LIPMAN LOG

Department of Biochemistry and Microbiology

Inside this issue

2018 Edition

RUTGERS
School of Environmental and Biological Sciences

News from the Chair

Department Chair, Max Häggblom

We are pleased to present this latest issue of the Lipman Log, with highlights from the 2017-2018 academic year. This has been an eventful year, with new additions to our faculty and staff, tenure promotions, awards, and theses defenses.

Maria Gloria Dominguez-Bello joins the department as the Henry Rutgers Professor of Microbiomes and Health. She is internationally recognized for her study of the role of animal-microbe interactions in health, including the human microbiome. Her research focuses on understanding symbioses between microorganisms and their hosts, their coevolution, the contribution of microbial genes to the function of microbe-dominated organs, and the effect of perturbations.

We congratulate **Jeff Boyd** on his promotion to Associate Professor with tenure, and the receipt of a National Science Foundation Career Award for his project "Iron-sulfur cluster assembly in *Bacillus subtilis*" and a National Institute of Allergy and Infectious Diseases grant for his project "Mechanisms of cellular respiration-dependent cell lysis and its impact on biofilm formation and disassembly in *Staphylococcus aureus*".

We welcome a new teaching faculty member, **Jessica Lisa** (Microbiology), and congratulate **Natalya Voloshchuk** on her promotion to Assistant Teaching Professor. Our non-tenure track faculty fill critical roles in our department's teaching, research, and engagement. **Diane Davis** retired from her position as Associate Teaching Professor in January after many years at Rutgers. As an instructor, she was a central force in the department and in the development of our microbiology undergraduate program. We wish her a happy retirement!

Peter Anderson, our polymath of IT operations, celebrates 30 years at Rutgers. He first joined the department as a Secretarial Assistant and later, with the development of office computers, took on the role of overseeing technological operations. His outreach in photography of departmental events has been truly superlative. Peter accomplishes his duties with boundless energy, attention to detail, and an enthusiastic smile.

It is a delight to follow the achievements of our students. Our graduate and undergraduate students are engaged in many exciting research projects with our faculty members. Our scholarship and undergraduate and graduate programs in biochemistry and microbiology continue to flourish. You can read more on the latest Ph.D. theses, the awards our students have received and about their other activities. Our department also continues to host visiting scholars and students from around the world.

I wish to thank all our donors!! Your contributions provide important student scholarships, awards and travel fellowships, and support our Fermentation Club seminar series. The Cuskey and Eveleigh Graduate Student Travel Awards continue to provide much-needed support for our students to travel to national and international conferences to present their work, network, and learn. Our Department Fund supports undergraduate awards, our Fermentation Club seminar series, and the annual microbiology symposium. We hope that you will continue to show your support for the department and our scholarly programs.

Jeff Boyd

I joined the Department of Biochemistry and Microbiology at Rutgers in the Fall of 2010. This spring I was promoted to Associate Professor with tenure.

I am originally from the Midwest and I primarily grew up in Iowa. My parents were hard-working middle class people who instilled in me a desire for investigation and discovery at an early age. If there was a problem around our house, Mom or Dad figured out a way to solve it. My parents fixed everything from cars to clothes, and as kids we were required to help them. My father's can-do attitude taught me to think logically when solving problems, whereas my mother taught me to think abstractly when searching for answers and not to be constrained by dogma. I believe the balance between these two philosophies helped me to become a well-rounded scientist; it taught me that the first step in solving problems is not to be afraid to try, and certainly not to give up once you hit a roadblock. This was my approach as I often disassembled and reassembled things on my own, including electronics and bikes. I was also given a great deal of freedom to explore, and spent a lot of time outside developing a passion for nature.

As an undergraduate at Iowa State University (ISU), I floundered through my freshman year of college trying different science majors. During my sophomore year, I took an entry level course in microbiology and I was hooked. I graduated with a degree in Microbiology, Immunology and Preventative Medicine. One of my most formative formal educational experiences was conducting research as an undergraduate in the laboratory of Prof. Alan DiSpirito. In Alan's lab, I studied the physiology of organisms that could grow on methane gas as their sole carbon and energy sources. This cemented my love for the diversity of life, which, as we know, is found in the microbial world. More importantly, I realized that I love to formulate and test hypotheses. It was in Alan's lab that I got my first "science high" after seeing the results of my own experiments. I have never looked back, and I look forward to a science high every day.

After graduation, I took a gap year in Crested Butte, Colorado with my soon to-be-wife, whom I met at ISU. We spent a lot of time exploring the landscape and enjoying nature. We subsequently moved to Logan, Utah where I conducted my Ph.D. studies in the laboratory of Prof. Scott Ensign at Utah State University (USU). USU was a great fit for me because I was studying the biochemical processes that make life unique, while also being encouraged to explore the mountainous surroundings and nature. In the lab, I examined unique bacterial metalloenzymes that detoxify environmental pollutants. I was also allowed the opportunity to work as a teaching assistant, where I learned that I truly enjoy educating others and helping students develop a toolset to ask and answer their own scientific questions. This experience cemented my decision to become an educator and a scholar.

After my graduate studies, my wife and I moved to the University of Wisconsin-Madison where I worked with Prof. Diana Downs as a National-Institutes-of-Health-funded postdoctoral scholar. The opportunity to work with Diana piqued my interest because the year prior she had won the American Society of Microbiology's award for being an outstanding graduate student mentor. Her husband Jorge had won the same award the year before. I knew that if I wanted to be a successful teaching scholar at a top research institution, I would need to hone my mentoring skills. Moreover, Diana studied metalloproteins. In Diana's lab, I studied the genetics and biochemistry of how bacteria make inorganic cofactors called iron-sulfur (FeS) clusters and maturate FeS proteins. These are still active projects in my lab at Rutgers. I also became a Howard Hughes Teaching Fellow and worked for one year as a teaching postdoctoral scholar. While in Madison, my first daughter was born. Given my new family dynamic, Diana's guidance helped me better balance my home and professional workloads. These experiences made it much easier for me to transition into my current position.

After leaving Madison, before starting at Rutgers, I worked as a postdoctoral scholar with Profs. Alex Horswill and William Nauseef at the University of Iowa. There, I enriched my molecular biology toolkit and learned to manipulate the genome of the bacterium *Staphylococcus aureus*. I initiated projects investigating how *S. aureus* responds to oxidative stress, and senses and responds to environmental perturbations, which are also current projects in my lab. I also discovered that I enjoy learning about how bacteria interact with the human body, especially, the innate immune system.

In my lab at Rutgers, we focus on deciphering how microbial cells function. Our goal is to understand what all genes in a bacterial genome do and how the gene products integrate into the metabolic network to produce a robust and responsive metabolism.

