Research Project Title: Analysis of persistent colonies of methicillin resistant Staphylococcus aureus biofilm after long term antibiotic treatment

Student Presenter: Jacob Brooks

Faculty Mentor: Paul Stoodley

Faculty Mentor Department: Joint appointments in the Departments of Microbial Infection & Immunity and Orthopaedics

Research Abstract: This project incorporates the comparison and analysis of persistent cells in response to various antibiotics (either single or in dual combination) on Staphylococcus aureus lawn biofilms by examination of zone of inhibition (ZOI). Persistent colonies—slow growing, multi-antibiotic tolerant forms of bacteria, were studied to improve the understanding of chronic biofilm infections. Calcium sulfate hemihydrate beads are often infused with antibiotics in an effort to prevent further infection after revision of an infected arthroplasty. In previous studies, it has been shown that antibiotics such as tobramycin and vancomycin impede metabolic activity of lawn biofilm; yet, after long periods of antibiotic diffusion, even with concentrations well above the minimum inhibitory concentration (MIC), persistent colonies may slowly arise with the ability to grow and form biofilms. A lawn biofilm of methicillin resistant S. aureus SAP231 (MRSA-USA300-NRS384 strain), a pathogen responsible for many surgical site infections, was grown on a plate for 24 hours, followed by the placement of an antibiotic infused calcium sulfate bead, to determine if a zone of complete killing (ZOK) could be obtained. SAP231 is a bio-engineered, bioluminescent strain that was used to track the suppression of metabolic activity through in vivo image analysis technique (IVIS). Various antibiotics (vancomycin, tobramycin, ciprofloxacin, gentamycin, rifampicin), were investigated for persister cell generation through the measurement of ZOI over time. Replica plating after nine days allowed for the quantification of remaining viable bacteria. This system was used to distinguish persistent cultures from resistant mutants. Colonies were tallied and plotted to determine killing of antibiotic on a log scale. Antibiotics in dual combination produced fewer persistent colonies than their respective counterparts. Specifically, the combination of ciprofloxacin and rifampicin formed the largest ZOI and seemed to eradicate all possible bacteria. Conversely, tobramycin and gentamycin, both belonging to the aminoglycoside class of antibiotics, produced rings of persistent colonies, and consequently, a smaller ZOI. This series of experiments targeted possible combination of antibiotics that can lower surgical site infections in total joint arthroplasties, as well as decrease the chances of biofilms, which are associated with significant morbidity and mortality.
Research Project Title: Comparative analysis of Salmonella enterica serovar Typhi isolates from acute and chronic infections

Student Presenter: Bradley Eichar

Faculty Mentor: John Gunn

Faculty Mentor Department: Microbial Infection and Immunity

Research Abstract: Salmonella enterica serovar Typhi (S. Typhi) is the causative agent of typhoid fever—a human-specific disease that results in approximately 200,000 deaths each year. With appropriate treatment, most patients recover from the acute stage of the disease. However, 3-5% of S. Typhi infections lead to a chronic infection and asymptomatic colonization in the host gallbladder allowing carriers to unknowingly infect others despite no outward signs of illness. While it is known that S. Typhi mediates carriage through the formation of biofilms on the surface of cholesterol gallstones in the gallbladder, molecular mechanisms for chronic S. Typhi carriage are not well understood. This project compared genetic, molecular, and functional characteristics of 22 different S. Typhi isolates from confirmed acute and chronic infections, hypothesizing that the components necessary to mediate chronic carriage in the gallbladder may vary and be unique from acute clinical isolates. Biofilms of the isolates were examined utilizing a crystal violet quantification assay, a tetrazolium salt (XTT) reduction assay, and confocal microscopy. The presence and relative abundance of Vi-antigen and lipopolysaccharide (LPS) were confirmed using dot blot assays with specific anti-Vi-antigen and anti-LPS antibodies and subsequent densitometric analysis. Additionally, immunofluorescent microscopy was used to evaluate Vi-antigen and LPS expression. The presence of cellulose was detected quantitatively via a microtiter-based calcofluor binding assay. Finally, the genome-sequence as well as pulsed-field gel electrophoresis (PFGE) patterns of all strains were determined. PFGE and the sequencing data informed phylogenetic relatedness determinations of the strains. Biofilm and extracellular matrix (cellulose, Vi-antigen, and LPS) expression studies revealed unexpected high variability between the S. Typhi strains. Preliminary analyses do not support the uniqueness of the chronic versus acute isolates. Additional analysis will provide a better understanding of how salmonellae enter and persist in the chronic carrier state, which may lead to targeted drug therapies to alleviate the carrier state.
Research Project Title: Mitigation of Pseudomonas aeruginosa virulence factors by novel kinase inhibitors

