Biological Sciences
Advisor: Nicole L. Achee
Coauthors: Brooke Rodriguez, John P. Grieco, Nicole L. Achee, Sean Moore, Stacy Mowry, Alex Perkins, and Benedicte Fustec

The Remoting Emerging Disease Intelligence-NETwork (REDI-NET) is a recently launched research initiative which aims to improve the surveillance, detection, and containment of emerging infectious diseases. REDI-NET will assess the presence and density status of a broad array of pathogens of human and animal health importance in Kenya, Belize, and Florida, USA, specifically those considered zoonoses which have the potential to spillover from animal to human populations. Thus, field teams in each location will conduct routine sampling of water, sediment, leeches and ticks from various sites. Field and laboratory data, as well as published data in the literature, will contribute to the development of mathematical models to produce spatial-temporal risk projection maps. Such risk projections are expected to guide health officials on timely preparedness for optimal mitigation strategies. Here we describe early-stage activities that were performed to build knowledge on reported tick-borne diseases within REDI-NET sampling locations to inform mathematical modeling based on a standardized and robust literature search on tick-borne pathogens in Florida. We searched various scientific literature databases as well as the Florida Department of Health for publications on the following tick-borne pathogens of interest: *Rickettsia spp., Ehrlichia spp., Anaplasma spp., Babesia spp., Borrelia spp*., and *Coxiella burnetii*. Presented are our summary findings including the availability of case and prevalence data, the challenges of building baseline model data, key considerations when interpreting data from risk model outputs, as well as activities planned for future REDI-NET research phases.

Fletcher David (Poster # 18)

Conformational Study of Apicularen A

David Fletcher

Major: Biochemistry
Advisor: Richard Taylor, Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, IN
Coauthor: Bryce Dye, Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, IN

Apicularen A is a natural product synthesized by several species of the genus *Chondromyces*. This polyketide is a potent vacuolar (V-type) ATPase inhibitor, which has been implicated in the possible treatment of certain cancers. Interestingly, apicularen A is not selective only for V-type ATPases, as it shows some mitochondrial (F-type) ATPase inhibition. Apicularen A shares structural similarities with other ATPase inhibitors: a macrolide core, salicylate moiety, and an enamide side chain. A subtle difference between these molecules is the stereochemistry of the C15 position, the carbon that connects the enamide side chain to the ester of the lactone. Here, we are conducting a conformational study on both apicularen A and its C15 epimer to elucidate whether the stereochemistry at the C15 position may affect the conformational preference of the macrocyclic core and whether this preference affects specificity to a specific ATPase. A total synthesis of both apicularen A and its C15 epimer, highlighting methodology developed in our lab, is currently underway. Once synthesized, computer methods will be used to analyze the conformational differences between the two diastereomers by probing their potential energy surfaces. High-field NMR experiments complimented with computational data regarding the two C15 epimers of apicularen A will confirm the conformational preference of this ATPase inhibitor and eventually whether this ATPase selectivity can be changed based on a simple stereochemistry modification.

Fulkerson Daniel (Poster # 19)

Impact of Targeted Mutations on Aquaporin-7 Structure and Breast Cancer Progression

Daniel E. Fulkerson, Verodia Charlestin, and Laurie E. Littlepage
Advisor: Laurie Littlepage, Dept. of Chemistry and Biochemistry, University of Notre Dame

Breast cancer is the most common cancer among American women and is projected to cause 43,250 deaths in 2022. Relative five-year survival rates associated with localized primary tumors are high (99%) but drastically decrease for individuals with metastatic disease. The development of metastatic potential remains poorly understood. Our lab has previously identified the water and glycerol channel Aquaporin-7 (AQP7) as a predictor of overall survival in breast cancer patients and a key metabolic regulator of breast cancer metastasis. However, the structure-function relationships that facilitate AQP7's pro-cancer phenotype are unknown. To further characterize these interactions, site-directed mutagenesis was used to introduce a point mutation in the mouse homolog of Aquaprorin-7, specifically targeting Serine-213, a residue known to be involved in pore selectivity. A Ser213Ala mutation was validated via restriction enzyme digestion and Sanger sequencing. The mutant AQP7 variant was introduced and expressed in stably infected 4T1 (mouse breast cancer) cells by lentiviral infection. The functional impact of the Ser213Ala mutation will be examined by evaluating its metabolic influence with a Seahorse XFp Real-Time ATP Rate Assay and by analyzing pro-metastatic cellular characteristics, including proliferation and adhesion.

Hammond Catherine, Strzalka Bridget, Andrysiak Nicholas, Nam Sandy (Poster # 20)

Analyzing phenotypic effects of current *norpA* mutants and genotype effects of novel *norpA* mutants in *Aedes aegypti*

Catherine Hammond, Bridget Strzalka, Nicholas Andrysiak, Sandy Nam
Advisor: Joseph O'Tousa, Dept. of Biological Sciences, University of Notre Dame

Aedes aegypti, a principal vector of the arboviruses dengue fever, chikungunya, and other neglected tropical diseases, use a combination of visual and environmental cues to locate its blood sources. To gain a better understanding of the visual system of *Aedes aegypti* in this process, we will be using *norpA* mutants in our project. From the *Drosophila* model, it is known that a key step in the invertebrate phototransduction cascade is the cleavage of phosphatidylinositol 4,5-bisphosphate (PIP2) into the secondary messengers inositol 1,4,5-trisphosphate (IP3) and diacylglycerol (DAG). The *norpA* gene encodes for Phospholipase C (PLC), the enzyme catalyzing this step. Three *norpA* mutants ($norpA^{CAT}$, $norpA^{DOG}$, and $norpA^{OWL}$) have previously been designed through CRISPR/Cas9 mutagenesis of the exon 2 region by the O'Tousa lab, but homozygous $norpA^{DOG}$ and $norpA^{OWL}$ mutants have yet to be found viable. This is potentially due to the loss of function of *norpA*, as it is anticipated that *norpA* is alternatively spliced into a form required for vision in adults (exon 4) and a form required for larval development (exon 4A). New CRISPR/Cas9 mutants have been generated with mutations in exons 4 and 4A to investigate this phenomenon. The course of this experiment established three main aims in order to examine the role of *norpA* in the *Aedes* visual system. A major rhodopsin of the phototransduction cascade, Aaop1 has been found to cycle into and out of the rhabdomere in response to changing light conditions. The first aim of this research is to use immunofluorescence to visualize Aaop1 localization in $norpA^{CAT}$ mutants during dawn and dusk time points to discern *norpA'*s role in such a process. Second, capillary analysis and FAST cloning will be used to genetically screen new exon 4/4A mutants in order to determine whether *norpA* is alternatively spliced into two forms and how these mutations affect the vision of *Aedes*. Lastly, the phenotypic characteristics of $norpA^{DOG}$ and $norpA^{OWL}$ will be studied by forming transheterozygotes of $norpA^{DOG}$ and $norpA^{OWL}$ crossed with $norpA^{CAT}$. The transheterozygotes' phenotypic characteristics will be assessed by their visual response in a locomotive activity monitor assay, and the differences in their behavior from wildtype and $norpA^{CAT/CAT}$ will be noted as the unique feature of each mutant.

Harkin Jamie (Oral Presentation)

Radio Frequency Quadrupoles Studies and Design for St. Benedict

Jamie Harkin

Despite successfully predicting the Higgs Boson and describing the fundamental particles of nature, the Standard Model (SM) fails to describe gravity, dark mat- ter, and the anti-symmetry between matter and anti-matter. However, the Stand- ard Model provides us with several frameworks within which we can probe for 'new' physics beyond the Standard Model. One such framework is the Cabibbo- Kobayashi-Maskawa Matrix, which describes the probabilities quarks under the weak interaction. This framework assumes that there are only three quark generations, and thus, that current probability matrix should be unitary. Testing this framework requires accurate and precise measurement of the matrix elements, particularly Vud, given that it contributes overwhelmingly to unitarity. To that end, the Superallowed Transition BEta NEutrino Decay Ion Coincidence Trap (St. Benedict) is under construction at the Notre Dame Nuclear Science Laboratory. St. Benedict will take Radioactive Ion Beams (RIB) from $TwinSol$ and will stop them in a Gas Catcher from Argonne National Labs (ANL) and extract the slow ions via a differential pumping system consisting of a Radio-Frequency (RF) Carpet and ion guide leading to an RF Quadrupole (RFQ) Cooler-Buncher which then injects bunches of ions into a Paul Trap for measurement. My thesis work consisted of studying the presence of contaminant bunches produced by the Cooler-Buncher and designing the ion guide that will follow the RF Carpet.

