Allegheny Branch ASM

Welcome to the

Allegheny Branch of ASM (ABASM)

Annual Fall Meeting

November 6-7, 2026

Hosted by

Mount Aloysius College

Schedule at a Glance: ABASM Annual Meeting 2026 Agenda

Mount Aloysius College, Cresson, PA

Friday, November 6, 2026:

4:00 – 5:00 pm Registration / Hang up posters Pierce Hall Lobby

5:00 – 6:00 pm Welcome and Dinner Cosgrave Meeting Rooms

6:00 – 7:00 pm **Dr. Cynthia Brame, Vanderbilt University** Cosgrave Meeting Rooms

Virtual via Zoom, Here's the LINK

Learning Assistants: A mechanism to promote belonging, confidence, and engagement in a variety of course contexts.

7:00 – 7:15 pm Return to Pierce Hall

7:15 - 8:15 pm **Students:** Launching your Microbiology Career Bertschi Center
Bring a hard copy of your resume or cover letter to discuss (optional).
Be prepared for a mock interview.
Faculty/Post Docs: Assessment Workshop Pierce Hall 208
Bring your microbiology assessments- what you love, what you'd like to improve. A hard copy is preferable so that we can swap/share.

Saturday, November 7, 2026:

8:00- 8:45 am Registration Pierce Hall Lobby
Faculty: Judging Assignments – Pierce Hall 208
Students: Poster Set up – Pierce Hall 1st and 2nd floor
Students: Upload Talks – Pierce Hall 105

8:55 – 9:00 am Welcome Remarks Bertschi Center

9:00 – 10:00 am Keynote Address Bertschi Center

Dr. Scott Lindner, The Pennsylvania State University

Ready, Steady, Go –How malaria parasites prepare for the unpredictable moments of their transmission

10:15 -11:15 am Poster Session 1 Graduate posters Pierce Hall 1st/2nd floor
Odd numbered undergraduate posters Pierce Hall 1st/2nd floor

11:15 -12:15 pm Oral presentations Pierce Hall 105/107/208

Students:

12:30 – 1:15 pm	Lunch Advice from Graduate Students Science and Art	Bertschi Center

Faculty/ Post Docs:

12:30 – 2:00 pm	Lunch Business Meeting	Cosgrave Meeting Rooms
2:15 - 3:15 pm	Poster Session 2 Even numbered undergraduate posters	Pierce Hall 1st/2nd floor
3:30 pm	Awards Presentation	Bertschi Center

\

Friday Nov. 6, 2026, 6:00-7:00 pm
Cosgrave Meeting Rooms
Guest Speaker: Cynthia Brame, PhD
Virtual via Zoom Meeting Link



Vanderbilt University

Professor of the Practice, Biological Sciences
Director, Learning Assistants Program
Associate Director, STEM Training and Education Program

Cynthia.brame@vanderbilt.edu

Learning Assistants: A mechanism to promote belonging, confidence, and engagement in a variety of course contexts

Cynthia Brame is a professor of the practice in Biological Sciences at Vanderbilt University, where she teaches introductory biology, genetics, biochemistry, and pedagogy courses. Originally trained as a biochemist, Dr. Brame focuses her research on developing, understanding, and sharing science teaching practices that improve the undergraduate experience for all students, with a particular focus on understanding ways that undergraduate learning assistants (LAs) can improve student experiences in gateway science courses. Dr. Brame is the author of *Science Teaching Essentials: Short Guides to Good Practice* (2019), served as founding co-editor of the *CBE Life Sciences Education Evidence-Based Teaching Guides*, is the director of Vanderbilt's LA program and the associate director of Vanderbilt's STEM Training and Education Project.

Saturday Nov. 7, 2026, 9:00-10:00 am
Bertschi Center
Keynote Speaker:
Scott Lindner, PhD, MBA, FASTMH



The Pennsylvania State University

Associate Professor, Dept. of Biochemistry & Molecular Biology
Co-Director, Center for Malaria Research
President, American Committee of Molecular, Cellular and ImmunoParasitology, ASTMH

sel27@psu.edu

Ready, Steady, Go – How malaria parasites prepare for the unpredictable moments of their transmission

Dr. Scott Lindner is Associate Professor of Biochemistry and Molecular Biology and Co-Director of the Huck Center for Malaria Research at Pennsylvania State University. His laboratory combines molecular parasitology, RNA biology, structural biology, and genomics to understand how malaria parasites prepare for transmission between mosquitoes and vertebrate hosts. A central focus of his research is translational regulation, the process by which parasites store and control messenger RNAs so that proteins can be produced rapidly when environmental conditions suddenly change during transmission. Research efforts in the Lindner laboratory include: 1) defining the molecular mechanisms that establish and release translational repression during key transmission stages, including gametocytes and sporozoites; 2) characterizing RNA-binding proteins, ribonucleoprotein complexes, and specialized ribosomes that regulate parasite development and infectivity; 3) applying proteomics, long-read genomics, CRISPR-based technologies, and structural approaches to uncover essential parasite functions; and 4) identifying vulnerabilities in malaria parasites that can be exploited to develop new transmission-blocking interventions. Through these studies, Dr. Lindner and his team seek to explain how malaria parasites anticipate unpredictable transitions between hosts and vectors, and how that knowledge can be leveraged to reduce the global burden of malaria.

Friday Night Student Activity: 7:15-8:15 pm Bertschi Center

Beyond the Petri dish: Launching your Microbiology Career

Presented by the TriBeta and Biology club students at Mount Aloysius College, this interactive session will provide practical advice on building your resume, interviewing, networking, and preparing for the job search. Whether you're just beginning to explore your options or getting ready to enter the workforce, this session will help you connect your passion for microbiology with your future career.

Optional: Bring a hard copy of your resume or cover letter to share.

Friday Night Faculty Activity: 7:15-8:15 pm Pierce Hall 208

Closing the Loop: Aligning Microbiology Learning Outcomes and Assessment

How do we know our students are truly learning microbiology? This session explores practical strategies for effectively assessing student knowledge, laboratory skills, critical thinking, and the ability to apply microbiological concepts to real-world situations. Faculty will consider a variety of assessment methods, from traditional exams and laboratory practicals to case studies, active learning activities, and authentic assessments. Participants will leave with ideas for aligning assessments with learning outcomes, providing meaningful feedback, and measuring student competency to better support student success in microbiology courses.

Optional: Bring a hard copy of exams, ideas for practicals, or active learning assignments for discussion. A shared drive will be used to exchange materials following the session.

The Allegheny Branch of ASM (ABASM)

This QR code links to the ABASM registration website.

ABASM's mission is to further the advancement of microbiology in all its phases through discussions and meetings, support of teaching, research, and research applications, and service as a branch of the American Society for Microbiology. ABASM draws its membership from the entire state of West Virginia and the western portion of Pennsylvania, bounded on the east by and including the counties of Potter, Clinton, Union, Snyder, Juniata, Perry, Cumberland and Adams. The Allegheny Branch belongs to ASM Region III, which includes five other branches: Western New York, Kentucky-Tennessee, Indiana, Ohio, and Michigan.

The Branch began in April of 1934 as the Central Pennsylvania Section of the Society of American Bacteriologists. It was primarily organized by a group at Penn State University with Dr. J.A. Sperry serving as first president. Meetings were held twice a year during the years 1934-1941. During this period, two joint meetings were held with the Central New York Branch. The branch was inactive during the "War Years". Starting in 1946, a concerted effort was made to establish a branch encompassing State College, Pittsburgh, and Morgantown, West Virginia. The first meeting of the new branch was held April 1, 1948. There were 75 people in attendance and it lasted well past midnight! The name, Allegheny Branch of the Society of American Bacteriologists (ABSAB), was proposed and accepted. The officers were as follows: Michael A. Farrell, President, Jonas E. Salk, President-elect, John C. Garey, Secretary Treasurer, and Mary Aiken, Councilor.

In 1961, the name was changed to Allegheny Branch of the American Society for Microbiology. The first newsletter was published in 1966 and the ABASM logo was introduced in March of 1970. After the national bylaws were changed in 1977, the branch switched to a single annual meeting in spring. A border dispute which erupted with the Eastern Branch in the latter part of the 1970's was resolved with the redrawing of the eastern boundary of the branch and changing of the bylaws in 1980. Starting in 1996 ABASM became an official sponsor of the Tristate Microbiology Teachers Conference. In 1996 and 1997 this meeting was held at Duquesne University. In the spring of 1998 there was an education symposium at the joint meeting in Ohio. Since 1983, seven joint meetings have been held with the Ohio Branch (1983, 1985, 1986, 1989, 1991, 1994, spring 1998), two joint meetings with Kentucky-Tennessee (1985 and spring 1998), and one with the Eastern Pennsylvania Branch (2012).

Jonas E. Salk is to this day the Branch's most well known member.

Oral Presentations:

3 Concurrent sessions 11:15 am-12:15 pm
Abstracts are included at the end of the program.
Names with an asterisk indicate the presenter.

Session 1: Pierce Hall 208

208-1 **Discovery and Characterization of Novel Bacteriophages Targeting *Acinetobacter baumannii* Patient Isolates**. Dominic Granata*, Daria Van Tyne. University of Pittsburgh– Greensburg, Greensburg, PA. (Undergraduate, Biomedical)

208-2 **Effects of *Pseudomonas aeruginosa* on Lifespan and Stress Responses in *Caenorhabditis elegans***. Katherine Bollinger*, Olivia Long. St. Vincent College, Latrobe, PA. (Undergraduate, Cell/Molec.)

208-3 **Determining Host-Binding Partners with *Listeria* Internalin Proteins**. Morgan McCann*, David Heisler. Duquesne University, Pittsburgh, PA. (Graduate, Cell/Molec.)

208-4 **Tandem Repeat Variation as a Source of Intraspecies Diversity in Biofilms**. Betsy Lewis*, Catherine Armbruster. Carnegie Mellon University, Pittsburgh, PA. (Graduate, Environmental)

Session 2: Pierce Hall 105

105-1 **Machine Learning Architectures and Multi-Omic Modalities for *Clostridioides difficile* Infection Diagnostics**. Manali Misra*, Regina Lamendella. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

105-2 **Dissecting the ECL1–RGI1/2 Link and Its Role in Sulfur Metabolism and Stationary Phase Survival in *Saccharomyces cerevisiae*.** Vicky Huang*, Jill Keeney. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

105-3 **A Bactericidal Monoclonal Antibody Synergizes with Antibiotics to Protect against *Pseudomonas aeruginosa* Murine Sepsis**. Spencer Dublin*, Mariette Barbier. West Virginia University, Morgantown, WV. (Graduate, Biomedical)

105-4 **Sensing kin death: Assessing the pervasiveness of lysis sensing across bacterial species**. Sophia Turecki*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA. (Graduate, Cell/Molec.)

Session 3: Pierce Hall 107

107-1 **Spatial Organization of Cutaneous Microbiomes Reveals Putative Microbial Contributions to Host Chemical Defenses in the American Toad**. Donovan McCammon*, Regina Lamendella. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

107-2 **Unmasking the Fungal Factor: The Overlooked Role of Fungi in CDI**. Eva Johnson*, Omkar Warke*, Regina Lamendella. Juniata College, Huntingdon, PA. (Undergraduate,Cell/Molec.)

107-3 **A nutrient-responsive transcriptional regulator coordinates biofilm formation and stress adaptation in *Pseudomonas aeruginosa*.** Anish Pyne*, Catherine Armbruster. Carnegie Mellon University, Pittsburgh, PA. (Graduate, Cell/Molec.)

Posters: 2 non-concurrent sessions
1st and 2nd floors of Pierce Hall
Abstracts are included at the end of the program.
Names with asterisks indicate presenters.

Session 1: 10:15 -11:15 am

All Graduate and Faculty Posters

Odd Numbered Undergraduate Posters

Session 2: 2:15 - 3:15 pm

Even Numbered Undergraduate Posters

Graduate and Faculty Posters: Session 1, 10:15-11:15 am, Pierce Hall 1st and 2nd Floor

G1. **Memory of Chronic Nitrogen Deposition in the Rhizosphere Microbiome.** Ayers Aguiar*, Ember Morrissey. West Virginia University, Morgantown, WV.

G2. **Effects of volatile 6-pentyl-2H-pyran-2-one (6PP) on the growth of aflatoxigenic *Aspergillus flavus* and *Aspergillus parasiticus***. Stacy Santiago-Garay, Maya Tanikawa-Brown, Josephine Wee. The Pennsylvania State University, State College, PA.

G3. **Exploring a role for HDAC3 in regulation of airway epithelial barrier integrity and bacterial infection response**. Erin Walsh*, Catherine Armbruster. Carnegie Mellon University, Pittsburgh, PA.

G4. **Computer vision-enabled high-throughput phenotypic compound screen using Vibrio cholerae**. Jesse Derringer*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA.

G5. **An mRNA Lipid Nanoparticle-Based Approach to Pertussis Toxin Antigen Development**. Ian Leighton*, Heath Damron. West Virginia University, Morgantown, WV.

G6. **A Treatment-Ready Model for *S. aureus* Bacteremia**. Barbara Wehle*, Heath Damron. West Virginia University, Morgantown, WV.

G7. **Screening Imidazole and Diimine Compounds as Potential Antibiotics**. Elias Griffin*, David Heisler. Duquesne University, Pittsburgh, PA.

G8. **Investigation of the Transcriptomic changes of *B. burgdorferi* to Identify Candidate Vaccine Antigen**. Annalisa Huckaby*, Mariette Barbier. West Virginia University, Morgantown, WV.

G9. **Fluorogen-Activating Proteins Reveal Spatial Gene Expression Patterns in *Vibrio cholerae* Biofilm Development**. Krutika Joshi*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA.

G10. **DbfQRS: A membrane stress-sensing pathway that balances protection and proliferation in *Vibrio cholerae***. Emmy Nguyen*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA.

G11. **Characterization of *S. coelicolor* Type VII Secretion System Involvement in Chromosome Segregation**. Lili Marcharashvili*, Joseph McCormick. Duquesne University, Pittsburgh, PA.

Graduate and Faculty Posters continued on the next page

Graduate and Faculty Posters: Session 1, 10:15-11:15 am, Pierce Hall 1st and 2nd Floor

G12. **Rising to the Challenge: Uncovering Species-specific Fructan Degradation to Optimize low-FODMAP Sourdough Breads**. Quinn Burnett*, Josephine Wee. The Pennsylvania State University, State College, PA

Faculty 1. **Metagenomes of lichens *Peltigera membranacea*, *Flavoparmelia caperata*, and *Physcia stellaris* include Acidobacteriae and *Nostoc* sp**. Welkin Pope*. Chatham University, Pittsburgh, PA.

Session 1, 10:15-11:15 am, Pierce Hall 1st and 2nd Floor

Undergraduate Odd-Numbered Posters.

U-1. **Water Chemistry-Guided Enrichment of Metal-Tolerant Bacteria from Acid Mine Drainage**. Ethan Buchleitner*, Liu Cao. Gannon University, Erie, PA.

U-3. **Water Quality and Microbial Diversity in Lake Erie**. Mattia Parrini*, Liu Cao. Gannon University, Erie, PA.

U-5. **Assessing Tick-Borne Illness Rates Through Processing of Ticks From Local Community Members**. Logan Cree*, Ilse Ness*, Ashley Robuck*, Jill Keeney. Juniata College, Huntington, PA.

U-7. **Persistence and Mitigation of Foodborne Pathogens in Hydroponic Lettuce Systems and During Seed Germination**. Gustaf Geremia*, Regina Lamendella. Juniata College, Huntington, PA.

U-9. **Assessing the Relationship Between the Gut Microbiome and Microplastic Accumulation in the GI Tract of American Eels, *Anguilla rostrata***. Juliana Onuskanich*, Maycie Kulp*, Regina Lamendella. Juniata College, Huntington, PA.

U-11. **Characterization of Phages Infecting *P. putida***. Maureen Johnson-Keitt*, Nicole McAllister Conrad. Seton Hill University, Greensburg, PA.

U-13. **Investigating the Presence of Bacteriophages in Soil Using Bacterial Hosts**. Peyton Cercone*, Nicole McAllister Conrad. Seton Hill University, Greensburg, PA.

U-15. **Diversity and Characterization of Bacterial Isolates from the Marr Ice Piedmont Glacier Forefield, Antarctic Peninsula**. Mackenzie Tickle*, Alicia Purcell. Marshall University, Huntington, WV.