Student Presenter: Anthony English

Faculty Mentor: Daniel Wozniak

Faculty Mentor Department: Microbial Infection and Immunity

Research Abstract: Psuedomonas aeruginosa (P.a.) is a Gram-negative opportunistic bacterium that causes serious acute and chronic nosocomial infections. The ability to fight bacterial infections, as such, is a growing concern in the world of medicine. With most antibiotics becoming ineffective against a mass of antibiotic resistant variants, controlling bacterial pathogenesis is crucial. We have put focus toward bacteriostatic alternatives that have shown reduction in both attachment and biofilm formation. Mitigation of these virulence factors could lead to a stronger immune response, thus helping to eliminate bacterial infections. A bank of 3000 kinase inhibitors (a type of drug primarily used in cancer treatment) was screened and of those, 5 molecules demonstrated efficacy above 50%. These inhibitors have been screened and have shown no inhibitory effects against bacterial growth. However, two of these candidates have shown reduction in attachment against a lab strain of P.a., as well as three clinical isolates. The other 3 candidates have indicated some degree of biofilm disruption capabilities and will be tested further.
Research Project Title: Identifying genes important for bacterial biofilm formation

Student Presenter: Nikolas Grotewold

Faculty Mentor: Daniel Wozniak

Faculty Mentor Department: Microbiology

Research Abstract: Introduction: Surface-bound bacteria in matrix-coated aggregates, called biofilms, are up to 1,000 times more resistant to antibiotics than planktonic cells (Rasmussen 2006). Rather than attempting to create new antibiotic treatments, disrupting biofilms would allow for a more effective way to use already existing ones. The formation and survival of a biofilm is paramount on having a strong initial cell-surface attachment by way of exo-polysaccharides (Palmer 2017). We hypothesize that interrupting bacterial attachment to surfaces will reduce disease burden.

Methods: Pseudomonas aeruginosa is a model organism in biofilm research due to its proficiency forming biofilms, its mechanisms for antibiotic resistance, and its medical impact in chronic infections. RNA sequence was performed to observe gene regulation upon surface contact within the first hour of biofilm formation. Rapid attachment assays narrowed down the list of regulated genes by seeing the degree of difference of biofilm formation. Clean deletions remove a gene from the organism and ability of biofilm formation can be observed when the gene is not present.

Results: RNA sequence results of cells attached within the first hour showed that 437 genes were regulated upon surface contact in the initial attachment phase of biofilm formation. Transposon mutants of these genes were screened for attachment to polyvinyl chloride. Of the 437 mutants of surface-regulated genes, 36% exhibit enhanced attachment and 15% have an attachment defect compared to the parental strain, PAO1. Mutants will be prioritized by the magnitude of attachment alteration and clean deletion mutants will be generated of the 20 highest priority genes. Future work will test the biofilm formation of clean deletion mutants.

Conclusions: Identification of essential genes for biofilm formation will facilitate the development of treatments specifically preventing biofilms.
Research Project Title: PmrA-regulated sRNAs and their effect on the pathogenicity of Francisella

Student Presenter: Victoria Kocsuta

Faculty Mentor: John Gunn

Faculty Mentor Department: Microbial Infection and Immunity

Research Abstract: Francisella tularensis is a Gram-negative, nonmotile, intracellular pathogen that is the causative agent of tularemia. Because of its virulence properties and ease of dissemination, F. tularensis is classified as a tier 1 (Class A) bioterrorism agent by the CDC. F. tularensis is classified by several subspecies that include tulanensis, holarctica, mediasiatica, and novicida. While most bacterial species contain many regulators including two-component systems (TCS) that regulate gene expression via a sensor kinase and a cytoplasmic response regulator, Francisella encodes a dearth of regulatory elements and lacks any classic TCS. However, PmrA is an orphan response regulator in F. tularensis that directly regulates the Francisella Pathogenicity Island (FPI) and affects intramacrophage growth and survival. Small RNAs (sRNAs) are important regulators of gene expression and protein production in prokaryotes and eukaryotes, and are also believed to play a role in gene expression in Francisella, especially given the lack of protein regulatory factors. The purpose of this study is to explore the role of sRNAs in regulating the virulence of Francisella, focusing on those regulated by PmrA. RNAseq was performed to identify sRNAs in F. novicida and an isogenic pmrA mutant. This data was used in conjunction with IntaRNA software to identify potential targets of the sRNAs. The first prioritized sRNAs were 539 and 543; however, intramacrophage survival and mouse virulence assays with mutants or overexpression strains showed no significant defects. Similar experiments are being performed on additional sRNAs from the IntaRNA-based priority list. This work will lead to a better understanding of how this bioterror agent responds to its environment and could lead to new therapeutic strategies to limit infection by F. tularensis.
Research Project Title: Defining the physiological changes occurring during biofilm formation in the filamentous fungus Aspergillus nidulans.