Henning Joseph (Oral Presentation & Poster # 21)

Development of Beam Profile Analysis Application: Design and Implementation

Joseph Henning, Manoel Couder

The St. George Recoil Separator is an important tool in the Nuclear Science Laboratory for studying inverse kinematic reactions. Having been brought online in 2019, significant effort has been made to correctly calibrate the machine to accurately make measurements. However, challenges still remain. Current data regarding beam position is very qualitative, and difficult to reproduce between runs. Therefore, there is a demand for a quantitative input of beam position and dimensions for St. George operators, which would allow for greater accuracy and reproducibility in tuning the beam. In order to obtain quantitative input, I utilized existing Beam Profile Monitors (BPMs) within St. George, and a Picoscope 2000 digital oscilloscope. Data from the oscilloscope could then be ported in to a computer and analyzed with an application that I would develop. There were multiple constraints and goals that my application would have to meet. In particular, it would be crucial that it provide information in real time, and be able to reject variable amounts of noise. The final application that I developed was fully capable of quantitative analysis of the beam. Upon starting the application, the user would be prompted to send a fiducial signal from the BPM to the oscilloscope, which would be recorded and used as a normalization point. The user would then be prompted to connect to the beam signal. Real time data on the width and position of the beam would then be displayed within the console, and would also be plotted in real time in a separate window. Statistics of the beam could be saved at any time, and plotted on screen for comparison. The completed application was uploaded to the St. George console computers, and can be used by researchers. Additionally, further development on this application will allow for more convenient use in the future.

Heston Emma (Poster # 22)

Long term impact on Juday Creek invertebrate populations from the 1997 restoration for construction of the University of Notre Dame Warren Golf Course, St. Joseph Co., Indiana

Emma Heston
Advisor: Dr. Ronald Hellenthal

In 1997, two four-hundred-meter reaches of Juday Creek were relocated to accommodate construction of the Warren Golf Course on the campus of the University of Notre Dame (Notre Dame, Indiana). Following golf course construction, benthic macroinvertebrate populations were monitored in stream sites in restored and unrestored parts of the golf course for 5 years, between 1997 and 2002. In this study, benthic macroinvertebrate populations in Juday Creek on the Notre Dame Warren Golf Course were sampled three times between September and December of 2022 at four previously monitored sites. Generally, 20 years after construction, the restored areas of the stream supported more benthic invertebrates than unrestored areas. This suggests that the restoration techniques used in the stream remain effective. However, there was an overall reduction in stream macroinvertebrate abundance and biodiversity in both restored and unrestored areas, indicating that stream water quality and habitat may have declined over the past 20 years. This study suggests that while site-specific stream restoration efforts may be effective for long periods, they can't completely compensate for deleterious changes in a stream's watershed.

Hines Regan (Oral Presentation & Poster # 23)

Investigating Cellular Senescence as a Novel Treatment for Pediatric Glioblastoma

Regan Hines[1], Kathryn Morris[1], Patricia Vaughan[1], Ted Hinchcliffe[3], Paula Traktman[4,5,6,7], and Kevin T. Vaughan[1,2]

[1]Department of Biological Sciences, [2]Harper Cancer Research Institute, University of Notre Dame, Notre Dame, IN, [3]Hormel Institute, University of Minnesota, Austin, MN, [4]Departments of Biochemistry & Molecular Biology, [5]Departments of Microbiology and Immunology, [6]Departments of the Hollings Cancer Center Medical University of South Carolina, Charleston, SC, [7]Department of Microbiology and Molecular Genetics, Medical College of Wisconsin, Milwaukee, WI 53226

The reformation of the nuclear envelope at the end of mitosis is a highly regulated process. We identified a novel pathway involved in nuclear envelope reformation that, when disrupted, induces defects in nuclear lamina assembly. These defects mimic Hutchinson Gilford Progeria Syndrome (HGPS) with blebbed nuclei and uneven accumulation of Lamin A around the nuclear perimeter. As seen in HGPS, nuclear blebbing can lead to cellular senescence through the cGAS-cGAMP-STING pathway. In order to form an intact nucleus, phosphorylation of both Lamin A and Barrier – to – Autointegration (BAF) are required for their interaction at the nuclear envelope. The protein vaccinia-related kinase 1 (VRK1) has previously been shown to phosphorylate BAF. Inhibition of VRK1 through either genetic approaches or drugs in a glioblastoma (GBM) cell line resulted in blebbed and highly micronucleated nuclei. Our results indicate that targeting the reformation of the nuclear envelope could be used as a novel treatment pathway for GBM by avoiding targeting the cell cycle. Inducing nuclear blebbing and, therefore, cellular senescence would help circumvent the problems GBM treatments typically have in highly mutated GBM tumors.

Hlavin John, Knight Caroline, Buckner Hallie (Poster # 24)

Investigation of Aaop1 Cycling in *Aedes aegypti* and *Aedes albopictus*

John Hlavin, Caroline Knight, Hallie Buckner

Principal Investigator: Joseph O'Tousa, Dept. of Biological Sciences, University of Notre Dame
Mentor: Michelle A. Whaley, Dept. of Biological Sciences, University of Notre Dame

Aedes aegypti and *Aedes albopictus* are principal vectors for many arboviruses, including Zika, yellow fever, dengue, and chikungunya, which cause the deaths of hundreds of thousands of people each year. As crepuscular organisms, the females use vision within a multimodal sensory system to seek blood meals at dawn and dusk. Two genes essential to the visual system of these organisms are *norpA* and *aaop1*. Within the phototransduction cascade, the gene *norpA* encodes for the protein phospholipase C (PLC), which is responsible for cleaving PIP_2 into DAG and IP_3. The gene *aaop1* encodes for the protein Aaop1, the major adult rhodopsin in these organisms. Aaop1 is known to exhibit a pattern of maturation and migration within the photoreceptor cell in response to changes in light. However, this mechanism of Aaop1 cycling is not fully understood. Recently, our lab has utilized CRISPR/Cas9 technology to produce an *Ae. aegypti norpA* mutation, creating a mutant animal referred to as $norpA^{CAT}$. The consequent inability of this mutant animal to make PLC disrupts the phototransduction cascade, likely altering the wild type functionality of Aaop1. We utilized this downstream effect to understand the Aaop1 cycling mechanism over the course of the light-dark cycle. To characterize the expression and localization of Aaop1 in $norpA^{CAT}$ mutants, we performed a series of western blots and immunofluorescence assays using samples taken from time points throughout a 24-hour period. We are currently gathering additional data so that we may propose a complete mechanism for the cycling of Aaop1. To carry out a similar analysis in *Ae. albopictus*, we are using the CRISPR/Cas9 approach to generate viable *Ae. albopictus norpA* mutants. These mutant animals will allow a comparison of the Aaop1 cycling mechanisms in the two species of interest.

Hollmer Lauren (Poster # 25)

Mathematical Modeling of the CA19-9 Response to chemotherapy in patients with pancreatic cancer

Advisor: Dr. Eugene Koay, Department of GI Radiation Oncology, University of Texas MD Anderson Cancer Center

CA19-9 is the most widely used biomarker for pancreatic cancer, and multiple studies have demonstrated that normalization of CA19-9 is associated with a good prognosis. However, there is currently no method to predict normalization early during chemotherapy to determine treatment efficacy. A cohort of 732 patients with resectable, borderline resectable, or locally advanced pancreatic cancer between 2015- 2019 was identified to generate a model to predict the likelihood of normalization during the course of chemotherapy treatment. Patients were selected from this group if they met all of the following criteria: No CA19-9 normalization prior to therapy, normal bilirubin prior to therapy (<2.0 mg/dL), no metastasis, uninterrupted FOLFIRINOX or Gemcitabine/nab-paclitaxel for 6 months, and at least two CA19-9 measurements in addition to the baseline. Normalization was defined as CA19-9 levels below 40 U/mL at any point during chemotherapy. CA19- 9 data were fit to an exponential decay model (Y[t]=alpha*exp(beta[t]); where Y was the CA19-9 level at time t, and alpha and beta were model parameters describing the shape of the response curve to predict the presence or absence of normalization within 6 months. If CA19-9 levels increased to time "T" within the first 60 days but then decreased, data was fit to a piecewise curve with magnitude for the rate of increase equivalent to the rate of decrease and the turning point at t=T. Model predictions were compared to ground truth CA19-9, followed by an assessment of misclassifications, progression trends, and ROC analysis. 86 patients (34 normalizers and 52 non-normalizers) met all inclusion criteria, resulting in accurate classification for 73 patients. Ongoing work will characterize and model responses for other subsets while improving predictive capacity for use in a clinical setting.