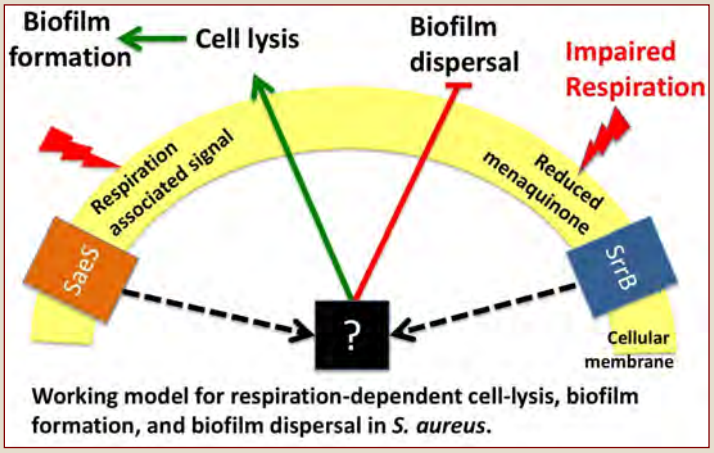
Our research group currently concentrates our efforts on three major projects and a few smaller ones. We focus most of our attention on the gram-positive bacteria *Bacillus subtilis*, which is a model organism, and *Staphylococcus aureus*, which is a pathogenic bacterium that affects mammals. *S. aureus* lives on about 30% of the human population asymptomatically; however, it is also a major cause of hospital- and community- acquired infections. In fact, it is a

Jeff Boyd

leading cause of infectious- disease-related illness and death in the United States. It can cause infections ranging from mild skin and soft tissue infections to invasive life-threating infections. The penultimate goal of our research is to apply our findings to decrease the burden of bacterial pathogens or modulate the behavior of these pathogens to improve disease outcomes.

Project 1: *Staphylococcus aureus* biofilm formation and dispersal.

In a project funded by the Cystic Fibrosis Foundation and the National Institute of Allergy and Infectious Diseases, we examine the mechanisms by which *S. aureus* forms biofilms or disperses biofilms once formed. Biofilms are groups of cells that act as a community to circumvent the immune system or hunker down to survive with limited resources. Biofilm formation and dispersal are important aspects of the infection lifecycle; it has been postulated that prevention of biofilm formation or the dispersal of biofilms could improve infection outcomes. The ability of *S. aureus* to form biofilms is thought to be a pre-requisite for disease; the dispersal of biofilms can result in the spread of infection to other human tissues, but it also makes *S. aureus* more susceptible to certain antibiotics.

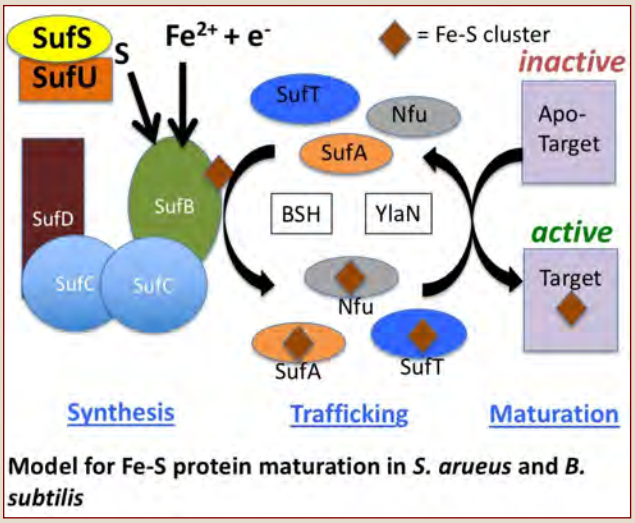


Working model for respiration-dependent cell-lysis, biofilm formation, and biofilm dispersal in *S. aureus*.

For *S. aureus* to colonize and invade human tissues, it must successfully respond to environmental perturbations and transition between individualistic and multicellular (biofilm) behaviors. However, the regulatory, genetic and molecular mechanisms underpinning the committed movement of planktonic (single) cells towards multicellularism are largely unknown. This project aims to examine the environmental signals and mechanisms that influence biofilm formation and dispersal in *S. aureus*. One of the major signals that *S. aureus* responds to is the presence or absence of oxygen. Many human tissues have low oxygen tension. We have found that when oxygen tension decreases, the number of *S. aureus* cells found in biofilms increases. We have identified two global regulatory systems that sense oxygen (cellular respiration) and alter biofilm formation. Both of these regulatory systems are necessary for *S. aureus* pathogenesis, but their molecular stimuli are currently unknown. We focus on how *S. aureus* senses the presence or absence of oxygen, the molecular components that alter biofilm formation and dispersal, and how the detection of oxygen results in altered expression of these factors. We also examine if small molecules can be used to trick *S. aureus* into thinking that oxygen is present or absent to modulate its behavior and improve infection outcomes.

Project 2: Building FeS clusters and maturating FeS proteins.

In a project funded by a National Science Foundation CAREER award, we are examining how gram-positive bacteria build FeS clusters and maintain proteins that require FeS clusters. Many bacterial pathogens are resistant to numerous commonly-prescribed antibiotics, so there is a great need to discover new antibiotics. Described antibiotics act upon a limited subset of metabolic reactions that are essential for growth and survival. We would like to expand the list of targets. The acquisition of iron (Fe) and the processes of building FeS clusters and maintaining FeS proteins is essential for most organisms. Importantly, the mechanisms by which bacteria conduct these processes is different than how mammals do, suggesting that they are viable antimicrobial targets. Before these targets are considered for antibiotic development, we need to determine all of the gene products necessary for the processes and assign biochemical functions to them.



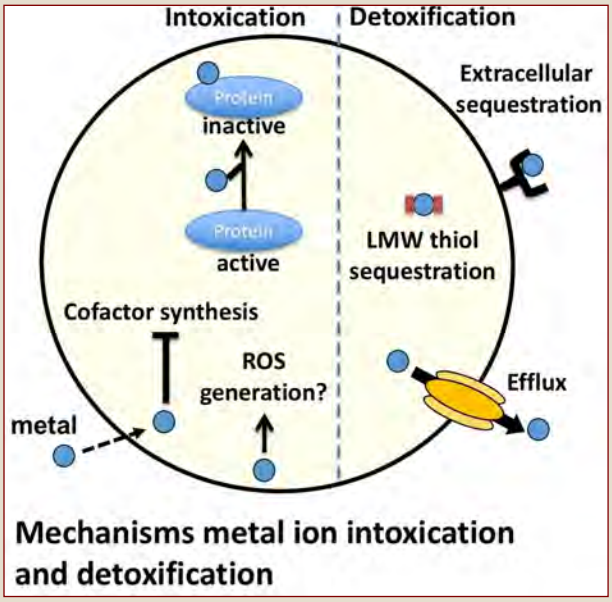
Model for Fe-S protein maturation in *S. arueus* and *B. subtilis*

Bacteria acquire Fe from the environment and transport it into cells using specific uptake systems. A large proportion of internalized Fe is housed in inorganic prosthetic groups called iron-sulfur (FeS) clusters. These cofactors are composed of Fe and sulfur (S) atoms. Because free Fe and S are toxic to cells, elaborate protein systems are used to build these cofactors. Once built, the FeS clusters must be trafficked to, and inserted into, proteins that require them for function. The proteins that utilize FeS clusters have many roles; there are few

aspects of metabolism that are not impacted by Fe-S cluster proteins. The metabolisms of most organisms are reliant on FeS protein function; failure to properly maturate FeS proteins results in widespread metabolic disorders and often cell death. The NSF-funded project combines classic and molecular genetics and biochemistry with state-of-the-art, next-generation technologies and computational biology to improve our understanding of how the model gram-positive bacterium *Bacillus subtilis* maturates and maintains FeS proteins. The results of these studies will impact the understanding of iron-dependent processes from bacteria to humans.