Student Presenter: Dale Lingo

Faculty Mentor: Stephen Osmani

Faculty Mentor Department: Molecular Genetics

Research Abstract: Fungi generate multi-layered biofilms resulting in gradients of cell crowding and oxygen concentration. Biofilm formation contributes to fungal persistence and drug resistance during infection. A recent study in our lab using the model filamentous fungus Aspergillus nidulans has revealed that the initiator cells at the base of a forming biofilm disassemble their microtubules (MTs). Notably, in the absence of the transcription factor SrbA that mediates adaptation to hypoxia, cells fail to depolymerize their MTs indicating that MT-disassembly in forming biofilms occurs as part of a regulated response to hypoxia. Additionally, we found that treatment of growing cells with hydrogen sulfide (H2S) mimics biofilm-mediated MT-disassembly. If MT disassembly is the sole cell biological modification occurring in fungal biofilms remains to be addressed.

The focus of my project is to investigate if other physiological changes occur in fungal cells as they form a biofilm beyond MT disassembly. Initial experiments indicate that the dynamics of the Golgi apparatus (GA) is also modified as cells form a biofilm. My goals are therefore to test the hypotheses that the dynamic changes in GA organization occur as a result of adaptation to hypoxia and that these alterations will be mimicked in growing cells by H2S treatment. Using spinning disk confocal microscopy, I will record time-lapse images to capture the dynamic changes in GA in wildtype cells as well as in cells lacking SrbA as they form biofilms. I will also examine the changes in GA organization in growing non-biofilm cells after treating them with H2S and whether the typical organization of GA is restored upon washing out H2S. Using genetic-crossing I have generated strains expressing fluorescently-tagged marker proteins to visualize GA in wildtype and SrbA-deleted backgrounds and I am currently imaging these strains to obtain a more thorough understanding of fungal physiology within biofilms.
Research Project Title: Unlocking a new therapeutic target of NTHI: separation of diverse binding sites is the key

Student Presenter: Nikhil Pramod

Faculty Mentor: Kevin Mason

Faculty Mentor Department: Nationwide Childrens- Center for Microbial Pathogenesis

Research Abstract: Nontypeable Haemophilus influenzae (NTHI) is a gram-negative bacteria that commonly causes respiratory tract infections including otitis media (OM). NTHI persists in the human body by resistance to host-derived antimicrobial peptides (AMPs) and import of essential heme-iron. The Sap Transporter (sensitivity to antimicrobial peptides) is the inner membrane protein complex that confers these activities. SapA, the periplasmic binding protein, binds both AMPs and heme-iron for delivery to the Sap complex and transport of these substrates into the bacterial cell. We are interested in mapping the binding sites for these two diverse substrates in SapA to ultimately design peptide inhibitors to block AMP binding without affecting virulence. Computational modeling of substrate bound SapA, utilizing the recently solved Apo crystal structure, revealed several residues that participate in binding of each substrate. Through genetic recombineering, we created specific point mutations in SapA and assessed the viability of these strains when confronted with AMPs. We found that SapA residues S290 and Y291 contribute, in part, to AMP binding, whereas S169 does not. Importantly, mutation of residue S290 decreases affinity for heme, in contrast to residues S169 and Y291. We have generated a double mutation in S290/Y291 to assess whether removal of both of these residues confers an additive affect in resistance to AMP killing. On-going work has identified an additional residue (R101) that participates in heme-binding but we predict does not recognize AMPs supporting our ability to separate the diverse binding sites. Since SapA is highly conserved across species our ability to design peptide inhibitors of the AMP binding site will support the testing of an advanced therapeutic of NTHI to assess affects on colonization and infection by NTHI.
Research Project Title: The use of traditional medicine in the treatment of malaria in immunocompromised individuals