Kacey William (Oral Presentation)

Measurement of PFAS in Chicken Egg Yolk and Development of Standards using Ion-Beam Analysis

Advisor: Graham Peaslee, Dept. of Physics, University of Notre Dame

Per and poly-fluorinated alkyl substances (PFASs) are a group of fluorinated organic compounds that have been identified as hazardous to human health. Because of their presence in a variety of commercial products and firefighting agents as well as their ability to persist against degradation, PFASs have come to be known as ubiquitous environmental pollutants, appearing in groundwater, dust, soil, and animal tissue. PFASs have been found to bioaccumulate in the yolk of bird eggs, primarily as a result of the ingestion of contaminated feed. The PFAS contamination of eggs has been studied up to this point using ultraperformance liquid chromatography coupled to tandem mass spectrometry. The purpose of this study was to find a method of measuring PFAS contamination of chicken eggs using the St. Andre 9S tandem pelletron accelerator in the Nuclear Science Laboratory. Development of a method based on using ion-beam analysis would provide quicker and cost-efficient measurements of this contamination. To prepare a target fit for the accelerator, a chemical extraction procedure was attempted to separate the PFAS from the egg's proteins. The organic extract was put on filter paper, bombarded with 3.7 MeV protons, and analyzed for fluorine using particle-induced gamma emission (PIGE) spectroscopy. It was found that this extraction did not successfully extract PFASs from egg yolk, and further research is needed to determine a more successful method of extraction. However, in the process of preparing targets, we successfully developed an effective new method of preparing standards for the measurement of fluorine using plaster of Paris and sodium fluorine salt. These new standards have been unlike previous standards, as they have been shown to resist day-to-day change and deterioration due to beam. This result will be published after we show its utility for the calibration of several other elements.

Kautzky Jenna (Poster # 26)

Generation of a Collection of *N*-Heterocyclic Small Molecule Inhibitors of Protein-Protein Interactions Between DYRK1A and DCAF7

Advisor: Brandon Ashfeld, Dept. of Chemistry and Biochemistry, University of Notre Dame
Jenna Kautzky

Dual-Specificity Tyrosine-Phosphorylation Regulated Kinase 1A (DYRK1A) is a kinase implicated in neurodegenerative diseases including Down Syndrome and Alzheimer's Disease. The main focus of this project is to design inhibitors for DYRK1A which do not affect its upstream involvement in many necessary processes including development and the cell cycle. This research worked toward the generation of a collection of small molecules with the potential to disrupt protein-protein interactions (PPIs) between DYRK1A and DCAF7. PPI inhibition is explored rather than active site inhibition due to the relative active site homogeneity among many different kinases. Instead, the DYRK1A-DCAF7 interaction provides a specific target for altering the intended metabolic pathway, which is related to neuronal cytoskeleton axonal transport and signaling of cellular processes. To expand upon our collection of the spirooxindole family of products, we have begun investigating a palladium-catalyzed, formal [3+1]-cycloaddition for the generation of spirooxindole cyclobutane products bearing an exocyclic alkene. We were inspired to generate these products both by the chemotherapeutic potential of the *strychnos* and *cyranthos* family of spirooxindole alkaloid natural products as well as the promising results observed with other members of the spirooxindole family of products in our previous investigation with DYRK1A. To date, we have optimized the cycloaddition and are continuing to expand our diverse collection of small molecules bearing interesting three-dimensional topographies. Future direction will include testing these molecules both *in vitro* (with ELISA and Co-IP experiments) and *in vivo* (with a whole organism *drosophila* model).

Kerner Elizabeth (Poster # 27)

Unlocking Climate Science Literacy Through Art

Elizabeth Kerner

The accessibility and widespread use of digital resources has led to the development of a variety of media forms. While increased global communication through the internet has led to better access to information across demographic regions and socioeconomic classes, it has also made less credible sources far more widespread and intermixed. In the lens of climate change the abundance of information and variety of sources has posed a challenge for acquiring information that is credible, scientifically accurate, and written to be accessible to the general public. The visual arts have a history of providing a widely accessible and quickly perceived media form to communicate personal, social, and political expression and movements. Through multimedia artwork, this capstone expresses challenges of establishing scientific literacy surrounding climate change when such an abundance of information is available, relaying the present discrepancies in translating climate science literature from scientific journals to popularly accessible media.

Khouzam Nadim & Amir (Poster # 28)

Processing and Analyzing data in order to establish trends in the unpredictability of Respiratory Syncytial Virus (RSV)

Amir R. Khouzam
Nadim R. Khouzam
College of Science
Biological Science
Advisor: Dr. Alex Perkins - Associate Professor of Biological Sciences
Concurrent Associate Professor of Applied and Computational Mathematics and Statistics

Respiratory syntactical virus (RSV) is a contagious virus that spreads seasonally through contact with droplets from the nose and throat of infected people when they cough and sneeze. Due to the recent pandemic, however, the regular season for RSV has been skewed, most likely due to usage of preventative measures like masks, which have lessened the spread of droplet-based viruses. Now that the pandemic restrictions have lessened substantially, RSV is beginning to resurge. The hypothesis that was postulated is that states that will have the greatest resurgence of RSV will be states that have fewer pandemic restrictions, such as social distancing, mask mandates, etc.
RSV data was collected using the Center for Disease Control (CDC) and Collection on RSV state trends. Collection was done monthly after several long-term predictions and hypotheses were made. Data was collected and stored in a google spreadsheet where states with the highest RSV Antigen and PCR tests were ranked first and observed closely. We are seeking to overcome the technical challenge of unpredictability in the RSV season recently caused by a season shift potentially through Covid restrictions.

Komater, Dante (Poster # 29)

Dynamically Tagged Groups of Metal-Poor Stars from The Radial Velocity Experiment Data Release 6

Dante Komater

A sample of ~8000 metal-poor stars, primarily selected from the RAdial Velocity Experiment Data Release 6 (RAVE DR6), complemented with astrometric information from GAIA EDR3, are used to derive orbital parameters for dynamical analysis. Stars are selected based on their metal-poor ([Fe/H] $\leq$ -0.8) status according to photometric metallicity determinations from the recalibration of Sky Mapper Southern Survey (SMSS) by Huang et al.; an additional set of stars are included with spectroscopic metallicity measurements from various medium-resolution follow-up efforts between 2014 and 2017. The orbital energies and cylindrical actions of 7957 stars in the sample are calculated using the AGAMA package, then analyzed with the HDBSCAN unsupervised learning algorithm to cluster the stars into dynamical groups. This procedure identifies 179 Dynamically Tagged Groups (DTGs), ranging in size from 5 to 35 member stars, with 67 clusters containing at least 10 stars. Of the DTGs, some are found to belong to various Milky Way (MW) substructures, including Gaia-Sausage-Enceladus, the Metal-Weak Thick-Disk, Thamnos, the Splashed Disk, and the Helmi Stream. A total of 10 DTGs are associated with globular clusters, while none are found to be part of a MW dwarf galaxy. Our DTGs are associated with previously identified dynamical groups, while possible new identifications are considered. A search for chemical peculiarity among these DTGs found 22 of them to be associated with r-process-enhanced stars, and carbon-enhanced metal-poor (CEMP) stars are found among the targets with available spectroscopy.

Kortick Genesee (Poster # 30)

An Assessment of the Herbicide Fluridone as an Invasive Aquatic Plant Treatment Option in Alaska (USA) Wetlands

Genesee Kortick

The Copper River Delta (CRD) of south-central Alaska contains ecologically important wetlands that are threatened by the invasive aquatic plant species, Elodea canadensis, known as Canadian waterweed. Elodea is extremely difficult to eradicate, so the herbicide fluridone has been proposed as a potential control method for infested water bodies. In this study, the effects of fluridone application on water column dissolved organic carbon (DOC), total nitrogen (TN), and chlorophyll-a (chla) were examined, as they are important indicators of water quality and ecosystem productivity. I hypothesized that concentrations of DOC and TN would initially increase as a result of plant death and then would decrease as fewer plants persist in the water body. Further, chla should increase as the fluridone kills plants because this increases the light in the water column needed for algal growth. The study took place in two invaded pond systems in the CRD near Cordova, Alaska. The first system (Cannery) had one pond divided by a barrier into reference and treatment ponds (WCW and WCE) as well as an uninvaded reference pond (EYS) monitored in case of contamination. The second system (Wrongway-Wooded) had separate reference and treatment ponds (WD and WW). Study data were collected from May to October for four consecutive years for the Cannery system (2016-2019) and six consecutive years in the WW/WD system (2016-2021). Fluridone treatments in both systems occurred for three years (2016-2018 for Cannery, 2019-2021 for WW/WD). Fluridone treatment had no significant effect on DOC or TN in either system but had a small negative effect on chla in the WW/WD system. These results suggest that fluridone treatments may have relatively minor impacts on water quality in CRD ponds, although further research may be needed to understand long-term impacts on water chemistry along with other community and ecosystem parameters.