Undergraduate posters continued on the next page

U-17. **Functional Genomic Insights into Predatory Bacteria Responding to Environmental Warming in Antarctic Soils**. Sarah Ellis*, Alicia Purcell. Marshall University, Huntington, WV.

U-19. **Evaluating Metal Tolerance in Bacteria with Light Rare Earth Element Biorecovery Potential**. Ellena Perdue*, Michelle Valkanas. PennWest University–California, California, PA.

U-21. **Evaluating the Synergistic Properties of a Monoclonal Antibody against Antimicrobial Resistant Strains of *Pseudomonas aeruginosa***. Sarah Rahin*, Mariette Barbier. West Virginia University, Morgantown, WV.

U-23. **Optimization of PCR to streamline *B. burgdorferi* in preclinical models of Lyme Disease**. Mauren Miller*, Mariette Barbier. West Virginia University, Morgantown, WV.

U-25. **Ionizable lipid nanoparticles for the inhibition of STAT5 and treatment of B-ALL**. Aidan Murray*, Sharan Bobbala. West Virginia University, Morgantown, WV.

U-27. **SEA-GENES: Finding Clues to Gene Function in Mycobacteriophage ZoeJ**. Hailee Gunn*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

U-29. **Is *Enterococcus* Auxotrophic for Lactose? Implications in Graft Versus Host Disease in Recipients of Allogenic Bone Marrow Transplants**. Abrielle Brown*, John Trimble. Saint Francis University, Loretto, PA.

U-31. **The impact of nutrient and oxygen availability on gut Clostridial growth in a heart failure model**. Amber Terry*, Michelle Valkanas. PennWest University–California, California, PA.

U-33. **The effects of hygiene on antibiotic resistance genes in the oral microbiome**. Arica Collier*, Michelle Valkanas. PennWest University–California, California, PA.

U-35. **GLP-1 Receptor Agonist Therapy Reshapes the Gut Microbiome**: A Longitudinal Genomic and Bioinformatic Study of Fecal Microbial Dynamics. Omkar Warke*, . Juniata College, Huntington, PA.

U-37. **The Role of Myeloperoxidase in Tumor Cell and Myeloid-Derived Supressor Cell Migration**. Gianna Moses*, Mariette Barbier. West Virginia University, Morgantown, WV.

Undergraduate posters continued on the next page

U-39. **Determining the Optimal Expression of *Borrelia burgdorferi* Outer Surface Protein A in BSK-II Culture**. Olivia Conaway*, Mariette Barbier. West Virginia University, Morgantown, WV.

U-41. **Whole-Genome Sequencing of Nine *Escherichia coli* Isolates Recovered from Retail Ground Beef in Puerto Rico** Alanis Velazquez Rivera*, Edward Dudley. The Pennsylvania State University, State College, PA.

Session 2: 2:15 - 3:15 pm Pierce Hall 1st and 2nd Floor Hallway

Undergraduate Even Numbered Posters.

U-2. **Establishing a Fluorescent Antibody Repository for Flow Cytometry Users of the WVU FCSCCF**. Caitlin Bissell*, Kathleen Brundage. West Virginia University, Morgantown, WV.

U-4. **Kinetic Characterization of *Clostridium butyricum* Enzymes and Pancreatin on Starch Substrates**. Gabriel Infante*, Darrell Cockburn. The Pennsylvania State University, State College, PA.

U-6. **The Effectiveness of a Laminated Antimicrobial Film to Control Microbes Associated with Low Moisture Foods**. Matthew Shue*, Catherine Cutter. The Pennsylvania State University, State College, PA.

U-8. **Whole Genome Sequence of 17 *Staphylococcus aureus*, Isolated from Ground Beef in Puerto Rico**. Nashalee Mercado*, Edward Dudley. The Pennsylvania State University, State College, PA.

U-10. **Investigating Macrophage Abundance and Polarization in Gemcitabine Treated Mice to Improve Therapeutic Outcome**. Callie Ancosky*, Timothy Eubank. The Pennsylvania State University, State College, PA.

U-12. **Testing Sensitivity and Resistance of *S. cerevisiae* YKL121W Gene Deletion and its Paralog Deletion, YMR102C, across Different Types of Media**. Madeline Hatch*, Jill Keeney. Juniata College, Huntington, PA.

U-14. **Exploring the Effects of YMR114C Gene Deletion**. Parker Thomas*, Jill Keeney. Juniata College, Huntington, PA.

U-16. **CRISPR-Cas9 and MDA-Enhanced Nanopore Sequencing for Culture-Independent Detection of *Staphylococcus aureus***. Liesl Stine*, Jasna Kovac. The Pennsylvania State University, State College, PA.

U-18. **Industry-Informed Peroxyacetic Acid Treatments Reduce *Campylobacter jejuni* Culturable Cells More Than Viable Cells on Chicken Wings**. Robert Monson*, Jasna Kovac. The Pennsylvania State University, State College, PA.

Undergraduate posters continued on the next page

U-20. **GLP-1 Receptor Agonist Therapy Reshapes the Gut Microbiome: A Longitudinal Genomic and Bioinformatic Study of Fecal Microbial Dynamics**. Ethan Achmoody*, Hailey Baker*, Brady Heath*, Joshua McMichael*,Regina Lamendella. Juniata College, Huntington, PA.

U-22. **Isolation of *Plasmodium yoelii* Ribosomes Using 3xMango-II Tag**. Brayden Wenrich*, Scott Lindner. The Pennsylvania State University, State College, PA.

U-24. **From Structure to Function: Biochemical Characterization of Four Proteins of Unknown Function**. Jamison Gaugler*, Giovanni Guido*, Emma Hyder*, Rosemary Mcgovern*, Olivia Long. Saint Vincent College, Latrobe, PA.

U-26. **Phage Purification: PEG Precipitation and Triton X-100 vs. Endotoxin Removal Resin Spin Column and Preliminary Work For LPS Exposed Mammalian Cells**. Briana Kochumuttom*, Nicole McAllister Conrad. Seton Hill University, Greensburg, PA.

U-28. **Characterization of *Bifidobacteria* spp. Lipoprotein**. Sam Carillo*, Timothy Meredith. The Pennsylvania State University, State College, PA.

U-30. **Green Microbiology: Determining if Single Use Plastics can be Reused While Remaining Accurate and Clean**. Liesl Allison*, Welkin Pope. Chatham University, Pittsburgh, PA.

U-32. **Annotation of *Arthrobacter globiformis* B-2979 phages**. Aislin Manzella*, Welkin Pope. Chatham University, Pittsburgh, PA.

U-34. **Effect of Oral Nicotine Pouches on Lifespan and Germline of *C. elegans***. Celia Cole*, David Smith. West Virginia University, Morgantown, WV.

U-36. **ButterNova: The Isolation and Characterization of a Novel Arthrobacter globiformis B-2979 Phage**. Santino Premozic*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

U-38.**Digging for Diversity: Isolation of the Soil Phage Trailhead A Newly Isolated Bacteriophage from Environmental Soil Samples.** Tyler Schlobohm*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

U-40. –Scratch--

U-42. **SEA-PHAGES: DirtyMert: A Filthy Bacteriophage**. Demetri Eori*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

2026 ABASM Oral Presentation Abstracts

208-1 **Discovery and Characterization of Novel Bacteriophages Targeting *Acinetobacter baumannii* Patient Isolates**. Dominic Granata*, Daria Van Tyne. University of Pittsburgh–Greensburg, Greensburg, PA. (Undergraduate, Biomedical)

Acinetobacter baumannii is a nosocomial pathogen responsible for infections that are often acquired within hospital systems and can readily develop resistance to the antibiotics used in treatment of these infections. To respond to this growing antibiotic resistance within infection-associated strains, novel treatment and therapeutic approaches are necessary to combat *A. baumannii* infections. Bacteriophages, which are viruses of bacteria, are an emerging opportunity to treat *A. baumannii* infections with specificity and complementarity to existing antibiotics. However, repositories of *Acinetobacter*-targeting bacteriophages are necessary to establish pipelines intended for patient isolate screening and possible treatment. We are working to discover and characterize novel *Acinetobacter*-targeting bacteriophages from diverse wastewater sources and to compare them with existing bacteriophages isolated previously by our lab and with bacteriophages sourced from research repositories. We will perform susceptibility screening of 53 clinical *A. baumannii* isolates collected from patients at UPMC hospitals against a panel of phages from multiple origins. The sequence type of each strain and the antibiotic resistance-associated genes present within these isolates were identified through whole-genome sequencing and revealed that the bacterial isolates are genetically diverse and encode an abundance of antibiotic resistance genes. Bacteriophage genomes will also be sequenced and significant differences between them will be explored. In future work, we aim to evaluate the utility of combining these phages with clinically relevant antibiotics, and to identify the ways that select *A. baumannii* isolates evolve resistance to the bacteriophages in our collection.

208-2 **Effects of *Pseudomonas aeruginosa* on Lifespan and Stress Responses in *Caenorhabditis elegans***. Katherine Bollinger*, Olivia Long. St. Vincent College, Latrobe, PA. (Undergraduate, Cell/Molec.)

Caenorhabditis elegans is a valuable model organism for studying biological stress responses due to its short lifespan, rapid reproduction, and ease of laboratory maintenance. Its ability to respond to environmental stressors makes it useful for investigating the effects of bacterial exposure on organismal health. This study aims to compare the lifespan and stress responses of two C. elegans strains, N2 and VZ892, following exposure to *Pseudomonas aeruginosa*, an opportunistic bacterial pathogen. Initial comparative lifespan analysis under normal, non-stressed conditions revealed similar lifespans between the N2 and VZ892 strains. Building upon these findings, ongoing experiments are investigating how exposure to *P. aeruginosa* affects survival compared to worms maintained under normal conditions using *Escherichia coli* OP50. These experiments aim to determine how bacterial exposure affects longevity and stress responses and whether these effects differ between the two strains. Additionally, fluorescence microscopy will be used to investigate stress responses under three conditions: normal OP50 exposure, heat-induced stress as a positive control, and *P. aeruginosa* exposure. The VZ892 strain expresses a GFP fusion protein, allowing visualization of a transcription factor involved in cellular stress responses. Comparing these conditions will help determine whether *P. aeruginosa* induces a measurable cellular response. Together, these experiments aim to better understand the relationship between bacterial exposure, stress responses, and survival in *C. elegans*.

208-3 **Determining Host-Binding Partners with *Listeria* Internalin Proteins**. Morgan McCann*, David Heisler. Duquesne University, Pittsburgh, PA. (Graduate, Cell/Molec.)

Listeria monocytogenes is a gram-positive opportunistic foodborne human pathogen with a high mortality rate in those who are elderly, immunocompromised, or pregnant. *Listeria* relies on its dissemination from initially infected intestinal mucosa cells to distal tissues for its pathogenesis. A class of proteins initially thought to be responsible for internalization of *Listeria* into cells, internalin proteins, have been shown to be involved in multiple steps of infection, but most remain understudied. All internalin proteins are defined by an N-terminal leucine rich repeat (LRR) domain, a well-conserved domain that mediates non-covalent protein-protein interactions. We aim to define the interaction between host proteins and LRR domains of internalin proteins to understand the roles of these proteins during an infection. Ubiquitin associated interaction trap (UBAIT) systems have been used to capture the protein targets of mammalian and bacterial ubiquitin E3 ligases. Here, we modified this approach by replacing the IpaH2.5 E3 substrate binding domain from *Shigella* with the LRR domains from the internalins to identify host-binding partners. Using mammalian cell lysates, we identified potential binding partners for eight of the internalin LRR domains that suggests roles in regulating mammalian gene expression and cell cycle. We also found that internalin Lmo0549 interacts with host autophagy proteins. Although evasion of autophagy by *Listeria* has been described, it has not previously been shown that internalin proteins directly interact with autophagic machinery. Further investigations will confirm direct host-binding partners with internalin protein LRR domains and determine the roles these proteins play to promote the pathogenesis of *Listeria*.

208-4 **Tandem Repeat Variation as a Source of Intraspecies Diversity in Biofilms**. Betsy Lewis*, Catherine Armbruster. Carnegie Mellon University, Pittsburgh, PA. (Graduate, Environmental)

Hypermutable tandem repeat regions (TRRs) are an underappreciated evolutionary mechanism for the generation of intraspecies phenotypic diversity in the absence of an immediate adaptive benefit. Methods: We computationally identified TRRs in the Pseudomonas aeruginosa (Pa) PAO1 genome and compared the abundance of repeats capable of causing frameshifts with that in scrambled genomes. We examined repeat-length distributions at selected loci across 22,569 publicly available Pa genomes. We also evaluated lipopolysaccharide production of an evolved TRR mutant using a column-based hydrophobicity assay and lipopolysaccharide (LPS) gel. Results: We identified 10,258 TRRs in PAO1, 85% of which were located within coding regions. Repeats with unit lengths not divisible by three can cause frameshifts following single-unit insertions or deletions. These frameshift-capable TRRs were less frequent in PAO1 than in scrambled genomes. Across publicly available genomes, selected frameshift-capable TRRs exhibited narrower repeat-length distributions than frame-maintaining TRRs. An evolved single-repeat deletion in wbpI, which encodes an epimerase required for O-specific antigen synthesis, resulted in loss of O-specific antigen production. Conclusions: The reduced abundance and narrower length distributions of frameshift-capable TRRs are consistent with evolutionary constraints on repeat variation within coding regions. Nevertheless, repeat-length mutations can generate phenotypic diversity, as demonstrated by loss of O-specific antigen production in an evolved biofilm isolate. These findings identify tandem repeat variation as a mechanism of diversification in Pa biofilm populations.

105-1 **Machine Learning Architectures and Multi-Omic Modalities for *Clostridioides difficile* Infection Diagnostics**. Manali Misra* , Regina Lamendella. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

In this study, we apply machine learning and deep foundation model architectures to our multi-omic *Clostridioides difficile* infection (CDI) cohort to benchmark diagnostic classification across diverse algorithms and data modalities. We systematically evaluate classical supervised classifiers (e.g., Random Forest, XGBoost, PLS-DA) alongside pretrained transformer backbones (e.g., BiomeGPT, MGM, MGM2) on matched 16S rRNA amplicon, metagenomic (MG) DNA, and metatranscriptomic (MT) RNA profiles. In multi-omic beta diversity evaluations across our dataset, metatranscriptomic KEGG Ortholog (MT KO) functional expression demonstrated the strongest statistical separation between CDI+ and CDI− status (PERMANOVA pseudo-$F = 4.83, p = 0.001$) relative to DNA-level taxonomic profiles (pseudo-$F = 2.56, p = 0.004$). While shallow supervised models yield high in-distribution accuracy, transfer learning using sample-level embeddings from species- and OTU-aware foundation models achieves superior resilience to cross-study distribution shifts. Furthermore, integrating trans-kingdom fungal taxa (*Candida albicans, Saccharomyces*) alongside bacterial profiles captures active co-exclusionary networks involving obligate anaerobic commensals (*Faecalibacterium, Roseburia*) that single-kingdom assays fail to resolve. Overall, applying machine learning across RNA-level functional activity, trans-kingdom fungal ecology, and pretrained contextual embeddings optimizes diagnostic accuracy and cross-cohort generalizability for clinical CDI applications.

105-2 **Dissecting the ECL1–RGI1/2 Link and Its Role in Sulfur Metabolism and Stationary Phase Survival in *Saccharomyces cerevisiae*.** Vicky Huang*, Jill Keeney. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

Saccharomyces cerevisiae is a leading model for eukaryotic aging, yet many of its genes remain functionally uncharacterized. We study two such paralogs, RGI1 and RGI2, to understand how yeast cells shift from growth and self-repair toward long-term, non-dividing survival. Reanalysis of an existing RNA-seq dataset (wild type vs. ecl1Δ, log vs. stationary phase) showed that RGI2 is strongly upregulated in the stationary phase, and even more so when ECL1, annotated as a regulator of chronological lifespan, is deleted. This points to an ECL1-dependent induction of the RGI2 gene that may control entry into stationary survival. This points to an ECL1-dependent induction of the RGI2 gene that may control entry into stationary survival. We hypothesize that RGI1/2 act downstream of ECL1 to promote stationary-phase survival, and are testing this through ecl1Δ rgi1Δ and ecl1Δ rgi2Δ double deletion. We observed H_2S production when strains are grown on methionine-limited plates. We plan to use BiGGY medium, on which colonies darken with active sulfur metabolism, to assay sulfur utilization in deletion strains. Sulfur availability tracks with the growth-to-quiescence switch: abundant sulfur sustains proliferation (log phase), whereas sulfur limitation slows division, triggering the energy-conserving stationary state that greatly extends lifespan. Together, these results lay the groundwork for dissecting how the ECL1–RGI1/2 link shapes yeast aging.