Student Presenter: Errienna McKenzie

Faculty Mentor: Jessie Kwiek

Faculty Mentor Department: Microbiology

Research Abstract: The practice of traditional medicine is a vital component of the culture in Tanzania. While the recent governmental regulation of the profession escalated its legitimacy, traditional healers have played a crucial role in the foundation of an integrated healthcare system. The objective of this study is to understand how healers diagnose patients and establish treatment plans, more specifically as it relates to Malaria. Historically, the derivation of chemicals from plants has led to breakthrough discoveries in the pharmaceutical field. While the natural products prescribed by the healers in Tanzania aren't tested for their medicinal qualities and instead monitored to insure they don't cause adverse effects. I hoped to learn whether there was a prevailing treatment used amongst the healers as this could point to legitimate medicinal benefits. Here we show through interviews of traditional healers there is a recurring preferred treatment for Malaria in immunocompromised individuals. During the interviews of three traditional healers from different regions of Tanzania, I learned that they confirmed their diagnosis of Malaria by evaluating the symptoms of their patients and presented a treatment plan considering the patients' demographic information. To combat the common symptoms of vomiting, diarrhea and fever, an herbal tea was prescribed. The remedy consisted of heating water and leaves from the Mvele Vele tree then straining the leaves before oral consumption. Observing the commonalities in treatment for this disease illustrates the possibility this remedy may have an actual medicinal effect since it is widely prescribed by the healers. From a small sample, it can be deduced that the usefulness of traditional healers in the treatment of immunocompromised individuals requires more in-depth research. The chemical structure of the natural products used to treat Malaria could be isolated and analyzed. This information could then be expounded upon dependent on the findings.
Research Project Title: Optimization of the isolation of RNA from antibiotic tolerant Pseudomonas aeruginosa "Phoenix"colonies

Student Presenter: Kelly Moore

Faculty Mentor: Paul Stoodley

Faculty Mentor Department: Department of Microbial Infection and Immunity, Department of Orthopaedics

Research Abstract: Pseudomonas aeruginosa is known to produce variance in isolated colonies, including classically resistant colonies and viable but non-culture-able colonies (VBNCs). When an antibiotic loaded cement bead is placed into a lawn biofilm of $5 \times 10^9$ CFUs per cm$^2$, 3.23 CFUs per cm$^2$ of these phenotypes emerge in the zone of clearance. Of these a quarter are antibiotic tolerant but not resistant mutants because they are susceptible to antibiotics when subcultured. Further, they are actively growing, indicating that they are not dormant â€œpersisterâ€ cells. We have termed these colonies â€œPhoenixâ€ colonies. Phoenix colonies are a phenotype of Pseudomonas aeruginosa which grow up within the zone of inhibition of a bone cement bead containing 12mg/ml of tobramycin, but become susceptible after being removed and cultured. The mechanism behind phoenix colony development is unknown. Our approach to elucidate the mechanism was to use a transcriptomic analysis of the colonies. When phoenix colonies were isolated, placed in RNAlater and subsequently cultured, they exhibited the wild-type susceptibility. Due to the large proportion of resistant and VBNCs, the phoenix colonies were difficult to isolate. RNAlater was used to preserve RNA for further examination, but its influence on short term viability of bacteria which was required to retrospectively determine the antibiotic susceptibility of a colony was unknown, leading to the hypothesis that the RNAlater may affect the growth of VBNCs. The effect RNAlater had on the colonies was examined, comparing growth with RNAlater and without RNAlater and we calculated a p-value of 0.986. This suggests the RNAlater had no effect on culturability. VBNCs were produced in the absence of RNAlater. The heritability of the phenotype was also examined, and it was found that there was an increased rate of susceptible colonies in the second generation. The process of removing, culturing and plating the phoenix colonies, was repeated for three generations to examine the heritability of the phenotype, and it was found that there was an increased rate of susceptible colonies. Further study is needed to determine the complete mechanism behind phoenix colony development.
Research Project Title: Patterned electroceutical dressing clears microbial biofilms while inducing wound re-epithelialization