Kowalkowski Hannah (Poster # 31)

Number of daily load cycles positively affects Haversian remodeling in the rabbit mandible

Advisor: Matthew J. Ravosa, Departments of Biological Sciences, Aerospace and Mechanical Engineering, and Anthropology, University of Notre Dame

Hannah Kowalkowski

Haversian or secondary remodeling is the process by which osteoclasts, bone-resorbing cells, and osteoblasts, bone-forming cells, respectively, break down and repair skeletal microdamage caused by repeated load-induced deformation during an organism's lifetime. In the mammalian skull, correlations between secondary osteon densities and oral feeding behaviors suggest that the number of daily load cycles, rather than loading magnitudes, affects the extent of hard-tissue remodeling. This hypothesis was tested using 30 male New Zealand white rabbits (*Oryctolagus cuniculus*) raised from weaning for 48 weeks on one of two different dietary protocols. All rabbits were fed pellets daily, but only half of the rabbits ate hay cubes in addition to pellets (n=15 "control" diet versus n=15 "overuse" diet rabbits). Compared to pellets, hay is notably tougher and stiffer, requiring significantly greater chewing investment and chewing duration to process. However, it does not impact peak mandibular bone strain compared to pellet mastication. Thus, the mandibles of all rabbits experienced similar loading magnitudes, while rabbits raised on hay experienced elevated daily chewing cycles, i.e., increased cyclical loading. Here, we quantified remodeling in histological sections from the postcanine region of the rabbit mandible where mastication occurs (M^2/M^3). Osteon population density (OPD) is the number of intact and fragmentary secondary osteons per mm^2 of cortical bone. Percent Haversian bone (%HAV) is the percentage of total cortical area composed of intact and fragmented second osteons. Employing ImageJ image processing and analysis software, OPD and %HAV were measured from 100µm coronal sections of the right mandibular corpus to evaluate secondary remodeling between treatment groups. Mann-Whitney U tests documented significant differences in both OPD (P=0.14) and %HAV (P=0.003), with greater OPD and %HAV in the overuse-diet group. These findings support the hypothesis that Haversian bone remodeling is influenced primarily by the number of daily load cycles rather than loading magnitude.

Lee John (Poster # 32)

Multi-fidelity Data Augmentation for U-Net Retinal Vessel Segmentation

John Lee[1], Lauren Partin[1], Daniele E. Schiavazzi[1]

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In the field of image recognition and segmentation, deep learning architectures have already exceeded humans in accuracy and efficacy. One such architecture that largely dominates segmentation in healthcare is the U-Net [1,2]. While U-Net architectures were designed to produce an accurate segmentation from limited data, the size of the training dataset required to segment high fidelity (or high resolution) images is still very significant.

Since the cost of acquiring images increases significantly with their resolution, one would be tempted to augment a dataset consisting of a limited number of costly high-fidelity images with a large number of inexpensive low-fidelity images. In this context, we study how the size and fidelity distribution in the input data affects the U-Net segmentation accuracy, but also quantify segmentation variability using Monte Carlo sampling combined with DropBlock layers [3] or by applying random image rotations.

We trained 12 identically parametrized U-Net models for semantic segmentation on the DRIVE retinal vessel dataset [4], augmenting the training set with a varying number of images at different fidelities. Low-fidelity images are generated by interpolating the high quality 584 x 565 images in the DRIVE dataset down to 256 x 256 and 128 x 128 pixels. We finally compare the predictions from these networks using various metrics of accuracy, and quantify both the spatial error distribution and the standard deviation in the network predictions produced by 1000 Monte Carlo samples.

Mignondje Kossivi (Poster # 33)

Characterizing ESX-1-responsive proteins in *Mycobacterium marinum*

Armel Mignondje, Kathleen R. Nicholson, Patricia A. Champion
Department of Biological Sciences, University of Notre Dame, Notre Dame, IN, USA

About one third of the human population is infected with *Mycobacterium tuberculosis*, which is the bacteria responsible for causing tuberculosis. When *M. tuberculosis* enters the macrophage, it lyses the phagosome using the ESX-1 secretion system. We use *Mycobacterium marinum*, a fish pathogen, as a model organism to characterize *M. tuberculosis* because of their conserved ESX-1 systems. A previous study from the Champion lab found that MMAR_2894 was an ESX-1 substrate in *M. marinum*. This same study found that the deletion of *MMAR_2894* led to broad changes in protein secretion. We hypothesize that proteins impacted by loss of MMAR_2894 may have a role in the ESX-1 system. We generated constructs of Strep fusion proteins to validate the secretion data in the *MMAR_2894* deletion strain using western blotting. We focused on MMAR_3129, MMAR_5025, and MMAR_0547 (EsxH), which were the top 3 secreted proteins in the Δ*MMAR_2894* background. EsxH is part of the ESX-3 secretion system in *M. marinum*; MMAR_3129 and MMAR_5025 have not been associated with an ESX secretion system before. We also wanted to characterize regulatory proteins of the ESX-1 secretion system. We recently identified MMAR_1626 as a novel transcription factor responsible for regulating multiple components, substrates, and other regulators of ESX-1. We worked to characterize potential protein-protein interactions of MMAR_1626 with itself and other components of the ESX-1 system using a LacZ bacterial two hybrid (B2H) system. Additionally, we have been working to determine transcriptional activity at the promoter region of *MMAR_1626* to interrogate the regulatory mechanism of this key ESX-1 regulator.

Mikol Grace (Poster # 34)

Impact of Sustainable Announcements on Company Performance and Perception

Grace Mikol

Millenial and Gen Z shoppers say they want to support sustainable brands and are willing to pay more for sustainably sourced products. Thus sustainable business practices should increase profitability and popularity, yet many large companies aren't taking on ambitious sustainable goals. This project is a first step in research I hope to inspire into how companies can profitability capture sustainability goals within their brand identity. I will analyze the financial statements and CRI Scorecard ratings of six publicly traded clothing brands before and after sustainability announcements in order to determine their impact on the company's bottom line and public perception. To further get at the public perception I will look at news articles about the sustainability announcements in order to determine public reaction to the announcement.

Nguyen Kayla (Poster # 35)

E. faecalis requires fibrinogen in re-catheterization in CAUTIs

Advisor: Ana Flores Mireles, Dept. of Biological Sciences, University of Notre Dame

Kayla Nguyen

Catheter associated urinary tract infections (CAUTIs) make up 75% of hospital acquired infections (HAIs) and can lead to sepsis with a 30% mortality rate. Treatment for CAUTIs consists of catheter removal and replacement, if the patient still needs catheterization, followed by a round of antibiotics. However, management of CAUTIs has become increasingly difficult due to biofilms formed on the catheter and bladder walls and the rise of antibiotic resistance. One of the most common CAUTI pathogens, *E. faecalis*, is a commensal bacteria found in the gut, but becomes a pathogen in the catheterized bladder environment. Importantly, it has been shown to bind fibrinogen (Fg), a serum protein found in the bladder due to catheter induced inflammation, enhances its initial binding to the catheter surface. However, later effects on biofilm formation have not been explored. In this study, *E. faecalis* biofilms were formed in urine with Fg, bovine serum albumin (BSA) or no protein coating the surface of 96-well plates for 48 hours. Prior to biofilm formation, inoculums were grown in either urine or rich media to mimic the bladder environment or the gastrointestinal environment, respectively. As initial binding is the first step in biofilm formation, we hypothesized that *E. faecalis* biofilms formed in the presence of fibrinogen will be significantly larger than those formed with BSA or no protein regardless of initial inoculum media. Biofilms were grown for 48 hours in urine, fixed and processed and quantified by immunostaining of both *E. faecalis* and Fg. Our results showed only slightly larger biofilm formation for wells coated with Fg compared to BSA coated or uncoated wells suggesting that: **A)** the bacteria are eating the Fg and this there is less of a scaffold to use as a binding platform shown in a loss of Fg signal compared to control wells or **B)** the stagnant nature of the biofilm formation doesn't recapitulate the bladder environment where urine is periodically washing out any bacteria free floating in the bladder. Thus, future work will aim to more accurately represent the bladder environment by occasionally replacing the urine during the 48 hour biofilm formation.