Project 3. Determining how copper kills *S. aureus* and the mechanisms utilized to prevent intoxication by copper. Our lab's newest project examines an age-old technology: using copper (Cu) to kill or prevent the growth of microorganisms. Copper has been used as an antiseptic and to coat surfaces to decrease bacterial loads; however, it is still not known how Cu kills microbes. Due to expanding antimicrobial resistance, Cu is being reevaluated for possible expanded use to prevent or treat diseases. We have discovered a gene operon in *S. aureus* that provides resistance to Cu. This operon is located within a transposon, a piece of DNA that can be transferred into the chromosomes of other bacteria. Within this transposon are genes that promote survival on human skin and increase virulence. These data suggest that selecting for Cu resistant *S. aureus* could aid the spread of genes that promote virulence.

We have also created mutant strains lacking all of the described genes that encode for proteins involved in Cu detoxification. We are using these strains to determine how Cu toxifies *S. aureus* and the physiological effects of Cu poisoning. Thus far, we have discovered that Cu treatment interferes with the usage of alternate metals. Treating with Cu affects both Fe and manganese homeostasis.



Mechanisms metal ion intoxication and detoxification

In the future, we plan to determine the gene products that are necessary for cellular fitness in the presence of Cu, and biochemically characterize the interactions between Cu and FeS cluster biogenesis and FeS protein maturation factors.

L to R: Alia Hasan, Tochi Unegbu-Ogbonna, Mary Foley, Hassan Al-Tameemi, Siamak Garabaglu, Adriana Van De Guchte, Nisa Mohammed, Javiera Norambuena Morales, Juan Cerezo, Cedar Boyd, Jeff Boyd, Rowan Boyd.

Department Newbies

Distinguished Professor Debashish Bhattacharya

Debashish Bhattacharya became a member of the DBM faculty in 2018 after transferring from the Department of Ecology, Evolution, and Natural Resources where he was since 2009, when he initially joined Rutgers University. The Bhattacharya group and collaborators have worked for many years in the field of algal genomics and evolution and established the complex paths of algal origin and their places in the eukaryotic tree of life. Debashish's current work focuses on endosymbiosis, the process that gave rise to the eukaryotic organelle plastids and mitochondria from captured cells. His group uses phylogenetics, genomics, and a variety of bioinformatics approaches and functional methods to understand how eukaryotes evolved and how organelles were integrated into "host" cell metabolism. His group works on the intriguing photosynthetic amoeba Paulinella that gained its photosynthetic organelle (plastid) independent from plants and algae, and provides an invaluable resource for understanding how organelles evolve. This area of research also addresses the green sea slug Elysia, a famous animal that behaves like a plant by stealing algal plastids to become photosynthetic ("leaves that crawl").

At Rutgers, he established the SEBS Genome Cooperative, which offers next-generation DNA sequencing and bioinformatic support for Rutgers faculty and both national and international collaborators. Several DBM faculty have worked with the Cooperative on genome projects. His group also pioneered marine single-cell genomics and developed methods to interrogate DNA associated with individual cells captured in nature. This work demonstrated that bacterium-sized algae called picobiliphytes are not photosynthetic as previously thought, and that individual cells contain unique mixtures of prey and pathogen DNA, including the discovery of a novel single-stranded DNA virus. This work opened new research avenues, including single-cell population genomics, the study of hidden marine biodiversity, and genetic transfer in individual cells.

Most recently, the Bhattacharya lab is involved in coral genomics and evolution research. A microbial biology graduate in his group, Alex Shumaker, won the 2017 SMRT grant from PacBio (www.pacb.com/blog/coral-microbiome-project-wins-2017-microbial-smrt-grant/) to generate microbiome data from bleached and healthy corals to figure out how microbes may contribute to coral health. In other work funded by the NSF, group members are using gene co-expression analysis to identify gene "hubs" that define key aspects of the coral stress response. These insights will help us identity and potentially exploit the most robust corals that can withstand current and future ocean warming that threatens reefs worldwide. The Bhattacharya group also maintains interests in novel approaches to microbiology, including work done with Mehdi Javanmard at Rutgers Electrical and Computer Engineering to develop a tool to determine cell health by studying their impedance response in an electrical field. In summary, the Bhattacharya group is excited to be affiliated with DBM and looks forward in the coming months and years to working together with the faculty, staff, and students.

left to right: photosynthetic amoeba Paulinella, green sea slug Elysia

Professor Maria Gloria Domínguez Bello

Maria Gloria Dominguez-Bello joined the Department of Biochemistry and Microbiology in 2018 as a Henry Rutgers Professor of Microbiome and Health. Maria Gloria received her undergraduate degree in 1983 from Simon Bolivar University in Venezuela, and her master's in 1987 and her PhD in 1990 from the University of Aberdeen in Scotland. She was a post-doc at the Institute National de la Recherche Agronomic in France, and worked at the Venezuelan Institute of Scientific Research in Venezuela, at the University of Puerto Rico, and at the NYU School of Medicine before joining Rutgers University.

Research in her lab focuses on the study of the co-evolution of microbiota and hosts, and on the impacts exerted by Western lifestyle practices. We study human microbiome development, structure and function, characterize the effect of perturbations, and explore restoration strategies. She also studies the role of the built environment in microbial transmission, integrating the fields of anthropology and architecture into microbial ecology. Her research work has involved the synergy of a network of collaborators in Venezuela, Bolivia, Peru, Brazil, and the US.

She is a member of the American Academy of Microbiology, an IDSA fellow, belongs to the editorial board of several journals, and has ~120 scientific publications.

Captain Octavio Colson with Maria Gloria Dominguez in the field with Dr. Monica Contreras's team, from the Venezuelan Institute of Scientific Research

CURRENT PROJECTS

C-section-like microbiota and alterations of immune responses. (Juvenile Diabetes Research Foundation, JDRF)
The major goal of this study is to determine microbial factors that increase or decrease T1D outcomes, using the NOD mouse model.

The ancestral and the early microbiome (C&D Fund)
Westernization leads to a reduction of microbiota diversity and to increased risks of diseases related to immune malfunction, such as T1D, celiac disease, autism, allergies, asthma, and obesity. There is evidence that microbial factors are associated with these diseases. This project will assess the magnitude of microbial losses in the human microbiome associated with Westernization, and restoration modalities.

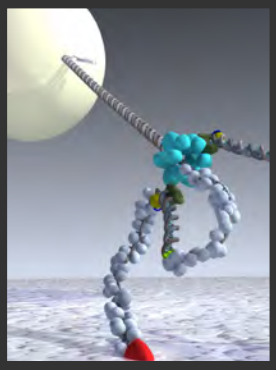
Dr. Dominguez-Bello and team departing a community

The microbiome of isolated peoples (Emch Fund)
Hunter-gatherer societies bring a unique opportunity to understand the microbiome before the impact of modern life practices. Little attention has been paid to the microbiomes of isolated peoples, away from practices including antibiotics, C-sections, and hygienic practices that may impact microbial populations. This project studies the community structure and function of the bacterial populations from traditional peoples, and their protective effect against current epidemic diseases of the modern urban world.