105-3 **A Bactericidal Monoclonal Antibody Synergizes with Antibiotics to Protect against *Pseudomonas aeruginosa* Murine Sepsis**. Spencer Dublin*, Mariette Barbier. West Virginia University, Morgantown, WV. (Graduate, Biomedical)

Antimicrobial resistance (AMR) rates for bacterial infections are increasing in prevalence, resulting in difficult-to-treat infections for at-risk patients. A common AMR pathogen in the healthcare system is *Pseudomonas aeruginosa*, an opportunistic, Gram-negative pathogen. It is paramount that new treatment strategies are developed to treat P. aeruginosa. We proposed the use of monoclonal antibodies (mAbs) as a method to supplement faltering antibiotics in the fight against antimicrobial resistant bacteria. WVDC-0496 is a monoclonal antibody developed by our group that reduces viability of *P. aeruginosa* directly without the need for additional immune components. We hypothesize this antibody alters bacterial membrane permeability and function, leading to bacterial cell death. Similarly, we hypothesize that WVDC-0496 will synergize with antibiotics as dual-administration treatments in murine models of sepsis, leading to increased bacterial clearance. To test these hypotheses, our lab measured bacterial survival following mAb exposure and osmotic shock conditions. Decreased bacterial survival was observed in high osmotic pressures following exposure to WVDC-0496, supporting our hypothesis that binding of WVDC-0496 interferes with membrane integrity. Checkerboard assays demonstrated a synergistic interaction between WVDC-0496 and many standard-of-care antibiotics. This result was mirrored with in vivo studies utilizing a murine model of sepsis. Dual-administration of WVDC-0496 with Gentamycin or Ciprofloxacin resulted in reduced bacterial burden and prolonged survival of mice with lethal sepsis infections. By determining the mechanism of action of this non-classical mAb, and by improving therapeutic efficacy of standard-of-care antibiotics, WVDC-0496 may provide alternatives to previously ineffective antibiotics families in the fight against these drug-resistant pathogens.

105-4 **Sensing kin death: Assessing the pervasiveness of lysis sensing across bacterial species**. Sophia Turecki*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA. (Graduate, Cell/Molec.)

Biofilms are complex, structured communities of microbes encased in extracellular polymeric substances which allow bacteria to withstand external threats, such as resource restriction, harsh chemical environments or bacteriophage. However, existing in these densely packed communities comes at the cost of nutrient competition or oxygen depletion. Therefore, some microbes have developed complex signaling pathways to transition between sessile and planktonic states. It was previously discovered in our group that exposure to lytic bacteriophages promotes robust biofilm formation in V. cholerae via detection of a danger signal released in kin lysate. This mechanism was thus termed “lysis sensing.” The prevalence of lysis sensing outside of the Vibrio genus remains understudied. We hypothesize that lysis sensing may be a common survival strategy across multiple bacteria. Using brightfield imaging and computer vision-driven phenotyping, we characterized the responses of 8 diverse bacterial species – *V. cholerae, E. coli, S. aureus, A. baylyi, A. baumannii, K. pneumoniae, P. aeruginosa and E. faecalis* – to kin lysate. Findings reveal that a robust biofilm formation response is specific to V. cholerae, although several other species showed distinguishable phenotypic responses. In contrast to *V. cholerae, S. aureus* and *A. baylyi* biofilm biomass was repressed when exposed to kin lysate. Future work will integrate transcriptional data with these phenotypes to get a more comprehensive view of how bacteria coordinate collective behaviors upon kin lysate detection.

107-1 **Spatial Organization of Cutaneous Microbiomes Reveals Putative Microbial Contributions to Host Chemical Defenses in the American Toad**. Donovan McCammon*, Regina Lamendella. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

Chemical defenses are widely evolved throughout the tree of life. Animals can exploit mutualisms with toxin-producing symbionts as a mechanism of chemical defense. However, this has only begun to be explored in depth, and how these mutualisms may relate to how animals synthesize or acquire their toxins has been even less studied. True toads synthesize their own toxins and offer a novel system to study the interplay between the cutaneous skin microbiome and how it may contribute to toxin synthesis or biotransformation. In this study, we investigated whether the cutaneous microbiome of the American toad (*Anaxyrus americanus*) was spatially structured across body surfaces in relation to toxin storage and secretion and assessed whether microbial communities exhibit distinctive bacterial taxa involved in toxin-related biochemical pathways. To do this, we used 16S rRNA gene sequencing, diversity metrics, differential abundance comparisons, functional pathway predictions, and ecological interaction networks. Our results indicate that the dorsal and ventral cutaneous surfaces harbor distinct bacterial assemblages, with the dorsal surface being enriched for bacterial taxa associated with the predicted potential to degrade or transform structurally complex organic compounds. This study provides insights into how the toad skin microbiome may contribute to the chemical defenses of toads and could reveal novel aspects of host-microbiome interactions in amphibians.

107-2 **Unmasking the Fungal Factor: The Overlooked Role of Fungi in CDI.** Eva Johnson*, Omkar Warke*, Regina Lamendella. Juniata College, Huntingdon, PA. (Undergraduate, Cell/Molec.)

Clostridioides difficile infection (CDI) arises within a perturbed gut ecosystem, yet most surveys emphasize bacteria alone. We profiled paired bacteriome–mycobiome signatures to distinguish CDI-positive (CDI+, n=50) from CDI-negative (CDI−, n=50) stool using metagenomic and metatranscriptomic sequencing. Reads were quality-filtered and taxonomically assigned. Community composition differed by CDI status at both DNA and RNA levels (PERMANOVA Bray–Curtis: MG taxa p=0.004; MT taxa p=0.002). Alpha-evenness was reduced in CDI+ for MG and MT taxa (Kruskal–Wallis: MG p=0.0001; MT p=0.0083), indicating dominance by fewer organisms. CDI− samples were enriched for obligate anaerobes typical of eubiosis, including *Bacteroides, Faecalibacterium, Roseburia*, and members of Lachnospiraceae/Ruminococcaceae. In contrast, CDI+ samples showed expansion of opportunistic/inflammation-associated bacteria (*Enterococcus, Escherichia–Shigella, Klebsiella, Streptococcus*) and fungal taxa within Saccharomycetaceae; BLAST refinement supported enrichment of Nakaseomyces (*Candida*) *glabratus* alongside *Candida albicans*. MaAsLin3 confirmed associations of *C. difficile* (MT) and Saccharomycetaceae/C. albicans with CDI+, with concurrent depletion of butyrate-associated commensals in CDI+. CoNet network analysis revealed reproducible transkingdom structure in CDI+, with significant co-exclusion between fungal taxa (*Candida, Saccharomyces*, unclassified Saccharomycetaceae) and commensal bacteria (e.g., *Ruminococcus, Bacteroides*), and selective co-occurrence with opportunistic bacterial genera. Together, these findings demonstrate that CDI is characterized by coordinated bacterial depletion and fungal blooms and that cross-kingdom interaction is a defining taxonomic feature of the CDI microbiome, yielding candidate microbial biomarkers of infection status.

107-3 **A nutrient-responsive transcriptional regulator coordinates biofilm formation and stress adaptation in *Pseudomonas aeruginosa*.** Anish Pyne*, Catherine Armbruster. Carnegie Mellon University, Pittsburgh, PA. (Graduate, Cell/Molec.)

Background: Bacteria encounter diverse environmental conditions that can shape their evolution and influence their ability to persist in newer environments. Opportunistic pathogen *Pseudomonas aeruginosa* (Pa) usually persist in nutrient-limited environments across both natural and built environments (buildings), including drinking water systems, where biofilms provide protection from environmental stress. However, it remains unclear how adaptation to these pre-infection niches influences Pa physiology and persistence during host colonization. Methods: We characterized PA3565 using isogenic deletion and complemented strains, independently evolved PA3565 variants, quantitative biofilm assays, live-cell imaging, oxidative stress survival assays, pyoverdine measurements, and an in vitro airway infection model. Biofilm formation was examined under both nutrient-rich and nutrient-limited conditions to determine how nutrient availability affects PA3565-dependent phenotypes. Results: Here, we identify PA3565 as a nutrient-responsive transcriptional regulator that was repeatedly mutated across independently evolved populations during 100 days of Pa biofilm experimental evolution in potable water, suggesting that it contributes to adaptation during nutrient-limited biofilm growth. Under nutrient-limited conditions, deletion of PA3565 impaired initial surface attachment but increased biofilm maturation at later timepoints, accompanied by increased expression of biofilm matrix genes. In contrast, under nutrient-rich conditions, loss of PA3565 reduced biofilm formation, increased susceptibility to oxidative stress, and impaired pyoverdine production. Additionally, PA3565 also contributed to competitive fitness in an airway infection model. Conclusions: These findings suggest that PA3565 coordinates biofilm development with stress adaptation in response to nutrient availability. Furthermore, our results suggest that adaptation during growth in nutrient-limited environmental reservoirs can alter bacterial traits relevant to subsequent host colonization.

2026 ABASM Graduate/Faculty Poster Presentation Abstracts -

G1. **Memory of Chronic Nitrogen Deposition in the RhizosphereMicrobiome.**

Ayers Aguiar*, Ember Morrissey. West Virginia University, Morgantown, WV.

Nitrogen (N) cycling across North American forests was altered by elevated N deposition during the twentieth century resulting from unregulated burning of fossil fuels. While forest associations primarily with arbuscular mycorrhizal fungi (AM) or ectomycorrhizal fungi (ECM) favor either inorganic or organic N cycling, the long-term imprint of N deposition on the rhizosphere microbiome and N cycling remains unclear. To understand how the effects of chronic N deposition persist in temperate forests, we sampled rhizosphere soil from forest plots dominated by either AM or ECM recovering from 30 years (i.e. 1989 to 2019) of whole-watershed simulated N deposition or from a reference watershed in the Fernow Experimental Forest in Parsons, West Virginia. Rhizosphere with N deposition shows reductions in the relative abundance of bacteria with putative roles in N cycling as identified with FAPROTAX. These include nitrate respiration, nitrate reduction, N fixation, and denitrification. ECM rhizosphere with elevated N deposition had significantly less ammonia ($p<0.05$) and inorganic nitrogen overall ($p<0.05$) compared to the reference rhizosphere. Lower relative abundances of bacteria putatively capable of ammonia oxidation in ECM rhizosphere with N deposition compared to reference AM rhizosphere appears to reflect lower inorganic N levels in ECM soils that had simulated chronic N deposition. While further efforts are needed, these results suggest accentuated organic N cycling in ECM rhizosphere recovering chronic N deposition. We would like to thank the U.S.F.S Northern Research Station for maintaining the Fernow Experimental Forest and supporting research activities. This research is funded by NSF grant # 2312514.

G2. **Effects of volatile 6-pentyl-2H-pyran-2-one (6PP) on the growth of aflatoxigenic *Aspergillus flavus* and *Aspergillus parasiticus***.

Stacy Santiago-Garay, Maya Tanikawa-Brown, Josephine Wee. The Pennsylvania State University, State College, PA.

Aspergillus flavus and *Aspergillus parasiticus* are mycotoxigenic fungi that produce aflatoxins B1, B2, G1, and G2 which impact the One Health framework (soils, plants, animals, and humans) and are the most widespread and potent carcinogens. Interest in environmentally friendly field level mitigation strategies of aflatoxigenic *Aspergillus* have resulted in the implementation of biological control agents (BCAs). Presently, commercially available BCAs contain atoxigenic *A. flavus* strains, which carry risks of regaining toxigenicity through genomic recombination and contributing to aflatoxin production. Alternatively, previous metabolomic work in our laboratory has identified four candidate volatile organic compounds (VOCs) produced by Trichoderma spp. for inhibiting aflatoxigenic *Aspergillus*. One of the four VOCs is 6-pentyl-2H-pyran-2-one (6PP), a compound with reported antifungal, plant growth-promoting, and anti-inflammatory activities[GU2.1][SS2.2]. Our study tested the effects of volatile 6PP alone on the growth of *A. parasiticus* B62, a mutant that accumulates norsolorinic acid (NOR), and *A. flavus* NRRL 3357. In a sandwich-plate assay, colonies of *Aspergillus* were exposed to 6PP at headspace concentrations of 0, 25, 50, 75, and 100 µg/L, with methanol as the solvent and control. [GU3.1] Growth, as defined by change in average colony diameter, was measured every 24 hours for five days, across two independent biological replicates (n=6). Although *A. parasiticus* B62 showed a reduced growth trend of 12% at 100 µg/L, 6PP did not significantly inhibit either strain at the concentrations tested. While no dose-dependent response was observed, these findings suggest further assay optimization and testing of the other candidate VOCs alone and in combination are needed.

G3. **Exploring a role for HDAC3 in regulation of airway epithelial barrier integrity and bacterial infection response**. Erin Walsh*, Catherine Armbruster. Carnegie Mellon University, Pittsburgh, PA.

Background: The airway mucosal epithelium protects the lungs from inhaled microbes through epithelial barrier function, mucus clearance, and coordinated immune responses. Like the intestinal epithelium, the airway epithelium must maintain barrier integrity while responding to microbial exposure. In the gut, histone deacetylase 3 (HDAC3) integrates microbial signals to regulate epithelial gene expression, barrier integrity, and immune responses. These shared functions suggest that HDAC3 may also regulate airway epithelial defenses. However, its role in maintaining airway barrier integrity and shaping responses to opportunistic bacterial pathogens remains poorly understood. Methods: Primary human bronchial epithelial cells (HBE) were cultured at air-liquid interface and treated with an HDAC3 specific inhibitor. Epithelial barrier integrity was assessed via transepithelial resistance. Cytotoxicity was quantified via lactate dehydrogenase release. Biofilm growth on HBEs was measured via both manual count and confocal imaging. Pathway enrichment was calculated from transcriptomics of HBEs pretreated with HDAC3 inhibitor 72 hours prior to *Staphylococcus aureus* infection. Results: HDAC3 inhibition of HBEs reduces airway epithelial barrier integrity in a dose-dependent manner. Inhibition of HDAC3 during infection exhibits differential effects on biofilm formation dependent on bacterial species and strain. During S. aureus infection, HDAC3 inhibition resulted in reduced TNFA inflammatory signaling via NFkB. Conclusion: The function of HDAC3 in the airways was observed to parallel its role in the gut as a regulator of barrier integrity and inflammatory signaling. When challenged by an opportunistic pathogen like S. aureus, HDAC3 activity in the airway epithelial influences bacterial colonization and biofilm production through mechanisms currently under investigation.

G4. **Computer vision-enabled high-throughput phenotypic compound screen using Vibrio cholerae**. Jesse Derringer*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA.

An attractive alternative to traditional antibiotic therapy is compounds that modulate bacterial behavior necessary for infection without exerting selective pressure. A common strategy to discover these compounds is a phenotypic drug screen, yet identifying a compound's molecular target remains a major hurdle. Biofilm formation is a pervasive behavior that enables treatment-resistant infection. My work aims to uncover compounds that alter biofilm phenotypes and streamline target identification. Leveraging our lab's automated, low-magnification imaging approach, I capture timecourse images of *Vibrio cholerae* treated with compounds. Our image processing pipeline computes 27 metrics to describe each frame, providing a numerical "barcode" for the biofilm development of each condition. Using numerical thresholds and considering the reproducibility of each compound-induced phenotype, I narrowed the 20,000-small molecule library to 25 hits. To identify their likely targets, I compared each compound-induced phenotype to those previously observed in V. cholerae transposon mutants, reasoning that a compound phenocopying a gene disruption likely acts on that gene's product. In tandem, we conducted a forward computational screen to identify compounds that target core biological pathways impinging on biofilm formation, 30 of which we experimentally verified. Across both screens, 10 compounds produce similar phenotypes to transposon mutants in motility, O-antigen biosynthesis, or pyruvate flux pathways. I am currently determining potency, assessing species specificity, and validating the relationship between compound-induced phenotypes and transposon mutants. Together, this work establishes a scalable phenotype to target pipeline, accelerating the discovery of anti-biofilm compounds that could serve as a foundation for anti-virulence therapeutics.