Nishimura Corey (Poster # 36)

Creation and Characterization of CRISPR Cas9 *Aedes aegypti norpA* Visual Mutants

Advisor: Joseph O'Tousa, Dept. of Biological Sciences, University of Notre Dame

Corey Nishimura

Aedes aegypti, also known by its common name as the yellow fever mosquito, is the primary vector responsible for spreading dengue fever, chikungunya, and Zika virus. *Aedes aegypti* uses multimodal host identification employing thermal sensing, olfaction, and the visual system to locate targets. This project has implications for informing the development of new vector control methods. However, the core focus of this project is characterizing the importance of the norpA gene in phototransduction in *Aedes aegypti*. The norpA gene encodes for the enzyme phospholipase C (PLC) which is responsible for cleaving the substrate PIP2 into two secondary messengers IP3 and DAG necessary for the phototransduction cascade. Electroretinograms (ERG) are used to measure the electrophysiological response of the retina to light stimulus in order to determine the degree of visual processing. The project aimed to mutate the norpA gene to disrupt phototransduction and subsequently the visual perception in *Aedes aegypti*.

The first phase of this project entailed the creation and rearing of norpA mutant animals. The CRISPR/Cas9 DNA-editing system uses Cas9 endonuclease to form a complex with a norpA-specific gRNA that matches the target DNA sequence selected to be cut to create nonsense mutation to knock out the norpA gene. Guide RNA sequences from the first coding exon of the norpA gene were selected. A successfully mutated copy of norpA with a nonsense point mutation and a set of 2 and 6 base pair deletions around the CRISPR-targeted sequence was found by capillary analysis. Eggs from pair mates of confirmed heterozygous animals each containing a single copy of the mutated norpA gene produced a viable homozygous *Aedes* mutant, identified as $norpA^{CAT}$. ERGs were recorded to characterize differences in extracellular electrical response involved in the light perception of the $norpA^{CAT}$ mutant. The $norpA^{CAT}$ mutant displayed a significant degradation in the amplitude of electrical response when compared to wild-type controls. Additionally, the ERG response indicated a delayed recovery period after exposure to light pulse due to the disruption of phototransduction via mutation of the norpA gene inducing mutations in PLC. These results indicate the successful creation of norpA visual mutants in *Aedes aegypti* with a deficit in electrophysiological light response and therefore defective in the perception of visual stimuli.

Nunez Zoe (Poster # 37)

Getting Student Athletes Outside

Zoe Nunez

This project's aim was to help cultivate a connection between student athletes and their environment. This connection will hopefully instill some responsibility in the student athletes by introducing even more reason to respect the environment. In order to build this connection, information about the health benefits associated with spending time outside was presented via social media and marketing materials around athletic facilities. This information took form as fliers posted around the Joyce and Guglielmino athletic facilities informing students of health benefits associated with spending time outside. These health benefits are followed by a call to action that encourages people to make small choices in favor of the environment so that there may be a big impact over time. The marketing campaign was measured using a preliminary survey to understand student athletes' baseline sentiments and behaviors followed by additional online and ethnographic surveys to analyze the effectiveness of the marketing campaign. I was able to gain just under 200 survey responses and I connected with 18 student athletes via ethnographic interviews. There were two findings that surprised me. The first one was that the survey didn't reach as many people as I thought it would. It only reached about 50% of the survey respondents, however, I believe this is due to the fact that there were some display malfunctions in the Guglielmino that will be discussed more in the results section. Next, I was surprised that a significant amount of student athletes were already aware of all or some of the health benefits associated with spending time outside. Nevertheless, once this information was either introduced or once again brought to their attention, they wanted to spend more time outside. The student athletes I was able to have real conversations with through ethnographic research shared with me that they believe spending more time outside will make them more conscious of the impact they make on their surroundings. Therefore, this project shows that building awareness about the health benefits of spending time outside can lead to a shift in the beliefs and behaviors that cultivate a stronger connection with the environment.

Pitts Caroline (Oral Presentation)

Survey of human pathogens from tick samples collected in Corozal and Orange Walk Districts, Belize, Central America

Caroline Pitts[1], Nicole L. Achee[1], John P. Grieco[1], Alex Perkins[1], Stacy Mowry[1], Donovan Leiva[2], Marla Magaña-Cansino[3], Marie Pott[3], Alvaro Cruz[3], Jailene Castilllo[3] and Benedicte Fustec[1]
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Vector-borne diseases represent 17% of the global human disease burden including those transmitted by ticks. Tick-borne diseases vary by ecology, and many represent zoonoses, spilling over from animal populations to humans. The objective of this study was to characterize tick species and identify circulating tick-borne pathogens of human health relevance in northern Belize, Central America. Two communities, San Lazaro and Copper Bank, which vary in ecology and associated climates were selected. San Lazaro represents a secondary forested area, while Copper Bank represents a marine coastal zone. Ticks were hand-collected in January 2020 from dogs within the communities of San Lazaro and Copper Bank in the Orange Walk and Corozal political districts, respectively. Ticks were maintained in 70% isopropanol prior to molecular testing using standardized protocols developed under the Remote Emerging Disease Intelligence-Network (REDI-NET) to enable viral and non-viral (bacterial, parasitic) pathogen detection via the Oxford Nanopore GridION. A total of 403 ticks were collected, 287 from San Lazaro and 117 from Copper Bank. All adult (361) and nymphal stage (43) specimens belong to the genus *Rhipicephalus* (396/403; 98.2%) or *Amblyomma* (7/403, 1.8%). *Rhipicephalus sanguineus* ticks comprised the majority species within the *Rhipicephalus* genus (348/396, 87.8%), followed by *Rhipicephalus microplus* (6/396, 1.5%). Of the few *Amblyomma* ticks collected, the most common was *Amblyomma ovale* (3/7, 42.9%). Data is intended to be used for the development of mathematical models to produce spatial tick-borne disease risk estimates, using ecological covariates including land cover, distance to nearest waterbody, elevation, Palmer Hydrological Drought Index (PHDI), Normalized Difference Vegetation Index (NDVI), long term climate, annual precipitation, and annual temperature. These models will provide public health specialists in Belize and the region guidance in preparing for and responding to potential emerging infectious disease threats.

Robinson Kathryn (Oral Presentation)

Anti-B7H3 Monoclonal Antibodies Induce Natural Killer Cell- Mediated Apoptosis In Triple Negative Breast Cancer

Kathryn Robinson[1,2], Anudishi Tyagi[2], Venkata Lokesh Battula[2]

University of Notre Dame[1], South Bend, IN

Department of Leukemia, University of Texas MD Anderson Cancer Center[2], Houston, TX

Background: Immune checkpoint blockade (ICB) therapies have shown promising results in treating a variety of cancer types; however, the median duration of progression free survival with these treatments in triple negative breast cancer (TNBC) is very low. A protein B7 homolog 3 (B7H3), or CD276, was found to be overexpressed in many cancer cells with little to no expression on normal cells. It initially was characterized as a costimulatory molecule promoting the activation of T cells but is now understood to act mainly as a coinhibitory molecule of the immune system. B7H3's mechanism of action and receptor remain uncharacterized, but its preference for malignant cells offers hope for a new therapeutic approach with less toxicity and more efficiency.

Objectives: The primary objective of this study was to determine the expression of B7-H3 in primary TNBC tumors and measure the effect of novel B7-H3 blocking antibodies in activation of NK cells and T lymphocytes against TNBC cells.

Methods: We performed immunohistochemistry to investigate B7-H3 expression in TNBC primary tumors (n=90) and adjacent normal mammary tissue (n=30). The data was quantitated using Vectra-Polaris®, multi-spectral imaging system. Natural killer (NK) cells and T lymphocytes were isolated from buffy coats of healthy donors by Ficoll density gradient centrifugation. Immune cell-mediated apoptosis was measured by IncuCyte® live cell imaging system. RFP-tagged $B7H3^{+/-}$ TNBC cell lines were co-cultured with primary NK cells at different NK to target cells ratios (2:1, 4:1, 8:1) or T lymphocytes at different T cell to target cell ratios (5:1, 10:1, 15:1). The cells were simultaneously incubated with annexin V-green and different concentrations of the anti-B7H3 mAb with IgG control antibodies or chimeric Ab (chAb) with rituximab control antibodies for 24 hours in IncuCyte.