Effect of water disinfection agent and by-products on the developing microbiome and host physiology
This work explores the antimicrobial effects of residuals in water on microbiota. The results will contribute to understanding the link between antimicrobials and urban diseases.

Assistant Professor Arek Kulczyk

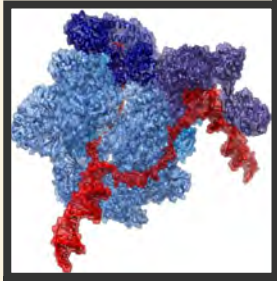
The replisome is a dynamic multi-protein molecular machine that synthesizes DNA, allowing for the passage of genetic information from one generation to another. The intrinsic dynamics and complexity of the replisome make it challenging for structural and biochemical studies. Thus, structural information is scarce and the molecular mechanisms for coordination of DNA synthesis are poorly understood. Nearly three hundred mutations have been identified in the sequence of mitochondrial replication proteins. These mutations play a causative role in the development of cancer and neurodegenerative mitochondrial disorders. Due to the lack of structural data, an exact mechanism by which altered replication proteins affect replisome function is not known.



single-molecule method used to study mtDNA replication.

One of the projects in the Kulczyk lab (kulczyk-lab.cryoemcorp.com) is the determination of the human mitochondrial replisome using cryo-electron microscopy (cryo-EM), which has recently revolutionized structural biology. Prior to joining Rutgers, Arek Kulczyk and his colleagues at Harvard determined a structure of the bacteriophage T7 replisome that is homologous to the human mitochondrial replisome. The cryo-EM structure defines an architecture of the entire replisome, and provides the first such structure of a functioning replication complex assembled on DNA, resembling a replication fork.

The transient nature of the protein-protein interactions that occur during synthesis of mitochondrial DNA (mtDNA) makes it challenging to study these processes by ensemble-averaging techniques. Thus, a number of questions remain unanswered, such as, what is the mechanism of mtDNA replication? To address such questions the Kulczyk lab develops methods combining the flow-stretching of DNA and the total-internal reflection fluorescence (TIRF) microscopy. These methods allow for simultaneous monitoring of the composition and dynamics of individual fluorescently-labeled replisomes during ongoing DNA synthesis in real time. The group investigates mutant variants of the mitochondrial proteins that have been associated with mitochondrial disorders and cancer using these methods. Although mitochondria were thought to lack DNA repair activity, recent data revealed the presence of multiple mtDNA repair pathways. Integrity of the mitochondrial genome is protected by Base Excision Repair (BER); the mechanism that functions interdependent of DNA replication. The Kulczyk lab studies the interplay between mitochondrial BER and DNA replication using single-molecule methods.



cryo-EM structure of bacteriohage T7 replisome

The group also combines single-molecule techniques and cryo-EM for development of the novel methods that allow simultaneous measurements of enzymatic kinetics and structure determination. These single-molecule correlative light and electron microscopy techniques (CLEM) will allow for systematic analysis of structural dynamics of the replisome, and in principle will be applicable to the study of any other biological system.

L to R: Arkadiusz Kulczyk, Primit Desai, Charles Vickers, Heineken Daguplo, Jai Shahani

Arek and his group expect that the structural, single-molecule and CLEM methods described above will yield new insights into the mechanism by which the mutant proteins alter activities of the replisome in human mitochondria. This information may subsequently facilitate development of novel therapeutics for treatment of cancer and neurodegenerative mitochondrial disorders.

L to R: Arkadiusz Kulczyk, Donald Gagne, Primit Desai, Raja Dey

Assistant Research Professor Yan Yan Lam

Date: One beautiful day in October 2016

Location: Sydney International Airport parking lot

Liping: *I'm starting a new lab in the States.*

Yan: *Are you hiring?*

Liping: *Yes. You want a job?*

[after two seconds… maybe three]

Yan: *Why not?*

That was how I started my journey at Rutgers.

When I became the first recruit of the Zhao Laboratory in 2017, many people thought I must have worked with Dr. Liping Zhao for many years to earn this position as his "second-in-command." The fact is, we barely knew each other. I first met Liping when he visited the University of Sydney in 2016. Back then I was a Research Fellow in nutrition and metabolic health and had just started to get into gut microbiota. Some colleagues approached me saying they had studies on weight loss, liver cirrhosis and diabetes and, "by the way," they also wanted to look at the gut bacteria. I could see myself becoming this go-to person for microbiota. But I wanted more than being a co-investigator on little side projects; I wanted my work on gut microbiota to take the center stage.

Joining the Zhao lab brings everything to a whole new level. Sequencing used to be a black box to me – I provided samples and someone would magically turn them into bacteria names and abundances. Over the past year, I have gone from picking up basics like DNA extraction and PCR, to learning about reads and OTUs. Bioinformatics is absolutely terrifying (even typing in the correct command is a challenge!). Lab management is also new to me. Before I left Sydney I had just started my N=2 group, and now I am looking after a N=10 lab. My typical day at the Zhao Lab is a crazy juggling act. I do everything from ordering consumables and supervising students, to writing IRBs and grants. Taking on these new roles in a new environment is not easy, but when my boss nominated me as the person-in-charge, I had nowhere to hide, so I soldier on!

Yan's birthday gift from Liping

The most exciting thing about coming to Rutgers is the science. As a clinical dietitian by training, I decided to pursue research because I believe there has to be better science behind what we advise people to eat or not to eat. Liping and I see our roles in the lab as "complementary" – we need good research and we need to make it possible in the real world. To me feasibility is crucial; we may have the most rigorous research to show that a high-fiber diet is good for gut microbiota, but in the end it all comes down to whether everyday people are able to follow a particular dietary regimen long-term. With our combined expertise in microbial ecology, nutrition, and clinical dietetics, I am thrived to have the opportunity to work side-by-side with Liping and lead a team to advance the concept of "microbiome nutrition." By flying the "feed me and my microbes" flag, we may one day revolutionize nutrition, and this will make my big move from Down Under to New Jersey all worthwhile.

Teaching Instructor Jessica Lisa

I grew up in Long Branch, NJ, where I developed a great appreciation for the ocean through surfing, swimming, and fishing. My interest in nature and curiosity to understand the natural world led me to focus my education on the life sciences. I graduated from Monmouth University with a BS in Biology with a concentration in Marine and Environmental Biology in 2007.

Following graduation, I worked as a research assistant for Monmouth University's Urban Coast Institute under the guidance of Professor John Tiedemann. I was involved in several endeavors to inform policymakers and the public about issues facing New Jersey coastal systems. I also engaged in applied scientific research using real-time data monitoring and microbial source tracking techniques to identify sources of fecal pollution in waterways. Through this work, I developed an interest in microbial ecology and decided to further my education to pursue a career in microbial ecology and marine science.

In May of 2015, I graduated from the Virginia Institute of Marine Science, College of William and Mary, with a PhD in Marine Science under advisor Dr. Bongkeun Song. My dissertation work coupled modern molecular techniques with sophisticated biogeochemical techniques link microbial community structure and function in the Cape Fear River and New River Estuaries in North Carolina. I used high-throughput sequencing techniques targeting present and expressed genes coupled with stable isotope tracing techniques to examine how microbial communities involved in nitrogen cycling respond to changing environmental conditions such as increased salinity.