G5. **An mRNA Lipid Nanoparticle-Based Approach to Pertussis Toxin Antigen Development**. Ian Leighton*, Heath Damron. West Virginia University, Morgantown, WV.

Bordetella pertussis is a Gram-negative, obligate human pathogen which utilizes a variety of adhesion proteins and toxins for colonization and immune evasion. Pertussis toxin (PT), the namesake virulence factor of B. pertussis, inhibits the early recruitment of leukocytes and is a critical antigen in all licensed pertussis vaccines. Conventional vaccine antigen production requires holotoxin purification from *B. pertussis*, a process complicated by co-purification of other virulence factors which limits antigen yield. However, employing mRNA technology allows for antigen development and evaluation without in vivo protein purification. Previously, we demonstrated that a secreted, genetically inactivated PT subunit A (gPTXA) delivered by mRNA-LNP induces neutralizing IgG responses in mice and rats while also recognizing native PT in a murine challenge model. Moreover, we compared secreted and surface-expressed gPTXA constructs with the latter inducing stronger antibody titers and toxin neutralization. To further enhance immunogenicity, we evaluated nanoparticle display of gPTXA. Incorporation of a flexible linker followed by a C-terminal 6×His tag increased expression, improved production scalability, and aided nanoparticle assembly, resulting in the modified gPTXA efficiently being bound to cobalt-containing Spontaneous Nanoliposome Antigen Particles (SNAP) incorporating cobalt porphyrin phospholipid (CoPoP). Importantly, SNAP-gPTXA nanoparticles were highly immunogenic in mice, eliciting antibody responses comparable to DTaP and conferred in vivo PT neuralization. Currently, an ongoing baboon challenge study compares naïve, DTaP, SNAP-gPTXA, control mRNA-LNP, and VDC-mRNA-0089 (surface-tethered gPTXA) groups to assess in vivo toxin neutralization. These studies will define the translational potential of recombinant nanoparticle and mRNA-based PT antigens as potential next-generation pertussis vaccines.

G6. **A Treatment-Ready Model for *S. aureus* Bacteremia**. Barbara Wehle*, Heath Damron. West Virginia University, Morgantown, WV.

Staphylococcus aureus bacteremia is a serious infection associated with substantial morbidity and mortality despite current standards of care. Treatment often requires prolonged intravenous antibiotics and extended hospitalization or outpatient therapy, increasing healthcare costs and exposing patients to complications such as medication toxicity, secondary infections, delirium, and loss of muscle mass and function. This burden is particularly concerning in West Virginia, where injection drug use has contributed to an increase in invasive *S. aureus* infections and where patients with substance use disorders may face barriers to completing treatment. The continued burden of disease highlights the need for improved therapeutics and experimental models to support their evaluation. This study was designed to establish a murine model of *S. aureus* bacteremia for testing therapeutic strategies against systemic infection. Model development evaluated infection conditions that produced measurable systemic disease while allowing comparison of disease severity. Prior bacterial exposure and infection route were examined as key variables: pre-exposure provided a framework for determining how previous encounters with *S. aureus* altered antibody responses and susceptibility to subsequent infection, while intraperitoneal and intravenous challenge compared infection initiated outside the bloodstream with direct bloodstream inoculation. Intraperitoneal *S. aureus* challenge was selected for future treatment studies. Model evaluation will integrate CFU enumeration in blood and organs to assess bacterial burden, serum anti–S. aureus IgM/IgG titers to characterize antibody responses, survival to assess lethality, and composite clinical scoring to track disease severity. Together, these measures provide a framework for evaluating treatment outcomes in invasive *S. aureus* infection.

G7. **Screening Imidazole and Diimine Compounds as Potential Antibiotics**. Elias Griffin*, David Heisler. Duquesne University, Pittsburgh, PA.

Antibiotic-resistant pathogens are one of the leading global health crises, causing ~48 million infections and $75 billion in healthcare costs annually. It is estimated that by 2050, about 40 million people will have died from antibiotic-resistant pathogens. Owing to the lack of new antibiotic, there is an urgent need to identify new scaffolds that possess potential antibacterial properties. Nitrogen-containing compounds, such as imidazoles and diimines, have been shown to have diverse bioactivities, including antibacterial. Therefore, we screened an initial library of imidazole and diimines compounds for their antimicrobial potential against common human pathogens (*Salmonella, E. coli, Shigella, Listeria, and Staphylococcus*) Using a zone of inhibition assay in conjunction with liquid growth inhibition assays, we identified one imidazole and five diimines with antibacterial properties against Gram-positive *Listeria* and *Staphylococcus*. One of these compounds was found to be bactericidal without being toxic towards mammalian cells at the same concentrations. This compound was also found to have a bactericidal function. Furthermore, we found that treatment of *Listeria* infected mammalian cells with the compound reduces bacterial burden by over 99%. These data collectively demonstrate the potential of diimines as novel antibacterial scaffolds, paving the way for their optimization to enhance their effectiveness.

G8. **Investigation of the Transcriptomic changes of *B. burgdorferi* to Identify Candidate Vaccine Antigen**. Annalisa Huckaby*, Mariette Barbier. West Virginia University, Morgantown, WV.

Lyme disease (LD) is the leading vector-borne disease in the United States and is caused by transmission of *Borrelia burgdorferi* (Bb) to humans through the bite of an infected tick. Without early treatment, LD can result in a variety of long-term symptoms, impacting the quality of life of those affected. Missed diagnoses, misdiagnoses, persistent symptoms after treatment, and projected increases in LD incidence rates highlight the need of preventive strategies, such as vaccines. Many LD vaccine efforts focus antigen formulation on the outer surface protein A (OspA) of Bb. Vaccine-induced antibody responses to OspA are thought to prevent transmission by neutralizing spirochetes during the tick blood meal. Because OspA is downregulated in the mammalian host, we hypothesize that vaccine-induced responses to OspA may not be sufficient to clear infections once spirochetes have colonized, suggesting that complete protection may require additional targets necessary for mammalian colonization and persistence. To this end, we used sequencing- and bioinformatics-based approaches to identify candidate vaccine antigens, followed by immunogenicity and efficacy screening. Candidate antigens were refined from the complete protein-coding sequences of the Bb genome based on (1) predicted/demonstrated surface expression, (2) expression ex vivo, and (3) conservation among three LD-causing species. This workflow narrowed 1,399 potential antigens to 24 candidates for screening. We selected four of these antigens for the first phase of preliminary immunogenicity, before future efficacy trials, with two inducing robust immune responses. Together, we hope these and future studies will inform the design of vaccines to prevent LD.

G9. **Fluorogen-Activating Proteins Reveal Spatial Gene Expression Patterns in *Vibrio cholerae* Biofilm Development**. Krutika Joshi*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA.

Background: *Vibrio cholerae* forms structured multicellular communities known as biofilms, where cells are encased in a self-produced protective matrix. Biofilms progress through a developmental lifecycle, from cell attachment to maturation to dispersal, driven by coordinated changes in gene expression across a clonal population. However, how gene expression varies spatially and temporally within a developing biofilm, remains unknown. Our project identifies spatial patterns of gene expression using an oxygen-independent labeling approach based on fluorogen-activating proteins (FAPs), with image analysis at near-single-cell (pseudocell) resolution. Methods: We constructed dual-reporter V. cholerae strains consisting of two FAPs driven by constitutive and gene-specific promoters respectively for per-cell fluorescence normalization. 3D images of biofilm development were captured over time using spinning disk confocal microscopy. We implemented a pipeline to pre-process 3D time-lapse images, isolate biofilm regions, and analyze spatio-temporal patterns of gene expression in BiofilmQ. Results: We found that the FAP signal is three-fold higher than that of fluorescent proteins (FP) in the oxygen-poor core of the biofilm. Using the dual-reporter system, the pipeline measures gene expression at pseudocell resolution, by partitioning the biofilm into cell-sized units and mapping transcriptional activity across biofilm regions. Preliminary imaging of quorum sensing reporter PluxC-FAP shows expression activating in the core, subsequently spreading outward, and then declining. Genetically identical cells therefore adopt distinct, position-specific expression states. Conclusion: This project uses FAPs to map gene expression across *V. cholerae* biofilms at near single-cell resolution. Together, these results begin to reveal how spatial position shapes gene expression heterogeneity during biofilm development.

G10. **DbfQRS: A membrane stress-sensing pathway that balances protection and proliferation in *Vibrio cholerae***. Emmy Nguyen*, Drew Bridges. Carnegie Mellon University, Pittsburgh, PA.

Two-component signaling pathways allow bacteria to sense and respond to environmental changes, yet the sensory mechanisms of many remain poorly understood. In the pathogen *Vibrio cholerae*, the DbfRS two-component system controls the biofilm lifecycle, a critical process for environmental persistence and host colonization. Here, we identified DbfQ, a small periplasmic protein encoded adjacent to dbfRS, as a direct modulator of pathway activity. DbfQ directly binds the sensory domain of the histidine kinase DbfS, shifting it toward phosphatase activity and promoting biofilm dispersal. In contrast, outer membrane perturbations, caused by mutations in lipopolysaccharide biosynthesis genes or membrane-damaging antimicrobials, activate phosphorylation of the response regulator DbfR. Transcriptomic analyses reveal that DbfR phosphorylation leads to broad transcriptional changes spanning genes involved in biofilm formation, central metabolism, and cellular stress responses. Constitutive DbfR phosphorylation imposes severe fitness costs in an infection model, highlighting this pathway as a potential target for anti-infective therapeutics. We find that dbfQRS-like genetic modules are widely present across bacterial phyla, underscoring their broad relevance in bacterial physiology. Collectively, these findings establish DbfQ as a new class of periplasmic regulator that influences two-component signaling and bacterial adaptation.

G11. **Characterization of *S. coelicolor* Type VII Secretion System Involvement in Chromosome Segregation**. Lili Macharashvili*, Joseph McCormick. Duquesne University, Pittsburgh, PA.

In many bacterial phyla, orthologues of the DNA translocase FtsK facilitate circular chromosome segregation during binary fission. Interestingly, FtsK is not required for genome segregation in *Streptomyces coelicolor*, which has simultaneous developmental-associated distribution of tens of copies of a linear chromosome during synchronous multiple septum formation in aerial hypha resulting in a string of unicellular compartments that mature into chains of spores. This fact led to our hypothesis that other proteins must function in segregation for this species. FtsK-family ATPases also function in large complexes for type VII protein secretion systems (T7SS). T7SSs are involved in pathogenesis and interspecies competition in Gram-positive organisms where they have been discovered and studied. Two T7SS ATPases are encoded in some *Streptomyces* species, including S. coelicolor, but not *S. venezuelae*. Here we show that the second T7SS ATPase, in the EssC family, encoded in a locus without typical secretion complex-associated auxiliary genes, is involved in chromosome segregation. Surprisingly, we found that while deletion of either ftsK or essC individually does not have a segregation defect, a ftsK essC double mutant does. Mutations in the lysine codon encoded in a Walker A box for ftsK and essC (D1, domain 1) results in the same null mutant phenotype. Finally, introducing the *S. coelicolor* essC+ gene, but not the essC(K721A) allele, into an *S. venezuelae* mutant complements the weak segregation phenotype of an ftsK-null mutant in that species. We propose that EssC is directly involved in chromosomal DNA transfer during development-associated genome segregation in *S. coelicolor*.

G12. **Rising to the Challenge: Uncovering Species-specific Fructan Degradation to Optimize low-FODMAP Sourdough Breads**. Quinn Burnett*, Josephine Wee. The Pennsylvania State University, State College, PA.

Sourdough bread relies on spontaneous fermentation driven by unique sourdough starter microbiomes of bacteria and fungi, which transform the physical, sensory, and nutritional properties of final breads. With inflammatory bowel disease (IBD) rates rising, consumers increasingly seek low-FODMAP alternatives. FODMAPS (fermentable oligosaccharides, disaccharides, monosaccharides, and polyols) are poorly absorbed in the small intestine and cause gut inflammation in individuals with IBD. Although studies have shown that certain sourdough microbiomes can reduce FODMAPs, how species-level differences across starter microbiomes influence FODMAP degradation remains unclear. We hypothesized that distinct sourdough microbiomes will differentially alter FODMAPs during fermentation, altering final levels in breads. Twenty distinct sourdough starters were baked into breads, and fructan (the key fermentable oligosaccharide in bread) and mannitol (a polyol produced by bacteria) concentrations were quantified using Megazyme K-Fruc and HPLC, respectively. Metagenomic sequencing provided species-level resolution of starter microbiomes. Microbial abundances were correlated with fructan levels, and minimal-media assays evaluated the growth of key species on inulin (a fructan) as a sole substrate. Distinct starter microbiomes drove significant differences in fructan and mannitol concentrations in final breads, with seven breads below the clinical low-FODMAP threshold (0.3 g/100g). Metagenomic analysis revealed *S. cerevisiae* abundance negatively correlated with fructan levels, while *Pichia kluyveri* positively correlated. Minimal media assays confirmed that *S. cerevisiae* efficiently utilized inulin for growth compared with *P. kluyveri*, highlighting the potential of *S. cerevisiae* as a driver of fructan degradation. Understanding these structure–function relationships enable the targeted design of starters to optimize low-inflammatory staple foods.

Faculty 1. **Metagenomes of lichens *Peltigera membranacea*, *Flavoparmelia caperata*, and *Physcia stellaris* include Acidobacteriae and *Nostoc* sp**. Welkin Pope*. Chatham University, Pittsburgh, PA.

Lichens are composite organisms composed of fungi and photobionts. In this announcement, we report the metagenome assemblies of two bacterial species, *Acidobacteriea* and *Nostoc*, recovered from foliose lichen species – *Peltigera membranacea, Flavoparmelia caperata*, and *Physcia stellaris*.

2026 ABASM Undergraduate Poster Presentation Abstracts - Odd Numbered Posters

U-1. **Water Chemistry-Guided Enrichment of Metal-Tolerant Bacteria from Acid Mine Drainage**. Ethan Buchleitner*, Liu Cao. Gannon University, Erie, PA.

Acid-Mine Drainage (AMD) forms when sulfide minerals exposed through mining react with water and oxygen, generating acidic, metal-rich water that can impair receiving ecosystems. Investigating bacteria that persist under these conditions can improve understanding of microbial metal tolerance and inform future studies of biological treatment. This study will characterize AMD water chemistry and use the results to guide the enrichment of metal-tolerant bacteria. Water samples will be analyzed for pH, conductivity, and metal concentrations. A target metal will then be selected based on its occurrence and concentration in the samples. Enrichment cultures derived from AMD samples will be evaluated across a range of concentrations of the selected metal. Other culture conditions, including pH, will be kept consistent to help distinguish the response to metal exposure. Microbial growth will be monitored over time to assess tolerance under the tested conditions. As a subsequent step, 16S rRNA gene sequence could compare the bacterial composition of the original water samples and selected enrichment cultures to identify taxa favored during enrichment. The study will provide an initial assessment of culturable metal-tolerant bacteria from AMD and a foundation for future tests of their metal-removal potential.

U-3. Water Quality and Microbial Diversity in Lake Erie . Mattia Parrini*, Liu Cao. Gannon University, Erie, PA.

Lakes and their tributaries are valued places for swimming, fishing, and relaxing. Bacterial contamination and nutrients can affect water quality. Routine monitoring relies on indicator counts such as E. coli, which show fecal contamination but do not describe the microbial community or its link to water chemistry. This study examines how water quality and microbial communities vary across Lake Erie shoreline and tributary sites in Erie County, PA, and how the two are related. We sampled six sites six times each (n = 36) from June 18 to October 3, 2026: Erie Bayfront Shoreline, Presque Isle Liberty Park, Presque Isle Beach 6, Elk Creek Access, Walnut Creek Access, and Mill Creek Lower Reach. We measured physical, chemical, and bacterial indicators and will use 16S rRNA sequencing to characterize microbial communities. Phosphate was above 0.1 mg/L in 25 samples (69%), E. coli above 235 CFU/100 mL in 15 (42%), and total coliform above 1,000 CFU/100 mL in 29 (81%). Every site exceeded at least one threshold, but patterns differed: E. coli exceeded its threshold most often at Elk Creek (6 of 6) and Walnut Creek (4 of 6), while phosphate and total coliform were more frequent at bay and lake sites. These patterns suggest bacterial and nutrient measurements capture different aspects of water quality and support location-specific monitoring. Sequencing will show whether site differences are reflected in the microbes. Results will be mapped to identify locations for further investigation, informing residents and local health departments.