Results: Expression of B7H3 was significantly higher in TNBC patients compared to healthy donors ($p<0.0001$). We found that high B7H3 expression was associated with poor progression free and overall survival ($p<0.01$). Co-culture experiments using novel anti-B7H3 mAbs triggered NK cell-mediated apoptosis in a matter of hours. The annexin V binding to RFP+ TNBC cells was significantly higher in TNBC cells treated with anti-B7H3 blocking antibody compared to TNBC cells treated with NK cells alone, mAb alone, or IgG control with NK cells. However, no difference in killing was seen in B7H3 negative cells.

Conclusions: Our data suggests that B7H3 is overexpressed in TNBC cells and anti-B7H3 mAb and chAb inhibits its immunomodulatory function and activate NK cells and T cells against TNBC cells.

Rodriguez Brooke (Poster # 38)

The Challenges of Zoonotic Disease Spillover Surveillance: Learning from a Literature Review and an Experience in Florida

Brooke Rodriguez[1], Nicole L. Achee[1], John P. Grieco[1], Alex Perkins[1], Stacy Mowry[1], Margaret Elliot[1], LTJG Edward Traczyk[2], Jason Fajardo[2], Melissa Vizza[2], Le Jiang[3], Yvonne-Marie Linton[4], and Benedicte Fustec[1]
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The current COVID-19 pandemic highlights the significant impact of transmission of pathogens from wild animals to humans (zoonotic disease spillover). The Remote Emerging Disease Intelligence-Network (REDI-NET) is a research program dedicated to enhancing infectious disease surveillance capacity in order to better detect, predict, and contain zoonotic pathogens. REDI-NET is currently establishing field sites for invertebrate and environmental sentinel sample collection in Florida, Belize and Kenya. As a component to the REDI-NET program, this study had two main objectives: 1) to conduct a literature review to extract relevant pathogen and/or human disease presence data in Florida for use in mathematical modeling of disease risk; and 2) to participate in field sampling activities in Florida to better understand the challenges in correlating surveillance data with risk projections. The literature search was performed using the Emerging Infectious Diseases (EID), PubMed, and Web of Science repositories based on the search criteria of scientific and common names of pathogens and associated diseases listed in a baseline hazard report for Florida, and 'FLORIDA'. Extracted data were integrated into mathematical models, as appropriate. Direct field observation of tick, leech, water and soil sampling was conducted alongside REDI-NET consortium partners in Florida in December 2021. Our literature search sourced a total of 923 unique publications, 40 of which contained study-relevant data viable for modeling; an assumed underrepresentation of actual zoonotic pathogen transmission in Florida given the geographical scale within the state where animals and humans may interact. Observations from field sampling underscored the difficulty in capturing leech and tick specimens during routine collections; thereby preventing the ability to test for pathogens. Active field surveillance by REDI-NET consortium partners in Florida will continue with data outputs on pathogen presence from collected samples used to supplement data sourced online and subsequent refinement of zoonotic disease risk projections.

Ruelle Julia (Poster # 39)

Assessing Exposure of Urban Air Pollution with Citizen Science Data

Julia Ruelle

Air pollution, especially particulate matter 2.5 micrometers or smaller (PM2.5), has serious effects on human health, including heart disease and lung cancer, making it a leading cause of death around the world. As such, it is of scientific interest to measure the concentration of PM2.5 to inform policymakers and the public at large, as well as develop approaches to mitigate the associated negative effects. Current approaches to measuring and quantifying air pollution rely on sparse sensors, typically just one in a relatively large region, or on satellite data, which are also sparse in time and space. Here, I investigate the potential of using citizen science data to develop a more nuanced spatiotemporal analysis of the PM2.5 in the Research Triangle region of North Carolina. The citizen data is shown to be reliably accurate when compared with the higher-cost sensors from the EPA, and resulting in maps with considerably finer spatial information on local emissions. These results suggest the viability of using citizen science to more dynamically model the distribution of air pollution in cities, offering more specific information for the mitigation of effects of air pollution and the targeting of major sources of air pollution.

Sauter Jack (Poster # 40)

The Role of Platelet-Derived Growth Factor in Regeneration of the Zebrafish Telencephalon following Severe Blunt-Force Traumatic Brain Injury

Jack Sauter, Kaylee Cloghessy, David R. Hyde

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Advisor: David Hyde, Dept. of Biological Sciences, University of Notre Dame

Blunt-force traumatic brain injury (TBI) has an increasingly profound impact on human health throughout the world. The initial damage occurs as a generally irreparable blow to the head and the loss of brain neurons, which can then lead to chronic complications that occur throughout life. Due to the relatively limited regenerative potential of the adult human brain, current treatment strategies mainly focus on reducing or slowing these secondary complications. To address the primary defect of neuronal cell death, it is necessary to induce neuronal regeneration from an endogenous cell population. Zebrafish serve as an ideal model to examine neuronal regeneration due to their wide range of severity-dependent regenerative potential throughout the central nervous system. To investigate the genetic mechanisms behind neuronal regeneration in the telencephalon, we used a scalable damage paradigm to induce severe blunt-force TBI in adult zebrafish. Platelet-derived growth factor (PDGF) is a candidate genetic pathway for neuroregeneration because it is involved in regeneration of several other zebrafish cell types and has multiple functions within neural systems. Utilizing quantitative reverse transcriptase PCR, we found that PDGF is expressed in the zebrafish telencephalon, the center for learning and memory within the zebrafish brain. Initial data shows increased pdgfa and pdgfb expression that corresponds to peak cell proliferation at 72 hours post-injury, suggesting that PDGF could contribute to the regenerative process. Further investigation will show how both underexpression and overexpression of pdgf ligands will affect the regenerative phenotype with the goal of uncovering a more complete picture of the cellular and genetic basis behind zebrafish TBI recovery.

Schiefelbein Grace (Oral Presentation)

A Single RNA Modification Destabilizes a Pyrimidine-Motif RNA●DNA-DNA Triple Helix

Grace E. Schiefelbein, Charlotte N. Kunkler, Jessica A. Brown
Department of Chemistry and Biochemistry, University of Notre Dame

The formation of pyrimidine-motif RNA●DNA-DNA (R●D-D) triple helices, in which '●' and '-' represent Hoogsteen and Watson-Crick interactions, has been proposed for over 60 years, but the stability of these structures with RNA modifications has not been studied. For this study, eleven RNA modifications were chosen: 5-methylcytidine (m^5C), 5-methyluridine (m^5U), pseudouridine (Ψ), 2′-*O*-methyladenosine (Am), 2′-*O*-methylcytidine (Cm), 2′-*O*-methylguanosine (Gm), 2′-*O*-methyluridine (Um), 3-methyluridine (m^3U), 4-thiouridine (s^4U), inosine (I), and N^6-methyladenosine (m^6A). Several of these were previously found to stabilize or destabilize other nucleic acid double and triple helix structures. Using native gel-shift assays and microscale thermophoresis, the relative stability of a single modified position in a pyrimidine-motif R●D-D triple helix was measured at neutral pH. For the canonical R●D-D base triples (Z●A-T and Z●G-C), the Nm modifications (Um●A-T) were the least destabilizing, whereas modifications that directly interfered with Hoogsteen interactions (m^3U●A-T) were the most destabilizing, ranging from 2-fold to complete disruption of binding. A database search for biological examples of R●D–D triple helices whose formation could be controlled by modified RNA yielded three potential lncRNAs, but only one, containing three m^5C sites in a 22-nucleotide long pyrimidine-rich region, showed triple helix formation under conditions tested. As the formation of R●D-D triple helices in promoter regions of DNA leads to transcriptional enhancement and repression, this study reveals that RNA modifications could inhibit R●D-D triple helix formation as an additional level of transcriptional regulation.