Afterwards, I worked as a post-doctoral fellow with the Gulf Ecology Division, US Environmental Protection Agency in Pensacola Beach, Florida. My research involved using molecular tools to develop microbial indicators of water quality focusing on nutrient loadings, hypoxia, and land use. My project was developed within the Office of Research and Development's Safe and Sustainable Water Resources Research (SSWR) Program's strategic research action plan to develop scientific solutions that help protect and restore watersheds and aquatic ecosystems.

In January 2018, I joined the Department of Biochemistry and Microbiology as a Teaching Instructor. Since then, I have taught General Microbiology laboratory courses and designed a new course, the Microbiology of Agricultural Products in New Jersey, which we implemented this fall. My goal as an instructor is to facilitate the development of analytical skills that are critical to the student's success as a person and scientist. I am grateful for the opportunity to join the department and look forward to sharing my passion for microbiology with students in a way that will allow them to experience the same excitement and fascination that I experience learning about new breakthroughs in the field.

Dr. Lisa and her post-doctoral mentor, Dr. Richard Devereaux, water column profile sampling at Jackson Lakes, Florida

Visiting Professors

Pin Gao

December 2017 — November 2018

Dr. Pin Gao is visiting Dr. Max Häggblom's lab from the College of Environmental Science and Engineering at Donghua University in Shanghai, China to research anaerobic microbiology, specifically in the areas of environmental microbiology and microbial ecology, by applying complementary molecular and analytical approaches for monitoring the activity of microbial populations in soils and sediments. The project's goal is to develop methods to enhance microbial bioremediation of contaminated sediments.

Xiaorui Liu

December 2017 — October 2018

Dr. Xiaorui Liu is visiting Dr. Liping Zhao's lab from International Peace Maternity & Child Health Hospital, School of Medicine, Shanghai Jiaotong University, Shanghai, China. She earned her PhD in Microbiology at State Key Laboratory of Microbial Metabolism, Shanghai Jiaotong University in 2013. Her primary research interest is vaginal microbe-host interactions (how microbes in the genital tract affect the host's immune system). Presently she is working on reproductive immunology and researching the vaginal microbiome in adverse pregnancy outcomes/complications.

Kyoung-Ho Kim

August 2017 — July 2018

Dr. Kyoung-Ho Kim visited Dr. Max Häggblom's lab from the Department of Microbiology at Pukyong National University in Busan, Korea to research environmental microbiology and biotechnology. He studied the "unusual appetites" of bacteria. His project's aim is to characterize the bacterial communities active in carbon and nitrogen cycling in these environments and to assess the selection mechanisms promoting the dominance of key bacterial taxa under changing temperature regimes.

Folasade Olajuyigbe

October 2017 — June 2018

Dr. Folasade Olajuyigbe visited from the Department of Biochemistry at Federal University of Technology in Akure, Nigeria as a Fulbright Fellow to work with Dr. Max Häggblom and Dr. Gerben Zylstra on her research project, Biochemical and molecular studies on aerobic degradation of crude oil by *Actinomyces viscosus* and *Actinomyces israelii* at varying temperatures. While in the US, she established The Women's Dignity Initiative, a charitable organization dedicated to supporting the education and career preparation of girls and young women in Nigeria.

Our Faculty in Print

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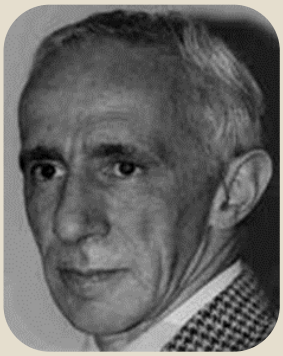
Norberto Palleroni

In Memoriam (1922 - 2018)



The bacterial taxonomist Norberto J. Palleroni passed away on March 5th 2018, at the age of 96. He was a colleague, dear friend, and mentor, and we have lost a leading force in discovery and characterization of the bacterial world. Palleroni was an internationally recognized authority in bacterial taxonomy, particularly the genus *Pseudomonas*. His work on this genus culminated in the metabolic studies based on carbohydrate degradation tests and the first development of ribosomal RNA (rRNA) homology experiments as a tool of general use in bacterial taxonomic and phylogenetic studies. The bacterial classification utilizing genomic DNA-DNA hybridization techniques commenced the exploration of the genome complexity of *Pseudomonas* and other bacterial taxa. This work stimulated research on other microbial groups, resulting in the development of new approaches in the study of bacterial phylogeny that eventually led to the "Tree of Life."

Born in Buenos Aires, Argentina, Palleroni earned his Ph.D. in Microbiology in 1947 at the University of Buenos Aires. The influence of Beijerinck and the "Delft School" of microbiology can be traced through his family tree of scientists: Palleroni's microbiology teacher, Santos Soriano, studied with Beijerinck. Early in his career, Palleroni received a Rotary International Fellowship to work on yeast genetics with Carl Lindegren at Southern Illinois University. He returned to the faculty of the University of Cuyo, in Mendoza, Argentina as Professor of Microbiology (1949-1968) and Director of the Institutes of Microbiology and of Industrial Fermentations. Shortly after this appointment, he received a John Simon Guggenheim Memorial Foundation Fellowship to study bacterial carbohydrate metabolism. This led to an almost 20-year association with two giants in microbial biology and biochemistry: Roger Stanier and Michael Doudoroff, at the University of California, Berkeley Department of Bacteriology.

Norberto's research with Stanier and Doudoroff (1950s-1970s) focused on the biochemistry and taxonomy of the genus *Pseudomonas*. This work resulted in the modern classification of this bacterial group, for which he is best known. The results of the morphological and physiological characterization of *Pseudomonas* species was published in the Journal of General Microbiology. To better understand the great diversity of the genus *Pseudomonas* Norberto began experiments to define the heterogeneity of their genomic DNA. One of the major advances was the use of rRNA hybridization experiments, which demonstrated that the various species assigned to the genus *Pseudomonas* behaved as an entity of several different genera. With the development of 16S rRNA phylogenetic analysis, the various pseudomonads have since been reclassified into different classes of the *Proteobacteria.*

In the early 1970s Palleroni joined the Hoffman-La Roche Research Division in Nutley, New Jersey where he was in charge of maintaining the central microbial culture collection used in organic synthesis and in the production of antibiotics. During this period (1973-1985) he worked on the cultivation and characterization of a range of poorly known bacteria, including the *Actinoplanes*, an actinomycete with motile spores. To enable the isolation of *Actinoplanes* strains he invented a novel method which consisted of trapping the motile spores inside of capillary tubes.

After retiring from Hoffman-La Roche, Palleroni was a Visiting Scholar at the Waksman Institute of Microbiology at Rutgers University (1985-1986), then an Adjunct Professor in the Department of Microbiology at New York University School of Medicine. In 1992 he returned to Rutgers University as a Research Professor at in the Biotechnology Center for Agriculture and the Environment and in the Department of Biochemistry and Microbiology, where he continued the study of bacterial taxonomy, describing several new species of the genera *Burkholderia*, *Thauera*, *Azoarcus* and *Paenibacillus*. As the expert on *Pseudomonas*, he authored the central chapters on the pseudomonads in the many volumes and editions of Bergey's Manual of Systematic Bacteriology.