U-5. **Assessing Tick-Borne Illness Rates Through Processing of Ticks From Local Community Members**. Logan Cree*, Ilse Ness*, Ashley Robuck*, Jill Keeney. Juniata College, Huntington, PA.

Ticks are significant vectors of infectious diseases, most notably Lyme disease caused by Borrelia burgdorferi. A key biomarker associated with this pathogen is outer surface protein A (OspA), a lipoprotein located on the outer membrane of B. burgdorferi that facilitates bacterial survival and colonization within the tick host. Detecting the presence of the OspA gene in tick populations provides insight into the potential prevalence of Lyme disease within a given region. This study aims to examine community-collected ticks for the presence of OspA DNA using molecular analysis techniques. Tick specimens were obtained from a variety of local sources, including contributions from community members and collections from nearby trails and recreational areas such as state gamelands and the Peace Chapel area. The tick species analyzed predominantly included blacklegged ticks (Ixodes scapularis), the primary vector for Lyme disease, as well as American dog ticks (Dermacentor variabilis). DNA was extracted from individual tick samples using ethanol precipitation and subjected to polymerase chain reaction (PCR) amplification using two primer sets: actin primers as a positive control to verify successful DNA extraction and amplification, and OspA-specific primers to detect the presence of B. burgdorferi genetic material. The identification of OspA in locally collected ticks reflects the potential risk for Lyme disease transmission within the community. This study underscores the importance of ongoing environmental surveillance and supports the use of molecular diagnostics in assessing and mitigating public health risks associated with tick-borne diseases.

U-7. **Persistence and Mitigation of Foodborne Pathogens in Hydroponic Lettuce Systems and During Seed Germination**. Gustaf Geremia*, Regina Lamendella. Juniata College, Huntington, PA.

Controlled-environment agriculture, particularly hydroponic lettuce production, faces food-safety scrutiny because pathogens such as Salmonella enterica, Escherichia coli, and Listeria monocytogenes can persist within system biofilms and plant tissue from seeding through harvest. This study examined pathogen persistence and mitigation across two hydroponic configurations, Deep Water Culture (DWC) and Kratky (KR), and during lettuce seed germination. Building on prior work showing inoculated pathogens persisted in rockwool over a three-week cycle, 16S rRNA amplicon sequencing characterized biofilm microbial communities from DWC and KR systems. PERMANOVA revealed a significant difference in community composition between systems ($p = 0.001$), though system type explained only 13.85% of total variance ($R^2 = 0.1385$), indicating hydroponic design is a significant but partial driver of biofilm microbiota. A second experiment evaluated bacteriophage and bacteriocin treatments during seed germination. Rockwool cubes were inoculated with a pooled pathogen cocktail (10^4 CFU/mL; three bioreplicates per group); Salmonella-only groups received bacteriophage, and three-pathogen groups (Salmonella, E. coli, L. monocytogenes) received bacteriocin, with sampling from Day 0 through Day 21 via selective plating (XLD, EMB, ALOA). Both treatments significantly reduced pathogen loads versus untreated controls, but efficacy diminished over time, trending back toward control levels. These results show bacteriophage and bacteriocin treatments can meaningfully suppress pathogens early in germination, but neither achieved sustained, commercially viable control. Future work will test repeated treatment application, combined phage–bacteriocin regimens, phage delivery in nutrient solution rather than rockwool, and refined bioinformatic trimming to improve taxonomic resolution.

U-9. **Assessing the Relationship Between the Gut Microbiome and Microplastic Accumulation in the GI Tract of American Eels, *Anguilla rostrata***. Juliana Onuskanich*, Maycie Kulp*, Regina Lamendella. Juniata College, Huntington, PA.

Anguilla rostrata, the American Eel, is a significantly understudied yet incredibly valuable species whose unique migratory pattern and extended lifespan offer critical insight into environmental contaminants and their relationship with organism health. As catadromous organisms, American Eels migrate from freshwater habitats in northeastern North America to spawning grounds in the Sargasso Sea, exposing them to pollutants on a larger geographic scale than other aquatic organisms in Pennsylvania. To better understand how these organisms are impacted by contaminants, this project investigates the presence of microplastics and analyzes the microbial diversity in American Eel GI tracts to understand the relationship between the two. This study uses 29 silver, or mature, American Eels collected from the Susquehanna River in the areas surrounding the Safe Harbor hydroelectric dam and Peach Bottom nuclear power plant by the U.S. Fish and Wildlife Service. GI tracts were removed from each sample, processed using KOH digestion with vacuum filtration, and analyzed using microscopy to identify microplastics. These samples were also used for metagenomic sequencing to determine microbial diversity and create a baseline for the American Eel gut microbiome, which to our knowledge, has not previously been done. Findings from this project will help develop our understanding of how environmental pollutants such as microplastics accumulate within key aquatic organisms. Additionally, findings will allow us to investigate the possible relationship between microplastics prevalence and microbial diversity within the American Eel gut microbiome.

U-11. **Characterization of Phages Infecting *P. putida***. Maureen Johnson-Keitt*, Nicole McAllister Conrad. Seton Hill University, Greensburg, PA.

To better understand soil and viral diversity, this study aims to discover and characterize phages that thrive in nutrient-rich soil. We used *Pseudomonas putida* as the primary host species due to its metabolic versatility, stress tolerance, and its critical role in degrading environmental pollutants. Understanding how these phages interact with *P. putida* is essential for maintaining soil health and developing new bacterial control methods in agricultural settings. Experiments so far have led to the successful isolation of potentially multiple environmental phages that infect *P. putida*. Because these are unknown environmental isolates, the current work of this research focuses on purifying the phages present and performing DNA extraction followed by restriction enzyme digests and gel electrophoresis. This molecular angle of phage analysis allows us to rapidly estimate genome sizes, differentiate between unique phage isolates, and identify distinct viral groups without requiring immediate whole-genome sequencing. These results contribute to our broader understanding of soil microbiology and may lead to different phage-based strategies for managing bacterial populations in diverse environments.

U-13. **Investigating the Presence of Bacteriophages in Soil Using Bacterial Hosts**. Peyton Cercone*, Nicole McAllister Conrad. Seton Hill University, Greensburg, PA.

This research mainly focuses on the collection, detection, and isolation of bacteriophages from environmental soil samples collected locally. Bacteriophages are vastly abundant viruses with the ability to infect and lyse specific bacteria that are found in everyday microbial communities. The soil samples collected were isolated through incubation and filtration to obtain samples that may potentially contain bacteriophages. These samples were then tested against three bacterial species, *Escherichia coli*, *Pseudomonas putida*, and *Pseudomonas fluorescens*, to observe potential phage activity through looking at bacterial lysis and spot tests. This research is still ongoing and aims to further investigate bacteriophages' interactions with certain bacteria and to isolate and archive phages for future lab use.

U-15. **Diversity and Characterization of Bacterial Isolates from the Marr Ice Piedmont Glacier Forefield, Antarctic Peninsula**. Mackenzie Tickle*, Alicia Purcell. Marshall University, Huntington, WV.

Terrestrial environments along the Antarctic Peninsula are rapidly changing due to increased temperatures. Consequently, increased glacier mass loss is exposing new environments. As climate change intensifies selective pressures, it is important to understand the shifts in community composition and impacts on biogeochemical cycling. This study aimed to isolate, identify, and characterize culturable bacteria from a recently deglaciated forefield of the Marr Ice Piedmont Glacier, Anvers Island, Antarctic Peninsula. Glacial till slurries were inoculated on TSA and Reasoner's 2 Agar, then incubated at 4°C, 15°C, and 20°C. Forty-two morphologically distinct colonies were recovered. Twenty-six isolates were selected for full length 16S rRNA gene sequencing and identification. Fourteen isolates were most closely related to Arthrobacter and seven to *Pseudoarthrobacter* within the Actinomycetota phylum. Two isolates were most closely related to the genus *Pedobacter* (Bacteroidota) and one to the genus *Rummeliibacillus* (Bacillota). Isolates APS1-27 and APS1-34 were chosen for further physiological characterization. Both exhibited 98.34-98.63% sequence identity to *Parafrigoribacterium mesophilum*, an aerobic, mesophilic bacterium previously isolated from agricultural soils. Staining results indicated APS1-27 as a Gram-negative bacilli, contradicting known characteristics of other Microbacteriaceae family representatives which are described as Gram positive cocci. Future work includes physiological comparisons between these Parafrigoribacterium isolates. This will include determining optimal growth temperature, motility, carbon substrate utilization, and presence of the enzymes cytochrome c oxidase and catalase. Overall, this study documents Antarctic microbial biodiversity and provides a collection of isolates for investigating bacterial adaptations to glacial environments.

U-17. **Functional Genomic Insights into Predatory Bacteria Responding to Environmental Warming in Antarctic Soils**. Sarah Ellis*, Alicia Purcell. Marshall University, Huntington, WV.

The Western Antarctic Peninsula continues to experience rapid warming, exposing nutrient-limited soils that have become valuable systems for examining how resident microbial communities may respond to future climatic changes. In these soil environments, microbes drive the biogeochemical cycles responsible for ecosystem growth, yet the precise role of predatory bacterial species within a community responding to environmental shifts is poorly understood. Bacterial predators function as top-down regulators obtaining their nutrients from the cellular contents of other microbial community members, where acquired biomass is used for replicative growth and remnants of their prey can become biologically active and re-enter the local microbial loop. Previous work identified several Antarctic Bdellovibrio-like Metagenome Assembled Genomes (MAGs) from experimentally warmed soil plots. Some MAGs exhibited increased in situ growth rates under warming, whereas others showed little or no measurable response relative to control plots. Among these putative predators, it remains uncertain whether these responses are linked to differences in genomic potential or expression patterns that are selectively advantageous within warming microbial communities. To address this question, seven Antarctic Bdellovibrionota MAGs were subjected to phylogenomic reconstruction, pangenome analysis, and comparative genomic characterization, and transcriptomic profiling. Predation-associated features including Type II secretion systems, Type IV pili, flagellar biosynthesis genes, Sec and Tat export pathways were evaluated. These features exhibited conserved patterns among predatory MAGs relative to non-predatory MAGs from the same experiment. Ongoing analysis suggests that warming-responsive predatory MAGs may exhibit different regulatory and accessory functions relative to lesser warming-responsive or non-responsive predatory MAGs.

U-19. **Evaluating Metal Tolerance in Bacteria with Light Rare Earth Element Biorecovery Potential**. Ellena Perdue*, Michelle Valkanas. PennWest University–California, California, PA.

Light rare earth elements (LREEs) and other metals can influence bacterial growth and metabolic activity. This study investigates the effects of lanthanum (La), cerium (Ce), neodymium (Nd), praseodymium (Pr), lithium (Li), and copper (Cu) on bacterial isolates to determine their respective minimum inhibitory concentrations (MICs). The bacterial isolates were grown overnight in R2A pH 4.6 and 1% methanol (MeOH) to account for the potential role of Xox-type methanol dehydrogenase (MDH), an enzyme associated with rare earth element-dependent methanol metabolism. A 96-well plate was then used to evaluate the bacterial growth in the presence of serial diluted metals. A 1:10 dilution of the overnight culture was aliquoted into the 96 well plate, the metals were serially diluted (1:2) ten times and the plate was incubated for 3 days at 30°C. Starting metal concentrations were as follows: La = 50 mM, Ce = 50 mM, N = 50 mM, Pr = 100 mM, Li = 2000 mM, and Cu = 15mM. Bacterial growth was measured on a microplate reader every 6 hours using OD600 to determine how each metal impacted bacterial growth. The results of this study will help to identify the concentrations of metals that inhibit bacterial isolate growth and improve the understanding of bacterial responses to metals under harsh conditions. This information can then be used to identify the best candidates for LREE biorecovery.

U-21. **Evaluating the Synergistic Properties of a Monoclonal Antibody against Antimicrobial Resistant Strains of *Pseudomonas aeruginosa***. Sarah Rahin*, Mariette Barbier. West Virginia University, Morgantown, WV.

Pseudomonas aeruginosa is an opportunistic, Gram-negative bacterium. This pathogen is prevalent in healthcare settings and displays increasing rates of resistance to standard-of-care antibiotics. Therefore, the development of new therapeutic strategies is crucial for improved bacterial clearance and patient recovery. Monoclonal antibodies (mAbs) are possible immunotherapies that, in combination with antibiotics, could effectively treat antimicrobial resistant (AMR) P. aeruginosa infections. Our lab has developed WVDC-0496: a mAb that directly kills P. aeruginosa without the need for traditional immune system strategies. We have observed the synergistic potential of this mAb with multiple antibiotics to kill non-AMR strains of *P. aeruginosa*. We hypothesize that WVDC-0496 will demonstrate similar antimicrobial properties and synergize with antibiotics against clinical AMR strains of P. aeruginosa. To test this hypothesis, we first identified clinical strains that were bound by WVDC- 0496. Next, we determined the minimum inhibitory concentration (MIC) of eight distinct antibiotics against these AMR strains. We then performed checkerboard assays with WVDC- 0496 and selected antibiotics these strains were resistant towards, to measure any synergistic potential. We found that, upon exposure of these AMR strains to the mAb and antibiotic, the MIC of these antibiotics was lowered, which demonstrates a synergistic relationship between the mAb and antibiotic. This synergistic relationship between mAb and standard-of-care antibiotics shows potential for the expansion of treatment options as lower drug doses may be effective for bacterial clearance. The treatment of these infections was previously limited by drug toxicity and efficacy, and now, could be improved with the mAb-antibiotic combination therapy.

U-23. **Optimization of PCR to streamline *B. burgdorferi* in preclinical models of Lyme Disease**. Mauren Miller*, Mariette Barbier. West Virginia University, Morgantown, WV.

Borrelia burgdorferi is a Gram-negative spirochete responsible for Lyme Disease. The incidence rate of Lyme Disease is at least 60,000 cases a year but could be higher due to it often being misdiagnosed. Together, this highlights the importance of developing new therapeutic and diagnostic strategies against this pathogen. Currently in our preclinical Lyme Disease vaccine models we test for *B. burgdorferi* dissemination by culturing organs for 14 days after harvesting. To screen these samples for the presence of *B. burgdorferi*, we use a combination of dark field microscopy and two separate PCR reactions. Although this screening process is effective, it can be time consuming for large-scale experiments. To offset these downfalls, we aimed to establish a high-throughput multiplex PCR protocol that can make screening experimental samples simpler and quicker. To do this, we designed multiple primer sets for three genes that are conserved in *B. burgdorferi*: recA, flaB, and fliD. We confirmed that each primer set individually and in different multiplex combinations by running PCR reactions with DNA isolated from *B. burgdorferi* cultures and previous experimental samples. In the beginning, we had 24 potential multiplex primer sets and through the optimization process we narrowed it down to 4 potential multiplex reactions. With additional protocol optimization, the development of a multiplex PCR protocol would decrease the amount of time required of the current screening process used for mouse experiments in our lab.

U-25. **Ionizable lipid nanoparticles for the inhibition of STAT5 and treatment of B-ALL**. Aidan Murray*, Sharan Bobbala. West Virginia University, Morgantown, WV.

Acute Lymphoblastic Leukemia (ALL) is the most common form of cancer in children aged 14 and under, accounting for approximately 20% of all diagnoses, with B-cell ALL (B-ALL) being the most prominent. Signal transducer and activator of transcription 5 (STAT5) is a cytokine-activated human transcription factor involved in the regulation of the cell cycle in immune cells. STAT5 is made up of two closely related isoforms, STAT5A and STAT5B, which serve differing roles in immune regulation. In many leukemic patients, overactivation of STAT5 proteins leads to both proliferation of malignant cells and upregulation of anti-apoptotic that are known to mediate chemoresistance. The downstream effects of STAT5 consequently result in unregulated growth and survival of B-ALL, two hallmarks of many malignancies. While much progress has been made in the development of selective small molecules inhibitors for the STAT5 isoforms, few have expanded past the preclinical phase. The delivery of nucleic acid therapeutics, such as small interfering RNA (siRNA), delivered through nanoparticle platforms such as ionizable lipid nanoparticles (LNPs) have acclaimed recent success in clinical trials for multiple cancers. We hypothesize that inhibiting the STAT5 pathway could be a viable treatment of B-ALL by repressing anti-apoptotic genes and assist with inducing cell death. This work demonstrates that transient knockout of STAT5A results in apoptotic-mediated cell death in primary B-ALL cells, validated using cytotoxicity and apoptosis assays. The findings presented here lay the framework for evaluating siRNA-LNPs as a potential adjunctive treatment for B-ALL.