Student Presenter: Aurko Shaw

Faculty Mentor: Sashwati Roy

Faculty Mentor Department: Surgery

Research Abstract: Bacterial infection is a considerable threat when addressing acute and chronic wounds, and commonly aggregate to form microbial biofilms. Biofilms can have adverse effects on wound healing and are difficult to eliminate due to their antibiotic resistance from their self-excreting extra-polymeric substance (EPS) and their quorum sensing abilities. Various therapies have been explored to assist in clearance of biofilms and to restore the skin function. Previous studies in our lab have shown that weak electric fields have been able to disrupt bacterial biofilm in vivo using a FDA approved wireless electroceutical dressing (WED) with no external power supply. This study scales up this dressing by utilizing a battery-powered patterned electroceutical dressing (PED), thus creating stronger electric fields, and increasing the dressing’s ability to eliminate more aggressive biofilms. Each dressing is comprised of a biocompatible silk base with an Ag/AgCl ink pattern powered by a 6 V portable battery. The dressings were tested at three different electrical resistances at 2 kΩ, 10 kΩ, and 60 kΩ to optimize biofilm clearance without affecting the re-epithelialization of the host tissue. In vivo testing with these dressings was performed on two white Duroc pigs, with the control pig receiving no power from the battery. The pigs were subjected to six 2â€x2â€ burn wounds and infected with a mixed culture of clinically relevant Pseudomonas aeruginosa, Acinetobacter baumannii, and Staphylococcus aureus 3 days later (d0). Each pig received two dressings at the three different resistance values at d7, d14, and d21 time points, and were powered for 24 hours. Biopsies of the wounds were taken after the dressings were removed at d7, d14, and d21 time points. Histological data has shown that each treatment significantly improved wound closure and reduced bacterial load in comparison to the control dressings. Currently, we are testing to see how inflammatory pathways are affected at the cellular level. Additional experiments will test other biofilm forming bacteria, including antibiotic resistant bacteria.
Research Project Title: The role of oral mucosal natural killer cells (NK)/ Innate lymphoid cells (ILCs) during HIV/SIV pathogenesis and HIV/SIV associated malignancies

Student Presenter: Nicole Reinhold-Larsson

Faculty Mentor: Namal Liyanage

Faculty Mentor Department: Microbial Infection and Immunity

Research Abstract: Although the incidence of HIV has fallen in recent years, it continues to spread globally, and AIDS is the fifth leading cause of death in low-income countries. HIV infects CD4+ T cells via CD4 receptor on the surface of the cell and chemokine receptor CCR5 or CXCR4. Dendritic cells (DCs) and macrophages also play a pivotal role in HIV virus dissemination. Interestingly, we and others have shown the protective role of Natural killer cells (NK) and gut mucosal Innate lymphoid cells (ILCs) in HIV and SIV infection. Vaginal and rectal routes are the most common mode of HIV transmission. However, HIV can spread via oral route in children through breast milk in the HIV untreated mothers. Although very rare, oral-genital HIV transmissions can still occur. Furthermore, studies have shown that 70-90% of individuals infected with HIV (vaginal and rectal routes) develop oral mucosal infections such as oropharyngeal candidiasis or hairy leukoplakia. Interestingly, HIV infected patients are at higher risk of developing Epsteinâ€™Barr virus (EBV)-associated B cell malignancy. However, the potential role of oral innate immunity in pathogenesis of EBV-associated oral lesions in HIV-infected individuals is unknown. Tonsils are considered as oral-pharyngeal mucosal associated lymphoid tissues and play an important role in oral mucosal immunity. Recent studies have shown the important role of NK cell subsets in preventing B cell transformation by EBV in tonsils. Thus, we hypothesize that the loss of protective NK cell subsets in tonsils during HIV infection, could lead to increased EBV mediated B cell transformation. In this study, we explore the role of NK cells and ILCs during HIV/SIV pathogenesis, and EBV related B cell transformation. Due to limited access to the tonsils from HIV infected humans, we use tonsils collected from naïve, acute and chronically SIV infected rhesus macaques to characterize the role of NK cell and ILC subsets during infection utilizing flow cytometry. Furthermore, by using in vitro experiments we will investigate whether loss of NK cell subsets during SIV infection could lead to transformed B cells by EBV-related rhesus lymphocryptovirus (LCV) in rhesus macaquesâ€™ tonsils.
Research Project Title: Characterization of a bifunctional salvage pathway for byproducts of S-adenosylmethionine metabolism