Several bacterial species and a genus have been named in Palleroni's honor, namely *Hydrogenophaga palleronii*, *Actinoplanes palleronii*, *Pseudomonas palleroniana* and *Palleronia marisminoris*. These taxon dedications recognize his expertise in general microbiology and bacterial systematics. Palleroni was Member of the National Academy of Sciences of Argentina and a Fellow of the American Academy of Microbiology. Among many honors are Honorary Doctorates from the University of Cuyo and University of Buenos Aires in Argentina, the Konex Foundation Prize in Biochemistry and Microbiology (1993), the Theobald Smith Society Selman A. Waksman Honorary Lectureship Award (1986), and the Bergey Medal (1995) in recognition of outstanding life-long contributions to the field of systematics of bacteria and archaea.

Norberto Palleroni was an exceptional person with a wonderful sense of humor and tremendous knowledge in science, art and music. He played the flute and delighted in the challenge of teaching himself to play the violin in his 80s. He was an accomplished photographer, of landscapes, flowers, and of course microbes. His photomicrographs of various bacterial species were indeed microbial "portraits." His friends and colleagues around the world dearly miss him.

PhD Theses

Kate Annunziato
Joint Graduate Program in Toxicology (PhD 2018)
Low Molecular Weight PFAS Alternatives (C-6) Result in Fewer Cellular and Behavioral Alterations Than Long Chain (C-8/C-9) PFASs In Larval Zebrafish
Advisor: Keith Cooper
Current Position: NIEHS Post-Doc at the University of Massachusetts in the laboratory of Dr. Timme-Laragy

This project examined the effects of low molecular weight perfluoroalkylated substances (PFAS) alternatives (C-6) compared to the longer chain (C-8/C-9) PFASs in larval zebrafish. These compounds have been found persistent due to their high energy C-F bonds, present in drinking water supplies, and once internalized have a half-life in humans of multiple years. This class of compounds is used in manufacturing many products such as stain-resistance products and fire-fighting foams. PFAS exposures have been associated with liver toxicity, developmental and reproductive damage, altered behavior, decreased antibody response and altered thyroid hormone levels. My results showed that the PFAS C-6 alternatives are less potent than the longer chain PFASs, but still resulted in altered morphometric and behavioral endpoints that could be related to altered gene expression and lipid distribution. The concentrations at which these effects were observed are consistent with environmental levels reported from impacted water systems around the world. An important finding was that each of the individual PFASs resulted in different gene and morphological effects across chain length and terminal group. Future directions of the research will examine effects on the yolk syncytial layer, lipid catabolism, thyroid hormonal control and connecting these effects through adverse outcome pathway.

Fatima Foflonker
Microbial Biology (PhD 2018)
Understanding the Genomic Basis of Stress Adaptation in Picochlorum Green Algae
Advisor: Debashish Bhattacharya
Current Position: Post-doc at Brookhaven National Lab

How do microalgae adapt to fluctuating environments and what are the impacts of climate change on primary producers? To answer these questions, I investigated habitat-specific differences in the salinity stress response in two green algal sister species, *Picochlorum oklahomensis* from salt plains and *Picochlorum* SENEW3 from a brackish lagoon. I found that the coordination of gene regulation and horizontal gene transfer are key to environmental adaptation. Genome organization of co-expressed genes under salinity shock resulted in "gene neighborhoods." These factors act together to allow rapid stress responses and niche expansion from a freshwater to hypersaline environment.

Ashley Grosche
Microbial Biology (PhD 2018)
Microbial Communities in Biofilms at Deep-Sea Hydrothermal Vents: Mapping the Microbial Landscape Across Space, Time, and Fluid Dynamics
Advisor: Costantino Vetriani
Current Position: Post-Doc in the Microbial EcoFenomics Group under Loïs Magnien at the University of Western Brittany, France

Deep-sea hydrothermal vents are a global phenomenon driven by reservoirs of geothermal energy that chemically transform seawater through the enrichment of minerals from the geothermally-heated basement crust. The chemical disequilibrium resulting from seawater-rock interactions at high temperature fuels microbial metabolism and enables life to flourish at ocean depths typically characterized by low biomass. This dissertation reconstructed the microbial biogeography of biofilm communities across the heterogenous landscape of a deep-sea vent ecosystem, constrained the functional diversity between subsurface and seafloor microbial populations, and compared the phenotypic profiles of pure-culture representatives with genotypes to verify gene function and explore novel adaptations that may impact the ecological success of these taxa in vent ecosystems.

Nicole Lloyd
Microbial Biology (PhD 2018)
Co-selection of Metal and Antibiotic Resistance in the Gut Microbial Community of the Mummichog Fish (*Fundulus heteroclitus*)
Advisor: Tamar Barkay
Current Position: Post-Doc at the Department of Laboratory Medicine, Clinical Center, National Institutes of Health

Microbial resistance to antibiotics is currently one of our most pressing health care concerns. Antibiotic resistance can

be selected for by metals through the process known as co-selection. Co-selection occurs through two primary mechanisms: i) co-resistance, when genes encoding both are located together in the genome and ii), cross-resistance, when the same mechanism provides resistance to both (e.g. efflux pump proteins). This thesis describes co-selection in the gut microbiota of a forage feeder fish, the mummichog (Fundulus heteroclitus). By comparing gut microbiota from fish from a mercury-contaminated site and a relatively clean site, we established the mummichog gut as a reservoir of antibiotic- and mercury-resistant microbiota. We examined three representative isolates with antibiotic- and metal-resistant profiles. Genome analyses revealed few instances of co-resistance, and instead presented various chromosomally-encoded resistance genes, including some of public health concern (i.e. a blaOXA carbapenemase), and contributions from cross-resistance. All three organisms contained a large number of efflux pump proteins, including multiple RND efflux pump operons. Testing of the strains shows that RND efflux pumps may be involved in resistance to several classes of drugs. A transcriptomic study is in progress to understand the regulation of arsenate resistance and the potential involvement of RND efflux pumps under metal stress. This work describes the abundance and inventory of antibiotic resistance genes and mechanisms in the mummichog gut microbiome and establishes the fish gut as a reservoir of such genes. This work adds to the understanding of the role of RND efflux pumps in resistance to antibiotics, which is critical in understanding multi-drug resistance in Gram-negative bacteria.