U-27. **SEA-GENES: Finding Clues to Gene Function in Mycobacteriophage ZoeJ**. Hailee Gunn*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

Bacteriophages, viruses that specifically infect bacteria, are the most abundant biological entities on earth and are valuable for studying bacterial genetics, evolution, and therapeutic applications. The SEA-PHAGES program, engages undergraduate researchers in phage discovery, genome sequencing, and phage characterization. Although, this program has contributed more than 1,500 sequenced mycobacteriophage genomes, an estimated 50-70% of phage genes still have no known function. SEA-GENES builds on the foundation from this research by pairing genome annotation with experimental gene characterization to determine what individual phage genes actually do. Our assigned mycobacteriophage was discovered at Providence College, infects a broad host range and is named ZoeJ. A genetically engineered version of ZoeJ was used to treat a 15-year-old patient with a drug-resistant *M. abscessus* infection, highlighting its potential as part of a phage cocktail. The function of many ZoeJ genes remain unknown. The ultimate goal of this project is to create a phage library in the pExTra plasmid and then determine if each individual gene in ZoeJ has a cytotoxic effect on the host *M. smegmatis*. A defense assay is also used to determine if the individual gene can impact phage infection. The genes of interest I was assigned were genes 1-6 and 36-39. PCR and isothermal assembly into the pExTra plasmid have been completed successfully. Electroporation into *M. smegmatis* has been performed on a select few. Understanding how individual ZoeJ genes behavior advances our knowledge of phage biology and evolution and supports the development of phage therapy as an alternative to antibiotics.

U-29. **Is *Enterococcus* Auxotrophic for Lactose? Implications in Graft Versus Host Disease in Recipients of Allogenic Bone Marrow Transplants**. Abrielle Brown*, John Trimble. Saint Francis University, Loretto, PA.

In this study, the ability of *Enterococcus faecalis* and *Enterococcus faecium* to grow without lactose was tested in order to determine whether or not it was auxotrophic. Auxotrophy is when an organism must be provided with a nutrient to be able to grow. Increases in the abundance of *Enterococcus faecium* (*Enterococcus* domination being considered ≥ 30%) are often seen in cases of graft versus host disease (GVHD), a complication of allogenic hematopoietic cell transplantation (allo HCT). GVHD is associated with decreased quality of life and survival rate of transplant recipients, with up to a 15% mortality rate. Lactose, a disaccharide “milk sugar,” has been found to fuel *Enterococcus* growth in several studies, and it has been suggested through these studies that *Enterococcus* species are auxotrophic for lactose. However, this has not been conclusive, and has raised concerns about the safety of transplant patients drinking milk and consuming dairy products and whether this might be responsible for some cases of GVHD in bone marrow transplant recipients. This was investigated by growing both species in Brain Heart Infusion (BHI) broth with and without lactase treatment. Cell growth curves were made using triplicate cultures measured via spectrophotometry. We predicted that *Enterococcus* is not auxotrophic for lactose due to its ability to grow in BHI, which likely contains little to no lactose. Further studies could examine the composition of BHI and identify what role lactose plays in the growth of *Enterococcus*.

U-31. **The impact of nutrient and oxygen availability on gut Clostridial growth in a heart failure model**. Amber Terry*, Michelle Valkanas. PennWest University–California, California, PA.

The connection between the gut microbiome and heart health (termed the heart-gut axis) has been recently acknowledged as an essential, relevant connection to cardiac failure/shock patient outcomes. The bacterial genus Clostridium has recently been shown to play an important role in this system, showing a significant increase in growth in heart failure patients, with the highest concentrations being found in the sickest patient population. Considering this, the aim of this research is to focus on how changes in nutrient availability and oxygen levels of the heart failure gut impact the metabolism of *Clostridum*. The organism *Clostridium butyricum* is used as a representative organism for the current experiment, and its fermentation activity is used to measure the effects of the nutrients and other elements being manipulated. The organism will be exposed to different factors whose levels differ significantly in heart failure patients compared to an individual with no heart condition(s). These factors include elevated levels of hemin, different levels of vitamin K (low, normal, high), elevated levels of choline and subsequently trimethylmine (TMA), and differing levels of oxygen and sodium, all of which can occur in heart failure patients as a result of the disease or associated medications. The goal of this research is to use its findings to further knowledge on the importance of the heart-gut axis in heart health and encourage further research to understand and use this connection to the benefit of the patients and create better outcomes.

U-33. **The effects of hygiene on antibiotic resistance genes in the oral microbiome**. Arica Collier*, Michelle Valkanas. PennWest University–California, California, PA.

Antibiotic resistance is when bacteria become resistant to medicines normally used to kill them. Despite current efforts, antibiotic resistance remains a relevant issue in the medical field, most commonly due to the overuse of antibiotics. One of the most common ways bacteria become resistant to antibiotics is through the expression of antibiotic resistance genes (ARGs) which can be used to deactivate antibiotics or remove them from the cell. Resistance in the oral microbiome caused by ARGs is understudied. ARGs can be shared through horizontal gene transfer through the formation of bacterial biofilms, increasing the percentage of resistant bacteria in the mouth. This research aimed to analyze full genomic sequences in the oral microbiota to determine if hygiene plays a role in the transfer/development of antibiotic resistance genes. Oral saliva samples were collected from twenty volunteers, following IRB approval, and separated into “good” and “bad” hygiene categories based on if they brushed their teeth, flossed, and/or used mouth wash. Selected samples were then sent to SEQCenter (Pittsburgh, PA) for Shotgun Metagenomic Sequencing. Full genomes will then be analyzed, looking for specific ARGs (e.g. tetM & ermB). It is hypothesized that while there will be ARGs present in both “good” and “poor” hygiene samples, but there will be a higher prevalence in the “less hygienic” hygiene group. This research seeks to better understand differences in the oral microbiota and the association of ARGs in relation to oral hygiene.

U-35. **GLP-1 Receptor Agonist Therapy Reshapes the Gut Microbiome**: A Longitudinal Genomic and Bioinformatic Study of Fecal Microbial Dynamics. Omkar Warke*, . Juniata College, Huntington, PA.

Glucagon-like peptide-1 receptor agonists (GLP-1RAs) are widely used in the management of type 2 diabetes and obesity due to their effects on glycemic control, appetite regulation, and weight loss. These agents function by triggering glucose-dependent insulin secretion from pancreatic beta cells. Moreover, GLP-1RAs like semaglutide enhance systemic insulin sensitivity and upregulate the browning of adipose tissue which makes fat cells much more metabolically active. Despite these therapeutic benefits, clinical application is frequently complicated by adverse gastrointestinal effects, primarily nausea and vomiting. Emerging evidence suggests that these agents may also influence the gut microbiome, a dynamic community of microorganisms that plays a critical role in metabolic health. GLP-1RAs restructure the microbial landscape by altering gastric emptying rates, intestinal transit time, and the local luminal environment. We are examining the bidirectional relationship between GLP-1RA signaling and gut microbiome composition, specifically focusing on how treatment could lead to possible dysbiosis. In this longitudinal blind study, we are receiving fecal samples from 55 individuals at 4 different time points; Pre GLP-1RA usage, 1 month after GLP-1RA initiation, 3 months post-initiation, and 6 months post-initiation. We will perform shallow shotgun metagenomics paired with the QIIME2/DADA2 bioinformatics pipeline on the 16S gene to characterize the microbiome shifts associated with therapies involving GLP-1RAs. In future works, we plan to pair this with a metabolomics short-chain fatty acid approach to support our 16S findings, as well as give us insight into the effects treatment has on the gut-brain axis and systemic inflammation.

U-37. **The Role of Myeloperoxidase in Tumor Cell and Myeloid-Derived Supressor Cell Migration**. Gianna Moses*, Mariette Barbier. West Virginia University, Morgantown, WV.

Metastatic disease, the spread of cancer throughout the body, is the primary cause of death among cancer patients. While immune checkpoint therapy has shown promise in treating some patients, many remain unresponsive to these treatments. One of the leading factors contributing to resistance is an immunosuppressive tumor microenvironment. Myeloid-derived suppressor cells (MDSCs) play a crucial role in immune suppression and contribute to an immunosuppressive tumor microenvironment. One immunosuppressive mechanism used by MDSCs is the increased production of reactive oxygen species (ROS). Myeloperoxidase (MPO), a myeloid lineage-restricted enzyme, is a major producer of ROS, and studies from our lab have shown that increased MPO activity in MDSCs contributes to their immunosuppressive functions. However, the specific role of MPO in regulating MDSC trafficking within the tumor microenvironment remains largely uncharacterized. We hypothesize that MPO drives MDSC migration. Bone marrow cells were isolated from the bone marrow in wild type CBL/6J mice and cultured in granulocyte-macrophage colony-stimulating factor (GM-CSF) to differentiate the cells into MDSCs. Transwell assays assessed the impact of MPO on MDSC and tumor cell migration across a semi-permeable membrane by treating MDSCs with vehicle control or an MPO inhibitor. Additionally, the effect of MPO on the mobility of MDSCs was examined using live confocal imaging with actin and tubulin fluorescent trackers over time. Understanding whether MPO influences the recruitment and localization of MDSCs could provide new insights into contribution of MPO in supporting cancer metastasis and identify potential therapeutic strategies to enhance antitumor immunity and treat metastasis.

U-39. **Determining the Optimal Expression of *Borrelia burgdorferi* Outer Surface Protein A in BSK-II Culture**. Olivia Conaway*, Mariette Barbier. West Virginia University, Morgantown, WV.

Lyme disease is the most common tick-borne illness in the United States, with an estimated 476,000 cases diagnosed each year. *Borrelia burgdorferi* is the causative agent of Lyme disease, and there is currently no vaccine on the market to prevent infection. Current vaccine development efforts center around providing immunity against OspA, which is an outer surface lipoprotein found on *B. burgdorferi*. OspA is typically highly expressed when the bacterium is growing inside the tick. In this study, we aim to establish the growing conditions of *B. burgdorferi* that lead to the highest level of OspA expression by changing factors like incubation temperature and media pH. In the tick midgut, B. burgdorferi grows at a pH of 7.4 and a temperature range of 23-37oC. Therefore, we hypothesize that B. burgdorferi grown at 27oC with 5% CO2 and a medium pH of 7.4 will express the highest amount of OspA because it replicates the conditions within the tick that the bacteria typically express high levels of OspA in. By determining the optimal growth conditions of *B. burgdorferi* that express high levels of OspA, we can create a more effective challenge model for vaccine development. Specifically, we aim to simulate a tick infection model using a needle challenge in mice, allowing us to better evaluate vaccine efficacy by challenging them with B. burgdorferi that expresses high levels of OspA.

U-41. **Whole-genome sequence of 9 *Escherichia coli*, isolated from retail ground beef obtained in Puerto Rico**. Alanis Velazquez Rivera*, Edward Dudley. The Pennsylvania State University, State College, PA.

Retail meats are considered one of the main sources of protein for humans. Continuous misuse of antimicrobial agents during animal growth and in processing plants may lead to raw meats harboring antimicrobial resistant bacteria. This study assesses the presence of antimicrobial resistant *Escherichia coli* (*E. coli*) in retail ground beef products. The samples were collected in Puerto Rico from 2024 to 2026 and then sent to Pennsylvania State University for whole-genome sequencing (WGS). Of the isolates received, nine isolates were sequenced and analyzed. The analysis resulted in the presence of antimicrobial resistance (AMR) genes in all of the isolates, with *blaEC-18* being the most prevalent, with a prevalence of 89% (8/9). No common pathotype specific markers were identified in the VFDB profile; however, this does not exclude the presence of other virulence associated mechanisms. Plasmid replicon analysis revealed the presence of plasmid replicons in all of the isolates, with an average of five replicons per isolate. These findings suggest genotypic resistance in the *E. coli* isolates and possible genotypic multidrug resistance (MDR) in one of the isolates. The bioinformatic data was published to support future surveillance and monitoring of AMR in retail meat products.

2026 ABASM Poster Presentation Abstracts - Even Numbered Posters

U-2. **Establishing a Fluorescent Antibody Repository for Flow Cytometry Users of the WVU FCSCCF**. Caitlin Bissell*, Kathleen Brundage. West Virginia University, Morgantown, WV.

The WVU Flow Cytometry and Single Cell Core Facility provides advanced instrumentation for analyzing the functional, physical, and chemical characteristics of cells and particles that are brought to the interrogation region in a fluid solution. Two of the Core's most popular instruments are the 4-laser, 17-color BD LSRFortessa and the 3-laser, 28-color spectral Cytek Aurora. Over the past three years, the Core has acquired over 300 fluorescent antibodies of varying reactivity, fluorophores, and age from surrounding labs. The objective of this project is to establish a centralized repository for WVU researchers. Since little is known about the previous storage and handling of the antibodies, we need to determine if they still bind their target and, in many cases, their optimal dilution before we can offer them to FCSCCF users. To make this repository useful to researchers, we are compiling all essential data for each antibody into a searchable document. So far, Jurkat (human T cell lymphoma), REH (human B cell ALL) cells, THP-1 (human monocyte) cells, and J774 (mouse macrophage) cells have been used to test the antibodies that should bind to these cells. Data is evaluated using FCS express software. The resulting repository will provide users with a comprehensive, user-friendly database containing the appropriate dilution of the antibody, fluorochrome information, and spectral graphs.

U-4. **Kinetic Characterization of *Clostridium butyricum* Enzymes and Pancreatin on Starch Substrates**. Gabriel Infante*, Darrell Cockburn. The Pennsylvania State University, State College, PA.

Resistant starch escapes digestion by human digestive enzymes but supports microbial fermentation in the colon and the production of metabolites such as butyrate. *Clostridium butyricum* can degrade resistant starch and produce butyrate. This study characterized starch degradation by two *C. butyricum* enzymes, designated CB1 and CB2, compared with pancreatin, a pancreatic enzyme preparation. Purified bacterial enzymes and pancreatin were evaluated using corn, potato, and HiMaize starches. Hydrolysis was quantified by measuring reducing sugar release using a bicinchoninic acid (BCA) assay with glucose standards. Conventional Michaelis–Menten analyses evaluated responses to varying substrate concentrations, while reverse Michaelis–Menten analyses evaluated responses to varying enzyme concentrations with potato starch. CB1 and CB2 exhibited lower apparent Michaelis constants (Km) than pancreatin for corn starch (53.75 and 10.42 versus 190 mg/mL) and HiMaize starch (4.42 and 3.20 versus 31.56 mg/mL). For potato starch, apparent Km values were 2.29 and 2.07 mg/mL for CB1 and CB2, respectively, while the pancreatin value could not be determined. Reverse kinetic analyses yielded estimated attack-site densities of 30 nmol/g for CB1, 83 nmol/g for CB2, and less than 1 nmol/g for pancreatin. CB2 exhibited the lowest apparent Km across tested starches and the highest estimated attack-site density on potato starch. These findings suggest that differences in access to susceptible sites on starch granules may contribute to bacterial degradation of starch that resists pancreatic digestion. Further biochemical and structural characterization is needed to determine the mechanisms underlying these differences and clarify their potential role in resistant starch utilization by the gut microbiome.

U-6. **The Effectiveness of a Laminated Antimicrobial Film to Control Microbes Associated with Low Moisture Foods**. Matthew Shue*, Catherine Cutter. The Pennsylvania State University, State College, PA.

A laminated antimicrobial film (LAF) was made by coating an ethylene-vinyl alcohol (EVOH) film with an edible biopolymer layer that contains pullulan, water, gelatin, glycerol, and the antimicrobial, lauric arginate (LAE). In an earlier study, LAF effectively inhibited foodborne pathogens associated with fresh and ready-to-eat meat. This study explores the effectiveness of the LAF to control naturally occurring microbes associated with low moisture foods such as hard salami (aw=0.8384) and aged Swiss (aw= 0.9665). Foods were evaluated for initial microbial populations (aerobic plate counts [APC] and lactic acid bacteria [LAB]) upon receipt. Shortly thereafter, food was temperature abused at 25℃ for 12 hours to increase microbes and resulting microbial populations were determined on day 0. Low moisture foods were treated with one of three film types: a control film (EVOH only), LAF made without LAE, and LAF made with 0.5% LAE. Treated samples were stored at either 4℃ or 10℃ and evaluated for microbial populations at days 2, 7, 14, 21, and 28. Homogenized samples were serially diluted and plated onto respective media; incubated for 72 hours at 31°C (APC) and 48 hours at 31°C (LAB). The LAF with 0.5% LAE was most effective at reducing microbial populations in both hard salami and aged Swiss cheese over a 28-day period; reductions were less for hard salami than for cheese. This research highlights an important limitation for LAFs that rely on surface moisture to release their antimicrobial agent.