Smith Carson (Poster # 41)

Medicinal plants in the diet of *Macaca fascicularis* may mediate microbiome variation associated with *Plasmodium* infection

Carson Smith
Advisor: Dr. Hope Hollocher
Co-authors: Chissa Rivaldi, Benjamin Gombash, and Hope Hollocher

Previous research has shown that *Plasmodium* infection may be associated with alterations in the gut microbiome, potentially due to illness-associated changes in the diet. Additionally, previous studies have suggested that nonhuman primates may deliberately eat medicinal plants to treat symptoms associated with parasite infections. However, there is a gap in the literature examining how these two phenomena may connect. This study used barcoding data of the 18S rRNA and 16S rRNA genes amplified from fecal samples of long-tailed macaques (*Macaca fascicularis*) in Bali, Indonesia, and Singapore to detect eukaryotes, including plant diet items and *Plasmodium*, and prokaryotes, respectively. Information about the medicinal qualities of plants identified in the macaque diet was determined through a search of the scientific literature on antiparasitic activity and general human medicinal uses of plants. Each plant item detected in the macaque diet was labeled as antiprotozoal, anthelmintic, antibacterial, antifungal, and/or general human medicinal according to documented properties; a plant was considered general human medicinal if it belonged to at least one category, and those that belonged to all categories were considered to be Anti-all. Partial mantel tests revealed positive correlations between *Plasmodium* infection and both general medicinal and Anti-all plants. Our data also show that there are significant differences in the abundances of general medicinal and Anti-all plants in comparisons between *Plasmodium*-positive and *Plasmodium*-negative samples. Positive linear relationships were identified between *Plasmodium* abundance and both general medicinal and Anti-all plant richness and between *Plasmodium* abundance and Anti-all plant abundance. A significant linear relationship was identified between observed bacterial richness and general medicinal plant richness. No direct linear relationships were detected between *Plasmodium* and bacteria. Our results provide preliminary support for medicinal plant ingestion being a potential mediating factor between *Plasmodium* infection and associated changes in variation in the macaque microbiome.

Steines Shannon (Oral Presentation & Poster # 42)

Characterizing the Retinal Pigment Epithelium During Zebrafish Neuronal Regeneration

Advisor: Dr. David Hyde, Dept. of Biological Sciences, University of Notre Dame

By 2050, over 22 million Americans are expected to suffer from disease related visual impairment that can highly affect their quality of life. To closely model the diseased human retina, constant intense light treatment has become a widely accepted method of retinal damage in adult zebrafish. Constant intense light causes degeneration and death of rod and cone photoreceptors, which induces Müller glia in the inner nuclear layer (INL) of the retina to de-differentiate and reenter the cell cycle. While there has been extensive research on the mechanisms that regulate Müller glia response to damage, research into the characterization of another cellular layer, the retinal pigment epithelium (RPE), during retinal regeneration is largely unexplored. The RPE is a monolayer of specialized pigmented cells in all vertebrate eyes that are critical for maintaining the function of the visual system, and RPE degeneration is a hallmark of age-related macular degeneration, a common blinding disease in humans. It has been suggested that the RPE is able to regenerate fully after complete genetic ablation in the zebrafish, which gives hope for uncovering potential modes of treatment for human disease. However, diseases like age-related macular degeneration are more gradual (chronic) processes of dysfunction and degeneration relative to the sudden (acute) constant light damage. Instead of complete annihilation of the RPE through ablation, I proposed to investigate the response of the RPE during retinal degeneration and regeneration in the zebrafish using two damage paradigms: (1) constant intense light treatment and (2) NMDA neurotoxicity. This study examined RPE tissue through two different methods: cryosectioning and whole mounting. These methods provided separate angles of visualization of the RPE to allow for greater understanding of any changes in RPE cell morphology. The zpr-2 antibody (a RPE-specific antibody detecting an unspecified antigen) was used to immunostain and identify RPE cells and their morphology. The results of this study found that there was a potential change in RPE morphology at 24 hours following the start of light damage due to increased zpr-2 staining intensity at that time point. I also found that there was a potential change in RPE morphology at 72 hours post-NMDA damage in both cryosectioned and whole-mounted zebrafish retinas due to an increased zpr-2 staining intensity at that time point. Through more experimentation to characterize the specific molecular mechanisms of how the RPE may be assisting the retina in regeneration during these timepoints, we could learn valuable insights that may allow us to stimulate similar environments in the human retina.

Sun Seunghoon (Poster # 43)

Senescence-associated secretory phenotype induces non-apoptotic cell death in normal mammary epithelial cells

Seunghoon Sun, Lisa Hom, Zachary T. Schafer

Cellular senescence is a state of permanent cell cycle arrest which occurs in response to different damaging stimuli. An important aspect of senescent cells is the ability for these cells to influence the surrounding microenvironment through the senescence-associated secretory phenotype (SASP). While previous studies have examined the role of the SASP in the context of cancer cells, the impact of the SASP on normal epithelial cells is not well understood which serves as the focus of this study. Our results show that when normal mammary epithelial cells are exposed to conditioned media from senescent fibroblasts, these cells undergo cell death. Furthermore, this cell death phenotype is maintained across different senescence-inducing stimuli such as the overexpression of the oncogene H-Ras and treatment with bleomycin, a DNA damaging agent. The data suggests that cell death caused by the SASP is mediated through caspase activation, but independent of traditional apoptotic pathways. Taken altogether, this study demonstrates a novel relationship between the SASP and induction of non-apoptotic cell death in epithelial cells.

Chou Brandon, Owusu Otoo Kingsley, Thanner Declan (Poster # 44)

Transcriptomic Analysis of the Defensive Response to Emerald Ash Borer in *Fraxinus pennsylvanica* (green ash)

Brandon Chou, Kingsley Owusu Otoo, Declan Thanner

Advisor: Jeanne Romero-Severson, Dept. of Biological Sciences, University of Notre Dame

Agrilus planipennis Fairmaire, better known as the Emerald Ash Borer (EAB), is an invasive species originating from North-East Asia. In the last two decades, EAB has spread from the Midwest to the northeastern parts of the continent, killing over 100 million ash trees. The cost of removal and replacement of dead and dying ash had risen to 10.7 billion dollars in 2012 and continues to rise. The mass die-off of green ash in riparian zones and northern wooded wetlands threatens the health of these essential ecosystems. In an effort to save this essential species and prevent further economic damage, this study focused on discovering the functional differences between the vast majority of green ash who succumb to infestation and the few who survive many years longer ("lingering ash"). To find out what makes almost all green ash deathly susceptible to EAB, our team performed a transcriptomic analysis of artificially infested families resulting from crosses between susceptible parents and crosses between lingering parents. We compared transcriptional data for the following contrasts: (1) high %larval kill, (2) low %larval kill, and (3) uninfested from the same families. Upon the completion of these comparisons, we discovered a range of differentially expressed genes between the three groups. In particular, the transcripts relating to spliceosomes, unsaturated fatty acids, and specific phytohormones were upregulated in high larval kill vs. low larval kill individuals, while other transcripts were upregulated compared to uninfested, regardless of larval kill phenotype. Armed with this information, existing ash breeding programs can assure funding agencies that the high % larval kill phenotype has a functional basis and can make progress towards the production of EAB resistant and locally adapted green ash for restoration in forested ecosystems and for the city green spaces essential for maintaining a sense of well-being in humans.

Weiss Laura (Poster # 45)

Investigating the structural properties of peptide-MHC complexes that contribute to immunogenicity

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Immunotherapy is a promising and rapidly developing avenue of cancer treatment that uses components of the immune system, like T cells, to treat cancer. The development of immunotherapies requires the identification of targets on the surface of cancer cells. Mutant peptides derived from intracellular proteins provide a possible therapeutic target that is specific to cancer cells. These mutant peptides, or neoepitopes, are presented by Class I Major Histocompatibility Complex (MHC) proteins, and this peptide-MHC (pMHC) complex can be targeted by T cells and initiate an immune response through interaction with T cell receptors. Not all mutant peptides, however, do initiate such a response, while some even generate a cytotoxic response. Predicting whether a peptide will be an appropriate therapeutic target is an ongoing challenge. Previous work in the Baker lab has suggested that the three-dimensional structure of neoepitopes as they are presented by MHC proteins is an important factor in determining the peptide's immunogenicity. In order to more fully understand the role of structure in immunogenicity, my project aims to solve a variety of pMHC structures, including both wild-type and neoepitope peptides, through X-ray crystallography. Here I present the solved crystal structures of two peptide-MHC complexes presenting the neoepitopes AVGSYVYSV and KLSHQLVLL, which were identified in a melanoma patient. These solved structures were compared to the model-predicted structures in order to analyze the accuracy of the modeling technique used, and they were also compared to their wild-type counterparts in order to evaluate and inform our current understanding of the ways in which structure affects immunogenicity.