C. Maximilian Miller

Technical University of Munich (TUM) Center for Doctoral Studies in Informatics and its Applications (CeDoSIA) (PhD 2018)
Functional Profiles of Health: elucidating genetics and microbiome of human disease
Advisors: Dr. Burkhard Rost, TUM, and Dr. Yana Bromberg, Rutgers
Current Position: Post-Doctoral Associate at Rutgers University

Discovering the molecular malfunction patterns leading to disease is one of the major tasks of this century. Multiple studies have explored associations between genetic variation and phenotypic outcomes of human disease. However, progress has been limited and fields like computational variant effect prediction have not seen significant improvement in method accuracy over the past decade. We took a new approach to elucidate the association between genetic variation, functionality and disease. We also introduced a new feature, characterizing protein sequence positions by the distribution of variant effects on protein function. We developed a Machine Learning approach to predict this feature with high accuracy, providing the foundation for a new variant effect predictor. In parallel we addressed the same question from an alternative perspective. Current research provides substantial evidence that microbiome function is also strongly associated with disease state. We developed two tools that firstly facilitated the analyses of microbiome function profiles between different disease states and secondly, permitted the investigation of microbial functional similarity with respect to different environments. To complement these tools and account for Big Data bottlenecks, we additionally developed an automated cluster load balancing software that allowed us to utilize both local and remote compute resources simultaneously and speed up analyses drastically. In summary, we developed new approaches which significantly improve identification of aberrant patterns and their association with disease states.

Javiera Norambuena Morales
Microbial Biology (PhD 2018)
Mercury toxicity and detoxification in *Thermus thermophilus* HB27
Advisor: Tamar Barkay
Current Position: Research Associate at TU Bergakademie, Freiberg, Germany

Mercury (Hg) is one of the most toxic and widely-distributed heavy metals. The thermophile *T. thermophilus* HB27 has a very peculiar *mer* operon; it consists of *merA* (mercuric reductase), a hypothetical protein (*hp*), *merR* (regulator), and *oah2*, which encodes for an enzyme that synthesizes homocysteine. I found that the *mer* operon has two promoters that are differentially regulated by *merR,* oah2 as well as other LMW thiols biosynthetic genes and the thioredoxin system are involved in Hg resistance. Bacillithiol (BSH) was the major LMW thiol in strain HB27 and Hg(II) caused depletion of the reduced BSH pool. This depletion was associated with an increase in reactive oxygen species (ROS) upon Hg(II) exposure. I showed that ROS were triggered by Hg(II) and that superoxide dismutase and pseudocatalase (ROS detoxifying enzymes) are involved in Hg(II) resistance. Collectively, this research describes how Hg(II) regulates the *mer* operon, interacts with LMW thiols and produces ROS.

Additional Microbial Biology Graduates

PhD

Firas S. Albayati, [PhD 2018]
Advisor: Paul Takhistov

Dina H. Al-Mansoori, [PhD 2018]
Advisor: Paul Takhistov

MS

Shiven Bhatt, [MS 2018]
Advisor: Jeff Boyd

Jacquelyn Deverell, [MS 2017]
Advisor: Gerben Zylstra

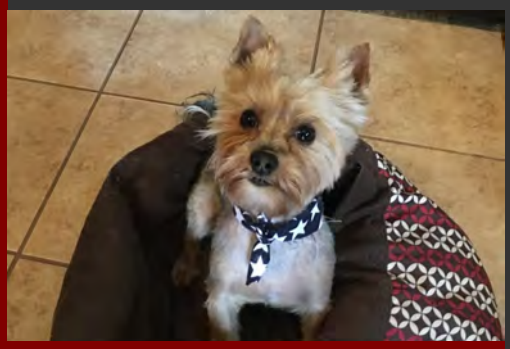
Adriana Van de Guchte, [MS 2018]
Advisor: Jeff Boyd

What's Shaking?

PhD student **Jie Liu** and her husband Yuanjun Zhou welcomed their first child, Keming Zhou, on May 30, 2018.

Microbial Biology PhD candidate **Michelle Zeliph** and Jessie Guillén-Sandi got engaged on June 17th, 2018 and will be married next May.

Congrats to **Lindsay Robinson** and Mark Vasy, married May 27, 2017 and honeymooned in Bermuda.



Allison Pohorence welcomes new addition "Elvis" to her family! He is a Yorkie with TONS of energy and lots of love.

Audrey Andrews purchased a new-to-her Honda CR-V, which doesn't break every other week. RIP Ford Taurus.

Peter Anderson's 30th Anniversary

I worked all 30 years in Lipman Hall, although I started at Rutgers in the fall of 1986 in the Vice President's office in Van Nest Hall as a temporary secretary. I started working in Lipman Hall in the fall of 1987 as a temporary secretary before being hired in the spring of 1988 as a full-time employee.

Rutgers is an intellectually rich and culturally diverse environment to work in. I feel fortunate to have worked here for so many years.

Retirement - Diane Davis

Dr. Diane Davis retired in January 2018 after many years at Rutgers. Diane contributed to instruction at Rutgers University by developing and teaching a wide range of courses, and was a key force in the development of our microbiology undergraduate program.

Diane earned her PhD in Biochemistry and Molecular Genetics at Rutgers in 1986. After post-doctoral positions, she was first appointed as Instructor in Microbiology in 1995, followed by an appointment as Instructional Laboratory Coordinator from 1999 to 2008, and again as Instructor in 2008. When the non-tenure track (NTT) for faculty was established at Rutgers, she was promoted to Assistant Teaching Professor in 2014, and Associate Teaching Professor in 2016.

Diane was truly engaged in the educational process and a highly successful instructor. She was a central force in the expansion of microbiology education at SEBS and the development of an innovative, forward-looking teaching program in microbiology. Diane led the restructuring and redesign of the General and Applied Microbiology laboratories, to bring our microbiology teaching lab physical facilities and teaching practices in line with 21st century technology and pedagogy. She designed laboratory class experiments, and integrated the use of updated approaches and instrumentation.

She developed laboratory manuals for student use in the General Microbiology and the Applied Microbiology classes and also developed and coordinated these courses' websites. Diane also initiated and implemented new courses that introduce microbiology to non-majors (such as Living in the Microbial World), guided the department faculty through establishing teaching goals and assessments, and continually sought to improve opportunities for our students. Diane reached thousands of students over her decades of service. In recognition of her achievements in education, she was presented with the Excellence in Teaching Award from Cook College in 2006.

Diane also served as an ambassador for Rutgers by organizing our Rutgers Day (Ag-Field Day) program, leading the microbiological displays in a tent in front of Lipman Hall. The displays included active microbes swimming under the microscope, microbial roles in food fermentations, discussion of food poisoning, and Diane's enthusiasm! This public outreach has been of continual success for over a decade.

Indeed, Diane has been a "mover-and-shaker" of microbiology instruction at SEBS, constantly generating new opportunities for our students, maintaining high standards of instruction, and nurturing students and faculty. We will miss her! Wishing Diane a Happy Retirement!!

Awards & Activities

Clement A. Price Human Dignity Award

Professor **Peter C. Kahn** was awarded the 2018 Clement A Price Human Dignity Award in acknowledgement of his activities over 41 years of service at Rutgers. At every opportunity he weaves matters of human dignity into his teaching and other activities, such as the Bosnian Student Project in which over a period of several years 17 students earned bachelor's degrees, while an 18th earned her doctorate. Prof Kahn has played a central role in forging intercultural cooperation and collaboration and made major efforts in reducing prejudice and promoting respect for diversity. He sets an example of what it means to act upon a sense of social responsibility.

Recent Grants

Tamar Barkay, Effects of wetland trophic status on microbial community structure/function and potential mercury methylation in Alaskan peat lands", DOE JointGenome Institute's Community Science Program.