U-8. **Whole Genome Sequence of 17 *Staphylococcus aureus*, Isolated from Ground Beef in Puerto Rico**. Nashalee Mercado*, Edward Dudley. The Pennsylvania State University, State College, PA.

This study focused on the whole genome sequencing and characterization of *Staphylococcus aureus* isolates recovered from retail ground beef. Bacterial isolates were cultured and characterized using microbiological media and phenotypic test using Mannitol Salt Agar. Genomic DNA was extracted from Gram positive *S. aureus* isolates and evaluated for concentration and purity using Qubit and NanoDrop. The WGS workflow was explored from DNA processing and library preparation through sequencing and downstream genomic analysis. Genomic data were analyzed using GalaxyTrakr and RStudio to characterize antimicrobial resistance genes, virulence factors, and plasmid replicon content. Additionally, *S. aureus* biofilm formation was evaluated under stress conditions, and biofilm associated genes were investigated through literature review. This work provided insight into the genomic characteristics of foodborne *S. aureus* isolates and their potential antimicrobial resistance and virulence profiles, contributing to the understanding of foodborne bacterial pathogens and their implications for public health.

U-10. **Investigating Macrophage Abundance and Polarization in Gemcitabine Treated Mice to Improve Therapeutic Outcome**. Callie Ancosky*, Timothy Eubank. The Pennsylvania State University, State College, PA.

Pancreatic ductal adenocarcinoma (PDAC) is the most common form of pancreatic cancer and remains highly aggressive, with a 5-year survival rate of only 13%. Although Gemcitabine/Nab-Paclitaxel and FOLFIRINOX are standard chemotherapy regimens, poor survival highlights the need for improved therapeutic strategies and biomarkers of treatment response. Macrophages are among the earliest and most abundant immune cells recruited into the pancreatic tumor microenvironment (TME). Although macrophages can initially support anti-tumor immunity, high macrophage abundance is associated with faster disease progression, cancer spread, recurrence, therapy resistance, and shorter overall survival. Tumor-associated macrophages (TAMs), particularly M2-like pro-tumor phenotypes, promote chronic inflammation, suppress anti-tumor immune responses, support metastasis, and contribute to treatment resistance. Because Gemcitabine remains a standard PDAC therapy, we aim to determine whether Gemcitabine alters macrophage abundance within the TME, shifts macrophage polarization from an M2-like pro-tumor phenotype toward a more M1-like anti-tumor phenotype, and whether this phenotype balance predicts treatment response. To test this, we used a murine orthotopic PDAC model in which tumor cells were implanted directly into the tail of the pancreas. After one week of tumor development, mice were randomized to receive five rounds of intraperitoneal Gemcitabine or saline. Following treatment, tumors were harvested and analyzed by immunofluorescence. Tissue sections were stained with DAPI and F4/80 to identify total macrophages, along with additional M1- and M2-associated markers to determine macrophage phenotype in Gemcitabine- and saline-treated mice. These studies will determine whether chemotherapy affects not only tumor burden, but also macrophage abundance, polarity, and function within the PDAC TME.

U-12. **Testing Sensitivity and Resistance of *S. cerevisiae* YKL121W Gene Deletion and its Paralog Deletion, YMR102C, across Different Types of Media**. Madeline Hatch*, Jill Keeney. Juniata College, Huntington, PA.

Saccharomyces cerevisiae, or baker's yeast, serves as a model organism used to study eukaryotic cellular function. S. cerevisiae is commonly used to identify gene functions due to the simplicity of genetic modification. The S. cerevisiae gene YKL121W has an unknown function and is a paralog of YMR102C. To date, the YKL121W deletion mutant is known to be resistant to 2-deoxy-D-glucose, a glucose analog that inhibits glycolysis by targeting hexokinase, causing cellular ATP depletion. The YKL121W gene is also reported to be sensitive to Congo Red, a compound known to inhibit yeast growth. This study investigates the effects of deleting the YKL121W gene and its paralog, YMR102C, on yeast growth across different types of media, including 2-deoxy-D-glucose, Congo Red, miconazole, and YPD. By plating the single deletions of both YKL121W and its paralog, YMR102C, we discovered that the YKL121W deletion strain showed resistance to 2-deoxy-D-glucose, but the paralog did not. This resistance was expected for the YKL121W deletion, a known 2-deoxy-D-glucose resistance marker. All strains failed to grow on miconazole plates, suggesting no resistance to miconazole. When plated on Congo Red YPD media, both the YKL121W and YMR102C deletion strains showed significantly larger colonies than the wild type, suggesting that in contrast to the reported phenotype, both single deletions are not sensitive to Congo Red. In summary, these results demonstrate that while YKL121W is essential for cell wall maintenance in this strain, it also plays a conserved, critical role in mediating 2-deoxy-D-glucose toxicity, which future research can further examine.

U-14. **Exploring the Effects of YMR114C Gene Deletion**. Parker Thomas*, Jill Keeney. Juniata College, Huntington, PA.

My yeast gene YMR114C has an unknown function. This study is to investigate whether this gene is involved in DNA replication or repair. Based on homology to the human gene HMCES, which is known to protect DNA from damage, I hypothesize that YMR114C contributes to enabling DNA binding activity to prevent mutations in DNA. To test this hypothesis,both wild type and YMR114C knockout yeast strains will be exposed to DNA damaging conditions, including ultraviolet radiation and hydroxyurea induced replication stress. In addition to this, XBP1 is a yeast gene that has known interaction with YMR114C and is only turned on through replicative stress. To test if this is a factor, the log growth and quiescence stages were measured and compared. Growth and DNA replication will be determined using a budding index and colony formation on YPD plates under varying treatment conditions. I anticipate that wild type yeast will demonstrate greater survival and repair capacity compared to knockout strains. This indicates a role for YMR114C in DNA damage response. Both the Wildtype and YMR114C strains of yeast grew among five, fifteen, twenty, and thirty seconds of UV and two and five millimolar concentrations of hydroxyurea. The results from the growth suggest that the gene is not necessary for repair or replication. However, the results of the budding index indicates that YMR114C gene promotes progression from the G1 phase to the S phase.

U-16. **CRISPR-Cas9 and MDA-Enhanced Nanopore Sequencing for Culture-Independent Detection of *Staphylococcus aureus***. Liesl Stine*, Jasna Kovac. The Pennsylvania State University, State College, PA.

Staphylococcus aureus is an opportunistic bacterial pathogen associated with a wide range of infections, highlighting the need for rapid and accurate detection methods. Conventional culture-based identification can be time-consuming and may limit detection in samples with low bacterial abundance. This project investigates a culture-independent detection strategy integrating CRISPR-Cas9-based target enrichment, multiple displacement amplification (MDA), and Oxford Nanopore Technologies (ONT) sequencing to facilitate *S. aureus* identification. CRISPR-Cas9 enables sequence-specific recognition and cleavage of targeted DNA, enriching genomic regions of interest for downstream analysis. MDA employs strand-displacing DNA polymerase to amplify DNA under isothermal conditions, increasing the quantity of genetic material available for sequencing. ONT sequencing analyzes DNA molecules as they pass through nanopores, enabling real-time sequence acquisition and genomic characterization. Integrating these techniques may improve the recovery and identification of pathogen-specific genetic sequences without requiring bacterial cultivation. The workflow evaluates the recovery and identification of S. aureus-associated DNA through targeted enrichment, amplification, and nanopore sequencing. Sequencing output and target identification can help characterize the effectiveness and limitations of this approach. Potential challenges include amplification bias, nonspecific enrichment, and distinguishing *S. aureus* from closely related bacterial species.

U-18. **Industry-Informed Peroxyacetic Acid Treatments Reduce *Campylobacter jejuni* Culturable Cells More Than Viable Cells on Chicken Wings**. Robert Monson*, Jasna Kovac. The Pennsylvania State University, State College, PA.

Peroxyacetic acid (PAA) is an oxidizing sanitizer used at multiple stages of poultry processing in the United States, whose efficacy in reducing *Campylobacter jejuni*, a known pathogen, is evaluated using culture-based methods. As *C. jejuni* can enter a viable but not culturable (VBNC) state when stressed, PAA efficacy may be overstated when measuring *C. jejuni* culturability. We aimed to determine how multiple industry-relevant PAA treatments affect both *C. jejuni* culturability and viability on chicken wings. Chicken wing portions (25 g) were inoculated with a three-strain *C. jejuni* cocktail (~6.0 log10 CFU/g). Condition 1 (C1) consisted of 50 ppm PAA for 2 hours, followed by 500 ppm for 20 minutes. Condition 2 (C2) included the same treatments as C1, but with the addition of a 10 second dip in 800 ppm PAA at the end. Both conditions were evaluated in three independent experiments with one untreated and four treated samples per experiment. Culturable cells were quantified by plating on Campy-cefex agar and membrane-intact cells by PMA viability-qPCR. Reductions relative to matched negative controls were analyzed using a linear mixed-effects model. Sequential PAA treatments resulted in a greater loss of culturability than membrane integrity, which is consistent with the potential presence of VBNC cells. The additional 800 ppm dip did not result in a significant additional reduction of C. jejuni, indicating limited added benefit under the conditions evaluated.

U-20. **GLP-1 Receptor Agonist Therapy Reshapes the Gut Microbiome: A Longitudinal Genomic and Bioinformatic Study of Fecal Microbial Dynamics**. Ethan Achmoody*, Hailey Baker*, Brady Heath*, Joshua McMichael*,Regina Lamendella. Juniata College, Huntington, PA.

Glucagon-like peptide-1 receptor agonists (GLP-1RAs) are widely used in the management of type 2 diabetes and obesity due to their effects on glycemic control, appetite regulation, and weight loss. These agents function by triggering glucose-dependent insulin secretion from pancreatic beta cells. Moreover, GLP-1RAs like semaglutide enhance systemic insulin sensitivity and promote adipose tissue browning, making fat cells far more metabolically active. Despite these therapeutic benefits, clinical application is frequently complicated by adverse gastrointestinal effects, primarily nausea and vomiting. Emerging evidence suggests that these agents may also influence the gut microbiome, a dynamic community of microorganisms that plays a critical role in metabolic health. GLP-1RAs restructure the microbial landscape by altering gastric emptying rates, intestinal transit time, and the local luminal environment. We are examining the bidirectional relationship between GLP-1RA signaling and gut microbiome composition, specifically focusing on how treatment could lead to possible dysbiosis. In this longitudinal, blinded study, we are collecting fecal samples from 55 individuals at four time points: pre-GLP-1RA use, 1 month after GLP-1RA initiation, 3 months post-initiation, and 6 months post-initiation. We will perform shallow shotgun metagenomics paired with the QIIME2/DADA2 bioinformatics pipeline on the 16S gene to characterize the microbiome shifts associated with therapies involving GLP-1RAs.

U-22. **Isolation of *Plasmodium yoelii* Ribosomes Using 3xMango-II Tag**. Brayden Wenrich*, Scott Lindner. The Pennsylvania State University, State College, PA.

Malaria remains one of the greatest global health concerns facing humanity in the 21st century. Its symptoms include intense gastrointestinal issues, high fever, and in select cases death. The parasite responsible for the disease (*Plasmodium*) contains three types of specialized ribosomes responsible for protein synthesis: A-Type, S1, and S2. It has been shown that these ribosomes express differentially throughout the life cycle of the parasite, suggesting stage-specific translational regulation. However, little is known about the structural and functional differences between the specialized ribosomes. This project aims to develop an experimental approach to isolate each type of ribosome from the parasite at large. Using 3xMango-II RNA tags which bind selectively on surface-accessible regions of each ribosome type, we are able to affinity-purify the ribosomes in an RNA-dependent manner. This is a novel approach that has never been reported before in eukaryotes, and only twice before in prokaryotes. Being able to isolate each type of specialized ribosome enables subsequent characterization experiments aimed at elucidating their structural and functional differences. Such possibilities include determination of protein composition through proteomics, identification of RNA modifications using Direct RNA-seq, and visualization of their structures via Cryogenic Electron Microscopy (Cryo-EM). Understanding the fundamental differences between the ribosomes of *Plasmodium* parasites will provide broader insight into the protein synthesis mechanisms critical to the organisms' success. Subsequently, this will open the door to future research that can identify and target translational weak points to ultimately compromise the survivability of the parasite.

U-24. **From Structure to Function: Biochemical Characterization of Four Proteins of Unknown Function**. Jamison Gaugler*, Giovanni Guido*, Emma Hyder*, Rosemary Mcgovern*, Olivia Long. Saint Vincent College, Latrobe, PA.

Despite advances in genome sequencing and structural biology, many proteins remain incompletely characterized, with their biochemical functions unknown or poorly understood. Through the Biochemistry Authentic Scientific Inquiry Lab (BASIL) project, we are investigating four proteins represented by Protein Data Bank (PDB) entries 3DS8, 3H04, 3L1W, and 2O14. Each of us is independently investigating one protein using an integrated approach combining molecular biology, protein biochemistry, and bioinformatics. We are expressing recombinant proteins in *Escherichia coli* using pET-based expression vectors. Our initial investigations have focused on optimizing bacterial growth and protein expression conditions to improve protein yield. We are currently refining protein isolation and purification procedures using nickel-affinity column chromatography, employing Bradford assays to quantify protein concentration, SDS-PAGE to assess protein expression and purity, and Western blotting to confirm the presence of our recombinant proteins. Our next steps will integrate bioinformatics analyses of protein sequence and structure, examination of potential ligand-binding interactions, and development of kinetic assays to evaluate predicted enzymatic activities. By combining computational predictions with experimental evidence, we aim to identify potential biochemical functions for these proteins and better understand how their three-dimensional structures contribute to their activities.

U-26. **Phage Purification: PEG Precipitation and Triton X-100 vs. Endotoxin Removal Resin Spin Column and Preliminary Work For LPS Exposed Mammalian Cells**. Briana Kochumuttom*, Nicole McAllister Conrad. Seton Hill University, Greensburg, PA.

Bacteriophages are viruses that kill bacteria by infecting and replicating within them. However, recent studies have suggested that bacteriophages also have the potential to interact directly with mammalian cells particularly by altering inflammatory cytokine activity. Lipopolysaccharide (LPS) is a component found on the outer membrane of gram-negative bacteria that provides stability and organization for bacteria but also exhibits pro-inflammatory effects. The objective of this project is to assess how LPS affects inflammatory cytokines production and how the T4 bacteriophage can alter this relationship in mammalian cells. The production of pro-inflammatory cytokine TNF-a and anti-inflammatory cytokine IL-10 as well as cell viability will be assessed after LPS treatment and phage exposure. Bacteriophages contain endotoxins or LPS which as mentioned before can have pro-inflammatory effects. Therefore, to ensure safety and achieve a purified bacteriophage sample, the sample must undergo a purification protocol. A comparative study of purification methods is being conducted as a preliminary step where the effectiveness of a PEG and Triton X-100 purification compared to an Endotoxin Removal Resin Spin Column purification. The most effective method will be utilized in the LPS induced co-culture system. Preliminary studies are underway, analyzing cell proliferation, percent attachment, and inflammatory cytokine levels in LPS exposed and non-exposed mammalian cells. These preliminary control experiments and the phage purification optimization studies are the first steps towards the LPS and phage co-exposure experiments that will aid in the understanding of how phages interact with mammalian cells.

U-28. **Characterization of *Bifidobacteria* spp. Lipoprotein**. Sam Carillo*, Timothy Meredith. The Pennsylvania State University, State College, PA.

The gut microbiome plays an important role in human health via its interactions with the immune system. *Bifidobacteria* are abundant gut bacteria that confer anti-inflammatory properties and are generally reduced in chronic gut diseases such as inflammatory bowel disease. *Bifidobacteria* membranes contain lipoproteins that perform vital cellular functions and are recognized by the human innate immune system's toll-like receptor (TLR) heterodimers 2/1 or 2/6. Differences in the lipid modifications of the conserved N-terminal cysteine (triacylated or diacylated variants) influence signal magnitude and downstream inflammatory or anti-inflammatory responses. In 5 bifidobacterial species tested, all activated TLR2/TLR6, consistent with diacylated lipoproteins. Due to differences in signal strength, lipoprotein structure was investigated through mass spectrometry, yielding two distinct lipoprotein candidates for further analysis.