Student Presenter: John Wildenthal

Faculty Mentor: F. Robert Tabita

Faculty Mentor Department: Microbiology

Research Abstract: S-adenosylmethionine (SAM) is a key sulfur-containing metabolite used in multiple biosynthetic processes. SAM serves as a methyl donor for DNA, RNA, and protein methylation. SAM also functions as a source of 5'-deoxyadenosyl radicals for radical SAM enzymes, which catalyze a diverse family of at least 85 different biochemical reactions. This results in the formation of 5'-deoxyadenosine (5dAdo) as a byproduct. Lastly, SAM is also used in polyamine synthesis for cellular growth and homoserine lactone production for quorum sensing, resulting in 5'-methylthioadenosine (MTA) as a byproduct. These byproducts are potent substrate inhibitors of enzymes utilizing SAM, and can accumulate to toxic levels and result in the loss of valuable organic sulfur and carbon if not recycled.

Recently, our lab discovered a novel salvage pathway in the photoautotrophic bacteria Rhodospirillum rubrum and Rhodopseudomonas palustris for the recycling of MTA. Herein MTA phosphorylase (MTAP), methythioribulose-1-phosphate isomerase (MTRI), and a novel class II aldolase (Ald2) sequentially convert MTA into dihydroxyacetone phosphate (DHAP) and methylthioethanol for carbon and sulfur salvage. Given the structural similarity between MTA and 5dAdo, we postulated that the same set of enzymes may also function to recycle 5dAdo into DHAP and ethanol for carbon salvage. To test this, we grew R. rubrum and R. palustris deletion strains in which MTAP, MTRI, and Ald2 were inactivated. Cell cultures were collected and analyzed by high-pressure liquid chromatography (HPLC) for the presence of 5dAdo. In both organisms growing anaerobically, inactivation of the MTAP and MTRI genes led to 5dAdo accumulation, whereas deletion of the Ald2 gene had no effect on 5dAdo levels. This shows that at least MTAP and MTRI function in 5dAdo salvage as well as MTA salvage. The role of Ald2 in 5dAdo metabolism, if any, remains unknown. Further experiments will confirm the chemical intermediates and unknown steps of this novel 5dAdo salvage pathway.
Research Project Title: The role of miR-155 on alveolar type II cellular gene expression during influenza infection

Student Presenter: Adam Bercz

Faculty Mentor: Ian Davis

Faculty Mentor Department: Veterinary Biosciences

Research Abstract: One of the most prevalent diseases in human history is influenza. Pandemics have claimed the lives of millions of people and annual epidemics continue to pose a major public health concern globally. As reported by the CDC, seasonal influenza-related illness around the world results in between 300,000-600,000 deaths every year. Commercially available antiviral compounds are limited in efficacy to treat the symptoms of influenza patients.

Investigations into host-pathogen interactions offer an alternative to current methods of combatting influenza. MicroRNAs (miRs) are non-coding nucleic acids which regulate multiple genes at a post-transcriptional level. We have shown that influenza infection induces higher levels of miR-155 expression in whole-lung cells of mice. This microRNA has been shown to regulate inflammatory processes. Furthermore, the increased abundance correlated with increased inflammatory activity in response to infection. Based on this pro-inflammatory function, we hypothesize that mir-155 plays a role in the physiological changes in the lung during influenza infection.

In healthy lung, alveolar type 2 cells (ATII) are critical in lung homeostasis. In addition to producing surfactant lipids and proteins in the lung, ATII cells are primary target of influenza viruses and express high levels of inflammatory markers upon infection. By isolating both virus-positive and virus-negative ATII cell populations from mice at multiple time points, the role of miR-155 can be observed. We used quantitative real-time PCR to determine expression levels of mir-155 and target genes. Virus-positive ATII cells express higher levels of miR-155 compared to virus-negative cells from the same lung. Angiotensin type II receptor is expressed at lower levels in virus-positive populations of ATII cells, while antiviral factors such as IFNγ receptor and NF-kB regulators are upregulated. The changes in target gene expression were also compared infected mice lacking miR-155 in ATII cells. In contrast to ATII cells from wild-type mice, the absence of miR-155 downregulates numerous target genes in virus-positive populations.

In conclusion, miR-155 influences gene expression of ATII over the course of influenza infection. The information drawn from this project may lead to investigating new targets for therapeutic agents which can mediate the host-response to more effectively treat influenza infections.
Research Project Title:

Student Presenter: John Thomas

Faculty Mentor: Howard-Varona Yes

Faculty Mentor Department: Cristina

Research Abstract: Isolation and characterization of 51 new phages for therapy against pathogenic Escherichia coli