Debashish Bhattacharya, Elucidating adaptive potential through coral holobiont functional integration. National Science Foundation OCE-BSF.

Jeffrey Boyd, Mechanisms of cellular respiration-dependent cell lysis and its impact on biofilm formation and disassembly in *Staphylococcus aureus*. Cystic Fibrosis Foundation.

Jeffrey Boyd, Mechanisms of cellular respiration-dependent cell lysis and its impact on biofilm formation and disassembly in *Staphylococcus aureus*. National Institute of Allergy and Infectious Diseases DHHS-PHS-NIH-NIAID-48.

Jeffrey Boyd, Iron-sulfur cluster assembly in *Bacillus subtilis*. National Science Foundation CAREER.

Keith Cooper, Impacts of Microplastics in the Urban Environment Regional Conference, National Institute of Health

Maria Gloria Dominguez, C-section-like microbiota and alterations of immune responses. Juvenile Diabetes Foundation International

Liping Zhao, CIFAR- Humans and the microbiome, Canadian Institute for Advanced Research

Departmental Awards

The **Douglas E. Eveleigh** and **Stephen M. Cuskey Travel Awards** enable graduate students in the Department of Biochemistry and Microbiology to present their research at conferences across the country and around the world.

Hassan Al-Tameemi: Gordon Research Conference, Mount Holyoke College, MA
Spencer Roth: ISME Conference, Leipzig, Germany
Yanran Wang: International Society for Computational Biology/ISMB Chicago, IL
Suha Eleya: SIMB Annual Meeting and Exhibition Conference, Chicago, IL
Preshita Gadkari: Ecology of Soil Organisms, Helsinki, Finland
Nicole Lloyd: ASM Microbe, Atlanta, GA
Javiera Norambuena Morales: ASM Microbe, Atlanta, GA
Aakansha Roberts: ISME Conference, Leipzig, Germany

The **Robert S. and Eileen A. Robison Award for Excellence in Graduate Studies**, established in 2003, is supported by the Robison family. It is awarded to a student who has demonstrated accomplishment in their academic program at Rutgers.

Jie Liu, **Nicole Lloyd**, and **Javiera Norambuena Morales**

Other Awards

Spencer Roth, National Science Foundation Graduate Research Fellowship

Michelle Zeliph, Bugs on Drugs: the influence of redox environments on the microbial degradation of pharmaceuticals in the Hudson River watershed Hudson River Foundation Tibor T. Polgar Fellowship .

NJ State Microbe

In New Jersey we are proud of our state flower, the Common Meadow Violet (*Viola sororia*), and the state bird, the American Goldfinch (*Spinus tristis*). Microbes are a major component of our soil's ecology: Filamentous bacteria (*Streptomyces*) give the soil that wonderful earthy aroma (geosmin), they maintain soil fertility, and are also a major source of antibiotics. Yet, we lack a State Microbe. The actinomycete bacterium, Streptomyces griseus, discovered in New Jersey, has dramatically advanced world health and thus merits state recognition.

The antibiotic, streptomycin, made by *Streptomyces griseus,* was discovered by Albert Schatz, Elizabeth Bugie and Selman Waksman at the New Jersey Agricultural School in 1944 at the dawn of the antibiotic era. It was truly remarkable in the breadth of pathogens that it attacked, including *Vibrio cholerae* (cholera) and *Mycobacterium tuberculosis* (TB), against both of which penicillin, the only other antibiotic at that time, had no effect. Streptomycin has saved millions of lives, extended human life span, and dramatically changed and improved the course of world health. It has been a major weapon in the war against bacterial infections: shortening and preventing illnesses, alleviating suffering and averting premature death.

Actinomyces

This producer of streptomycin, *Streptomyces griseus*, discovered in New Jersey soil and also isolated from the gullet of a healthy New Jersey chicken, was developed at the Department of Biochemistry and Microbiology at Rutgers, where its remarkable antibiotic properties were recognized. It was used in the development of large scale fermentation, a novel concept at that time. Thus streptomycin joined penicillin in the development of New Jersey's pharmaceutical industry. Within four years of the discovery of streptomycin in 1944, the initial yields in the milligram range were ramped up to 3,000 kilograms per month - a million-fold increase. This enabled animal and human trials by Drs. William Feldman and Corwin Hinshaw, at the Mayo Clinic in Rochester, MN. Within two years it was in use, helping Robert J. Dole, later Majority Leader of the United States Senate and Presidential candidate, rapidly recover from war injuries.

To date, only Oregon has recognized a state microbe – *Saccharomyces cerevisiae*, yeast, the basis of brewing – in recognition of the state's many small craft breweries. Wisconsin and Hawaii are considering naming state microbes as well. Three nominations for a New Jersey State stood out:

- *Azotobacter vinelandii* – discovered by Jacob Lipman in 1903 in Vineland, NJ soil. This was the second free-living aerobic nitrogen-fixing bacterium (the initial study was by M. Beijerinck - *Azotobacter chroococcum* 1901).
- *Thiobacillus thiooxidans* (or the updated name, *Acidithiobacillus*) – discovered by Jacob Jaffe and Selman Waksman in 1922 in acid mine waste and associated transformations from New Jersey.
- *Streptomyces griseus* – discovered by Albert Schatz, Elizabeth Bugie and Selman Waksman in New Jersey in 1944; produces streptomycin and is active toward gram-negative pathogens and the tubercule bacillus.

Streptomyces griseus clearly emerged as the winner. It saves millions of lives; it has created jobs – the development of the pharmaceutical industry in the 1950s was based in NJ; and it is recognized for its production of streptomycin, for which Selman Waksman won the Nobel Prize for Physiology or Medicine in 1952.

New Jersey can be proud of *Streptomyces griseus.* The designation of a New Jersey State Microbe will highlight the power of microbes and how microbial activities can help us discover novel bioactive compounds, characterize metabolic traits for degradation of hazardous chemicals, develop new biofuel production methods, and in the case of *Streptomyces griseus* promote human health.

Please write to your legislator to support this nomination.

John Warhol, president of the Warhol Institute, and Jessica Lisa, Douglas Eveleigh and Jeff Boyd, Rutgers microbiology professors, at the Senate voting session in Trenton on July 26, 2018

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Through the years, students in the Department of Biochemistry and Microbiology have been supported in many ways: grants, assistantships, corporate funds and fellowships endowed by individuals, just to name a few. Financial support is critical to the ongoing success of our students, and allowed them the opportunity focus fully on their education and research. The next generation of gifted students in microbiology and biochemistry need your support. As traditional funding mechanisms become more difficult to secure, we turn to our community of dedicated alumni and friends to support those who will come after them, and continue their legacy of achievement.

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2. Graduate Student Travel Awards (Stephen M. Cuskey and Douglas E. Eveleigh)
3. Department of Biochemistry and Microbiology Fund

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Department of Biochemistry and Microbiology | School of Environmental and Biological Sciences |Rutgers, The State University of New Jersey
76 Lipman Drive | New Brunswick, NJ 08901-8525| Lipman Hall | 848-932-9763 | Fax: 848-932-8965| dbm.rutgers.edu
www.facebook.com/RutgersDBM

Editors: Max Häggblom, Audrey Andrews, Lindsay Robinson
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