Wernecke Elena (Poster # 46)

Clinical characteristics may predict lymph node burden in hormone receptor-positive (HR+), human epidermal growth factor receptor 2-negative (HER2-) breast cancer patients

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The recent RxPONDER trial demonstrated that postmenopausal patients with hormone receptor-positive (HR+), human epidermal growth factor receptor 2-negative (HER2-) breast cancer (BC) and 1-3 positive axillary lymph nodes (LN) who have a low Oncotype DX Recurrence Score (≤ 25) may potentially forgo chemotherapy. This necessitates a method to assess the extent of axillary LN involvement, which is typically determined through complete axillary lymph node dissection (ALND) for patients who are clinically node-positive (cN1) and undergoing upfront surgery. This may be overtreatment for patients with limited axillary nodal burden. This study aims to analyze the associations between clinicopathologic factors and number of suspicious or pathologically positive LNs in patients with cN1, HR+/HER2- BC who underwent upfront ALND (2002-2016). Clinical characteristics based on imaging and physical examination were compared with pathology. Among 158 patients, preoperative ultrasounds (US) identified 1, 2, 3, and >3 suspicious LNs in 61.7%, 18.5%, 18.5%, and 1.3% whereas ALND identified 1, 2, 3, and >3 positive LNs in 26.6%, 21.5%, 14.6%, and 37.3%. This corresponds to a 96.6% false negative rate (FNR). Further, the median number of suspicious LNs reported in each cohort of ALND-identified involvement was 1, with no significant correlation between the number of suspicious US-identified LNs and total verified positive ALND-identified LNs. There was no statistically significant association between the number of positive ALND-identified LNs and LN palpability, histology, race, hormone receptor expression, or histologic grade. Pearson's correlation test revealed no association between ALND-identified LN burden and median age, tumor size, or size of index LN found on preoperative US. These results demonstrate that preoperative US has a high FNR in determining LN burden. Individual clinicopathologic features do not accurately predict the extent of LN involvement. Multivariate studies will evaluate whether clinicopathologic features can be used in combination to predict the extent of axillary nodal involvement.

Wilson Noah, Kuc Rafael (Poster # 47)

Targeting One-Carbon Metabolism in BPD Lung Vasculature

Advisor: Dr. Margaret Schwarz, Dept. Chemistry and Biochemistry, University of Notre Dame

A shift from glycolytic and fatty acid derivatives toward one-carbon metabolites has been detected in the developing lung during transitions of the early postnatal period. Moreover, altered methionine homeostasis was observed in a bronchopulmonary dysplasia (BPD) murine model during the transitions between saccular to alveolar stage. BPD is characterized by the simplified alveolar and pulmonary vascularization and our studies aim to investigate the ameliorative properties of one-carbon metabolites in BPD. By mass spectrometry and immunoblotting we assessed the one-carbon metabolites levels and enzymes involved in the pathway to specifically identify the altered steps in the pathway. Our histology studies showed that methionine supplementation could rescue hyperoxia- induced BPD in a murine BPD model by promoting alveolar and pulmonary vascularization. To elucidate the mechanism, we investigated the one-carbon metabolites and enzyme levels in lungs by mass spectrometry and immunoblotting. Altered MNA and Nicotinamide levels and altered DNMT/NNMT and NAMPT/NNMT ratios were detected in hyperoxia lung tissues compared to the normal lung tissues. Moreover, we explored the role of methionine supplementation in neovascularization of endothelial colony forming cells (ECFC) isolated from umbilical cords and found out that methionine can promote cell proliferation and angiogenic sprouting of ECFC. Taken together, our results suggest the potential of one-carbon metabolite-based therapeutics in BPD and future studies in dissecting the molecular mechanism is warranted.

Zhang Joshua (Poster # 48)

Antitumor effects and mechanisms of SOS1 KRAS inhibitors on pancreatic ductal adenocarcinoma in pre-clinical models

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The deadly nature of pancreatic ductal adenocarcinoma (PDAC) is mainly related to the early and aggressive nature of the disease, late onset of symptoms and high resistance to conventional therapies. The current standard chemotherapeutic treatment nab-paclitaxel (NPT) plus gemcitabine (Gem), has been able to give an average prognosis of 8.5 months after detection, but its effects in mitigating to progression of the disease are limited. PDAC genomic analysis revealed that the most frequently mutated genes in this disease are KRAS, TP53, p16, and SMAD4. Among these, the oncogene KRAS is mutationally activated in approximately 95% of PDAC cases. Recently, pan-KRAS inhibitors BI-3406 and BAY-203 have been developed that inhibit the protein SOS1, an activator of KRAS. These pan-KRAS inhibitors target a broad range of oncogenic KRAS variants, indicating a therapeutic potential for PDAC. In cell proliferation assays, inhibition of cell proliferation in KRAS mutant AsPC-1 cells was 53.3% (NG), 43.7% (BI-3406), 68.7% (BAY-293), 71.1% (NG+BI-3406), 90.1% (NG+BAY-293). For KRAS mutant Panc-1, inhibition was 41.5% (NG), 31.9% (BI-3406), 59.3% (BAY-293), 56.8% (NG+BI-3406), 76.3% (NG+BAY-293). Western Blot analyses of Panc-1 and stromal cells exhibited that BI-3406 and BAY-293 decreased expressions of oncogenic proteins phospho-Ref, phospho-ERK, phospho-AKT, phospho-MEK, phospho-p70S6K, and phospho-4EBP1. BI-3406 and BAY-293 increased the expression of pro-apoptotic proteins Bax, cleaved caspase-3 and cleaved-PARP, as well as the expression of cell-cycle inhibitor protein p27. Subcutaneous xenograft study in NOD/SCID mice using AsPC-1 cells demonstrated that NG, BI-3406, and BAY-293 decreased tumor volume by 48%, 72% and 66%, respectively. Importantly combination of chemotherapy with KRAS inhibitors showed additive tumor growth inhibition effects, 78% (NG+BI-3406) and 87% NG+BAY-2903. These results suggest SOS1 KRAS inhibitors can improve the standard of current PDAC therapy. Thus, combination treatment of BI-3406 or BAY-293 with NPT+Gem standard therapy could potentially be an effective treatment of KRAS-mutant PDAC.

Zlaket Caroline (Oral Presentation)

Wait, Should I Even Have Kids? — Redefining "Your 20s" in the Daunting Anthropocene

Caroline Zlaket

Youth in the modern world have a unique perspective as they enter adulthood: they have grown up in the midst of a climate crisis. Because of this, a pressing question has been presented to children that may not have been as urgent to older generations: what does the future look like? Further, should there be hope to have kids / place faith in the future if the planet itself is unstable? While many writers and researchers have contributed their thoughts on this topic, few have been able to do it in the present moment (rather than in hindsight, looking back at childhood or life "as it was before"). The purpose of this capstone is to illuminate the specific emotions youth encounter when actively living through environmental degradation and chaos. Before beginning research for this project, I had rarely read about the climate crisis from a young adult's perspective, and the readings I did find could not capture all the various anxieties, worries, and joys of coming of age in the Anthropocene. Thus, I felt that exploring my own journey, thoughts, and emotions through creative writing could be a fruitful way to provide raw honesty. I explore the sentiment of suffocation that comes from news and information influx. Additionally, I discuss emotions pertaining to my family and how it feels trying to lean on older generations' wisdom while the modern-day climate is ever-changing. Finally, I address the events that cast shadows of doubt on a young person to make them feel apathetic toward any sort of hope for themselves or the world around them. Ultimately, I analyze what makes the future worth having faith in despite the fear-inducing status of the natural world.

Spirit of Science Presenters—3:30 pm to 5:00 pm

The below Middle School students are the awardees of **The Northern Indiana Regional Science and Engineering Fair (NIRSEF)** that is open to schools in the counties of Elkhart, Fulton, Marshall, and St. Joseph. They will be presenting their data at COS JAM.

Plastic Bag Recycling
Michael Turba

Extending The Life of A Battery With A Generator
Seth Kirzeder, Saint Anthony De Padua School

Is the 5 Second Rule True?
Luis Garcia Sanabria, St Vincent DePaul School

Gender and the Brain
Adeline DePauw, Christ The King School

No Pollution Rubber
Alexis Gasanovas & Mikayla Beach, Culver MS

A test of fun: How video game time affects test scores
John Morin, Christ The King School

The below High School students are the awardees of Indiana representative to ISEF 2022 (International Science and Engineering Fair). They were selected to present their data at COS JAM.

The Effect of Antepartum Maternal Position Changes on Labor and Delivery Outcomes
Grace Weaver, Marian High School

The Evasion of Cell Death by Cancer Cells Detached from the Extracellular Matrix
Luke Reynolds, Marian High School

Real-time Imaging Reveals the Antimicrobial Effectiveness of Natural Bromelain on Bacteria
Madelyn Cerney, Marian High School

What is the role of PRPF39 in cisplatin treated cancer cells?
May Weston, Marian High School