U-30. **Green Microbiology: Determining if Single Use Plastics can be Reused While Remaining Accurate and Clean**. Liesl Allison*, Welkin Pope. Chatham University Pittsburgh, PA.

Plastic waste is a huge contributor to global pollution, as seen in the island of plastic in the Pacific. While single-use plastics are great for convenience and sterility, lab and medical waste, like micropipette tips, accumulate lots of unnecessary waste. In more recent years, our lab has started to reuse materials in order to reduce waste as much as possible. Cell culture was used to determine that reused micropipette tips remain accurate and sterile, concluding that no living cells remain. PCR and Gel Electrophoresis were used to determine if DNA remained on the surface of reused micropipette tips after cleaning and sterilization. Repeated testing has shown no presence of bacterial DNA on the washed and reused materials. Future directions are to test for infectious phage particles and phage DNA on reused materials.

U-32. **Annotation of *Arthrobacter globiformis* B-2979 phages**. Aislin Manzella*, Welkin Pope. Chatham University, Pittsburgh, PA.

Bacteriophages are viruses that infect bacteria as their hosts. With 1031 bacteriophages on the planet, all possessing different morphologies and functions, they are an important contributor to global biodiversity. Previously, Chatham University students isolated and sequenced phages that infect *Arthrobacter globiformis* B-2979 from environmental samples. Phages BellaJr, Merpity, and Marianna39 from clusters FN, FQ1, and FK respectively, have been annotated. These clusters are fairly small, containing less than 10 phages each. Specific genes in clusters FN and FK are well conserved across each cluster. Cluster FQ1 shows phages with two different heads but a conserved tail while Cluster FK genomes contain a section of short repeats.

U-34. **Effect of Oral Nicotine Pouches on Lifespan and Germline of *C. elegans***. Celia Cole*, David Smith. West Virginia University, Morgantown, WV.

Oral Nicotine Pouches (ONPs) are increasingly marketed as safer alternatives to cigarettes and e-cigarettes because they eliminate inhalation risks. However, evidence regarding their effects remains limited, and this study evaluated the impact of diluted ONP extract on the lifespan of *Caenorhabditis elegans* (*C. elegans*). Exposure to ONP extract significantly decreased the lifespan in both wild-type nematode and Huntington's disease model compared to untreated controls. The higher concentration correlated with accelerated mortality. These findings indicate that ONPs induce systemic toxicity and reduce longevity in a model organism. Future investigations are required to isolate the roles of specific nicotine concentrations, brands, and flavoring agents on long-term physiological health.

U-36. **ButterNova: The Isolation and Characterization of a Novel Arthrobacter globiformis B-2979 Phage**. Santino Premozic*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

Bacteriophages (phages) are viruses that infect bacteria and play a vital role in the regulation of bacterial populations. Characterizing bacteriophages improves the collective understanding of phage biology and potential applications. This study focuses on the novel discovery, isolation, and characterization of ButterNova, a bacteriophage that was discovered on *Arthrobacter globiformis* B-2979 and additionally found to infect *Arthrobacter globiformis* 2880. The goal is to achieve a high titer lysate of the phage to add it to the Science Education Alliance-Phage Hunters Advancing Genomics Evolutionary Science (SEA-PHAGES) database and characterize it as following the lytic or lysogenic cycle. ButterNova was isolated, purified, and amplified following the protocols given by the SEA-PHAGES program. Serial dilutions of phage samples were prepared and plated with Arthrobacter globiformis B-2979 host bacteria to observe plaque formation. Plaque morphology was examined to assess the appearance and consistency of bacterial clearing, with additional experiments conducted to investigate the potential of lysogeny. Observation through experimentation showed that ButterNova produced clear, uniform plaques on bacterial lawns. These characteristics are consistent with phages that undergo the lytic cycle. Plaque morphology alone cannot definitively determine a strictly lytic phage from one capable of lysogeny. Further experimental evidence is needed to definitively establish ButterNova's life cycle. These findings provide an initial characterization of ButterNova and establish a foundation for further investigation of its interactions with bacterial hosts. Future experiments examining lysogeny will help clearly define ButterNova's mode of infection and contribute overall to a better understanding of bacteriophages.

U-38.**Digging for Diversity: Isolation of the Soil Phage Trailhead A Newly Isolated Bacteriophage from Environmental Soil Samples.** Tyler Schlobohm*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

Phages that infect soil bacteria like *Arthrobacter globiformis* are understudied compared to some other groups of phages, despite these bacteria commonly appearing in the environment. Finding new ones helps us learn more about phage diversity and how they interact with their hosts. The goal of this project was to isolate a new bacteriophage from soil, confirm it was real, and prepare a high-titer lysate so the phage DNA could be extracted for further work. Soil samples were collected from different locations and processed using the standard SEA-PHAGES methods for *A. globiformis*. This included enrichment to increase probability of finding phage, filtration, plating to look for plaques, three rounds of purification to get a pure sample, and then amplification on plates to make a high-titer lysate. One phage produced clear plaques that possessed identical morphology after purification. It was successfully grown up to a high titer, and phage DNA was extracted from that lysate. The phage was named Trailhead. These results show that a new Arthrobacter phage was recovered from soil and that a pure high-titer stock is now available. Isolating Trailhead adds another phage to the growing list of Actinobacteriophages and shows that the enrichment approach works well for this host. Next steps include examining the phage under the Transmission electron microscope, sequencing the genome, and annotating it to compare to other phages, then archived.

U-40. –scratch—

U-42. **SEA-PHAGES: DirtyMert: A Filthy Bacteriophage**. Demetri Eori*, Sarah Swerdlow. University of Pittsburgh–Greensburg, Greensburg, PA.

Bacteriophages (phages) infect their host by inserting their genetic information into the bacterial host organism. Upon infection, the phage can go through one of two life cycles, the lytic or lysogenic cycle which both result in host lysis. When observed, virulent phages undergo the lytic cycle and leave a clear plaque on their agar plate. However, temperate phages carry out the lysogenic cycle which leave more hazy/clouded plaque spots. The bacteriophage population is large, with an estimated 1031 bacteriophages in the Earth's biosphere. Around ~5000 phages have been sequenced and the SEA-PHAGES program aims to sequence more. To complete this experiment, my initial sample collection came from Smithton, PA. The soil sample came from dark brown, moist dirt taken from an area between a tree and a garage, the ground receives both shade and sunlight throughout the day. The site of collection is a high foot traffic area. Isolation of the phage from the soil sample followed data collection. For plaque assays and the entire experiment Arthrobacter globiformis 2979 served as the host and PYCa is the media. Amplification, DNA extraction and characterization is the final step. The experiment resulted in the discovery of DirtyMert, a virulent phage with plaques of 1-3mm in diameter that forms a MESA. The host range experiment shows that DirtyMert infects Arthrobacter globiformis 2880 as well. Following my initial experiment, further data collection on the phages host range capabilities and mapping the genome would be key items in completing the SEA-PHAGES project.

Special Message of Thanks from President-Elect Dr. Merrilee Anderson

ABASM is a massive collaborative effort! The following individuals deserve special recognition for their contributions:

-The Leadership Team of ABASM (Dr. Drew Bridges, Dr. Sarah Swerdlow, Dr. Michelle Valkanas, Dr. Jill Keeney, Dr. Jennifer Koehl) – for all their guidance.

-Dr. Crystal Goldyn, Dr. Mike Engle, Dr. Penny O'Connor, Ms. Aimee Itle- MAC Faculty

-Ms. Erin Wise and Ms. Jeanine Farabaugh- MAC Administrative Assistants

-Mount Aloysius College – Dining Services, Maintenance, IT, Campus Safety

-Pitt Greensburg- Justin in IT

-TriBeta and Bio club students from MAC

-Dr. Cynthia Brame – Guest speaker

-Dr. Scott Lindner –Keynote Speaker

-Faculty judges- for providing great feedback to our students

-ASM- for providing the funds to support ABASM

MOST IMPORTANTLY: ALL ATTENDING AND PARTICIPATING STUDENTS-

We are so proud to see and hear you present your work, best of luck in your education and career!

Upcoming ABASM Meetings

2027 –Juniata College

Attendees

Omkar	Warke	orw100@juniata.edu	Juniata College
Ethan	Achmoody	eda100@juniata.edu	Juniata College
Ayers	Aguiar	aa00397@mix.wvu.edu	West Virginia University
Tara	Allison	drtallison15@gmail.com	Gannon University
Callie	Ancosky	cancosky@gmail.com	West Virginia University
Merrilee	Anderson	manderson@mtaloy.edu	Mount Aloysius College
Caitlin	Bissell	ceb00054@mix.wvu.edu	West Virginia University
Katherine	Bollinger	katherine.bollinger@stvincent.edu	St. Vincent College
Ethan	Buchleitner	Buchleit003@gannon.edu	Gannon University
Quinn	Burnett	qcb5019@psu.edu	The Pennsylvania State University
Liu	Cao	cao003@gannon.edu	Gannon University
Sam	Carrillo	carrillo.sam.216@gmail.com	Penn State
Peyton	Cercone	p.cercone@setonhill.edu	Seton Hill University
Darrell	Cockburn	dwc30@psu.edu	Pennsylvania State University
Celia	Cole	cc00207@mix.wvu.edu	West Virginia University
Celia	Cole	cc00207@mix.wvu.edu	West Virginia University
Arica	Collier	COL98567@pennwest.edu	PennWest University - California
Olivia	Conaway	oc00012@mix.wvu.edu	West Virginia University
Logan	Cree	creelr23@juniata.edu	Juniata College
Jesse	Derringer	jessederringer@cmu.edu	Carnegie Mellon University
Spencer	Dublin	srd0018@mix.wvu.edu	West Virginia University
Edward	Dudley	egd100@psu.edu	Penn State University
Meenal	Elliott	melliott@hsc.wvu.edu	West Virginia University
Sarah	Ellis	ellis362@marshall.edu	Marshall University
Mike	Engle	JEngle@mtaloy.edu	Mount Aloysius College
Jamison	Gaugler	jamison.gaugler@stvincent.edu	St. Vincent College
Crystal	Goldyn	cgoldyn@mtaloy.edu	Mount Aloysius College
Dominic	Granata	dmg168@pitt.edu	University of Pittsburgh at Greensburg
Elias	Griffin	griffine2@duq.edu	Duquesne University
Giovanni	Guido	Giovanni.guido@stvincent.edu	St. Vincent College
Hailee	Gunn	hag168@pitt.edu	University of Pittsburgh at Greensburg
Katie	Hackman	klh102@juniata.edu	Juniata College
Madeline	Hatch	mgh100@juniata.edu	Juniata College
Madeline	Hatch	mgh100@juniata.edu	Juniata College
David	Heisler	heislerd@duq.edu	Duquesne University
Hunter	Hoffman	hrh100@juniata.edu	Juniata
Vicky	Huang	yhu102@juniata.edu	Juniata College
Annalisa	Huckaby	abh0010@mix.wvu.edu	West Virginia University
Emma	Hyder	emma.hyder@stvincent.edu	St. Vincent College
Gabriel	Infante	gabriel.infante@upr.edu	PennState
Maura	Jodkin	maura.jodkin@stvincent.edu	Saint Vincent College
Eva	Johnson	johnsem23@juniata.edu	Juniata College
Maureen	Johnson-Keitt	m.johnsonkeitt@setonhill.edu	Seton Hill University

Jill	Keeney	keeney@juniata.edu	Juniata College
Briana	Kochumuttom	b.kochumuttom@setonhill.edu	Seton Hill University
Jennifer	Koehl	jennifer.koehl@stvincent.edu	Saint Vincent College - BioSci Department
Jasna	Kovac	jzk303@psu.edu	Penn State
Maycie	Kulp	mzk100@juniata.edu	Juniata College
Regina	Lamendella	lamendella@juniata.edu	Juniata College
Ian	Leighton	il0009@mix.wvu.edu	West Virginia University
Betsy	Lewis	betsylew@andrew.cmu.edu	Carnegie Mellon University
Scott	Lindner	sel27@psu.edu	Penn State
Olivia	Long	olivia.long@stvincent.edu	St. Vincent College
Lili	Macharashvili	macharashvilil@duq.edu	Duquesne University
Chris	Maltman	christopher.maltman@sru.edu	Slippery Rock University
Nicole	McAllister Conrad	nmcallister@setonhill.edu	Seton Hill University
Donovan	McCammon	mccamdd23@juniata.edu	Juniata College
Morgan	McCann	mccannm3@duq.edu	Duquesne University
Rosemary	Mcgovern	rosemary.mcgovern@stvincent.du	St. Vincent College
Mauren	Miller	maurmill6@gmail.com	West Virginia University
Manali	Misra	misramx23@juniata.edu	Juniata College
Robert	Monson	rhm5291@psu.edu	The Pennsylvania State University
Gianna	Moses	gak00019@mix.wvu.edu	West Virginia University
Aidan	Murray	am00276@mix.wvu.edu	West Virginia University
Ilse	Ness	ihn100@juniata.edu	Juniata College
Emmy	Nguyen	emmyn@cmu.edu	Carnegie Mellon University
Juliana	Onuskanich	jvo100@juniata.edu	Juniata College
Mattia	Parrini	parrini001@gannon.edu	Gannon UNiversity
Ellena	Perdue	PER33872@pennwest.edu	PennWest University - California
Welkin	Pope	w.pope@chatham.edu	Chatham University
Santino	Premozic	sap455@pitt.edu	University of Pittsburgh at Greensburg
Alicia	Purcell	purcella@marshall.edu	Marshall University
Sarah	Rahin	sar00034@mix.wvu.edu	WVU
Ashley	Robuck	robucaa23@juniata.edu	Juniata College
Bee	Rohrs	bailey.rohrs@chatham.edu	Chatham University
Stacy	Santiago-Garay	stacy.santiago1@upr.edu	The Pennsylvania State University
Tyler	Schlobohm	Tys65@pitt.edu	University of Pittsburgh At Greensburgh
Rebecca	Slate	slater@duq.edu	Duquesne University
Liesel	Stine	lps5747@psu.edu	Penn State
Liesel	Stine	lps5747@psu.edu	Penn State
Sarah	Swerdlow	sjs308@pitt.edu	University of Pittsburgh, Greensburg
Maya	Tanikawa-Brown	mmt5857@psu.edu	The Pennsylvania State University
Amber	Terry	TER20518@pennwest.edu	PennWest University - California
Parker	Thomas	plt100@juniata.edu	Juniata College
Mackenzie	Tickle	mackenzietickle@gmail.com	Marshall University

Mackenzie	Tickle	mackenzietickle@gmail.com	Marshall University
John	Trimble	jtrimble@francis.edu	Saint Francis University
Sophia	Turecki	sturecki@andrew.cmu.edu	Carnegie Mellon University
Sophia	Turecki	sturecki@andrew.cmu.edu	Carnegie Mellon University
Alanna	Vala-Kovac	jzk303@psu.edu	Park Forest Middle School
Michelle	Valkanas	valkanas@pennwest.edu	PennWest University - California
Erin	Walsh	erinwals@andrew.cmu.edu	Carnegie Mellon University
Josephine	Wee	jmw970@psu.edu	Penn State University
Barbara	Wehle	bjm00025@mix.wvu.edu	West Virginia University School of Medicine
Brayden	Wenrich	bjw6026@psu.edu	Penn State University
Michelle	Witt	mrwitt@hsc.wvu.edu	West Virginia University

Mount Aloysius College Address: 7373 Admiral Peary Highway, Cresson, PA 16630

Campus Maps: https://www.mtaloy.edu/about/our-campus/maps/

Parking: Parking will be held in Lots 7, 13, & 14. After using the **Near Entrance**, you will come to a stop sign at the back of the campus. Turning left will take you to **Lot 7** behind **Pierce Hall (J)**, while turning right will take you to **Lot 13** and **Lot 16**.

Events: Registration, poster and oral sessions will occur in Pierce Hall.
Friday night will be in **Cosgrave** and Saturday keynote speech will occur in **Bertschi Center (K)**. Bertschi is a short walk, visible from the main entrance to Pierce Hall.

Campus Map:

