Expression

People and Progress 2018 - 2019
UConn Department of Molecular and Cell Biology

In this Issue:

Expression

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Gulf killfish, Andrew Whitehead, UC Davis; Bri Diaz/UConn Photo; PSM photos, Elaine Mirkin; UConn photos, Sean Flynn, Peter Morenus, Kasia Thomas, and Kim Krieger.

ON THE COVER:

DUPLICATED DIVISION After fertilization, cells in fruit fly embryos synchronize division, or mitosis. Chromosomes (blue) attached by their centromeres to ropelike structures called microtubules (red) are tugged into two separate cells. From an on-line article about Dr. Mellone's work described on page 4. (Photo from Mark Berryman, ScienceNews)

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From the Department Head

Michael Lynes
Professor and Head

MCB continues on a path of growth and strength in our research, teaching, and outreach missions. Grants garnered by MCB faculty demonstrate the vigor of our research programs. Several are highlighted in this issue of *Expression*. Four MCB faculty have been awarded NIH R35 "Maximizing Investigators' Research Award" (MIRA) awards (Broderick, Core, May, and Mellone) and another received a K02 "Independent Scientist" Career award (Campellone). Others have received R01s, R21s, and STTR awards, and those from other federal agencies, non-profit agencies and corporate sponsors. A number of faculty members have been awarded intramural PITCH funds/service and PATH funds for the development of new intellectual property arising from their work, and several patent applications for some of these discoveries have been submitted.

Notably, we have also received a significant donation from Biohaven Pharmaceutical Company that was used in the summer of 2019 for a summer fellowship awarded to one of our doctoral students.

MCB space allocations are also changing. We are adding a fifth location, in Gant Science Center, which will house the large-scale laboratory course teaching that is done by MCB faculty. Beach Hall currently houses modular, high-end skill-based courses in the PSM program, summer workshops for non-UConn undergraduates, and the experiential learning courses "Tiny Earth Networking" and "SEA PHAGES/Virus Hunters." We are advocating for space in Torrey Life Sciences Building to enable us to add "team science" experiential research opportunities for the growing numbers of MCB Honors and University Scholars.

Changes have also occurred in the MCB administrative office to meet the expanding needs of the department. With the dissolution of Biology Central Services, several new staff members have been hired since the department assumed additional administrative responsibilities including graduate student program management, human resource management, travel, and procurement work.

Inside you can read about a number of exciting studies being conducted in MCB, including an analysis of the genome of horseshoe crabs and studies of a fish that beats the odds by rapidly adapting to new conditions. Fruit fly centromeres have been successfully sequenced in Dr. Barbara Mellone's lab, opening doors to new discoveries. A new feature, "MCB in Review," summarizes review articles recently written by MCB professors. Among these is an article co-authored by Dr. Broderick about apparent sex bias in the choice of first authors on research articles.

Finally, we invite MCB alumni to let us know of any new developments in your life that you would like to share here. We look forward to another year of outstanding achievements of our faculty, students, and alumni.

Malone Selected as AAAS Fellow

Professor **John Malone** was awarded a AAAS Science & Technology Policy Fellowship (STPF) with a placement at the Office of Science and Technology Cooperation in the Department of State. Malone is among 278 highly trained scientists and engineers who will spend a year serving professionally in federal agencies and congressional offices. The U.S. government benefits from the contributions of STPF fellows while fellows learn first-hand about federal policymaking and implementation.

The fellowship program is operated as part of the American Association for the Advancement of Science (AAAS) mission to advance science and serve society. The program aims to support evidence-based policymaking by engaging the knowledge and analytical mindset of science and engineering experts, and foster leaders for a strong U.S. science and technology enterprise. Fellows represent a broad range of disciplines, backgrounds and career stages.

The 2019-20 class is comprised of 278 fellows sponsored by AAAS and partner societies. Of these, 33 will serve in Congress and 245 in the executive branch among 19 federal agencies or departments.

Prof. **Joerg Graf** was elected into the American Academy of Microbiology, an honorific leadership group within the American Society for Microbiology. Fellows are elected annually through a highly selective, peer-review process, based on their records of scientific achievement and original contributions that have advanced microbiology. Fellows are from several countries and represent all subspecialties of the microbial sciences and involved in basic and applied research, teaching, public health, industry, and government service.

MY EMOTIONAL BUNKER

The Story Collider convened in October 2018 in Hartford to present stories about intellectual humility in science told by UConn scientists, including Prof. **Sarah Hird**. Story Collider travels the country presenting true, personal stories by about science told by professional scientists, engineers, doctors, and science students. The Hartford event was presented in partnership with the University of Connecticut's College of Liberal Arts and Sciences and Public Discourse Project.

Hird holds a Master's degree from the University of Idaho and a PhD from Louisiana State University. After receiving her degree, she and her husband took postdoc positions at the University of California, Davis. Her story was about the time that she and her husband moved to California to start their positions. The time was filled with anticipation at the starts of their new scientific careers and at the prospect of starting a new family. At the time she was five months pregnant. As one does, she got a new doctor and went in for a baby check up. Her doctor told her there were some apparent abnormalities in her baby and this was the start of months of additional tests and profound anxiety for both parents-to-be. Hird told an emotional story of their journey and its impact on both their professional and personal lives.

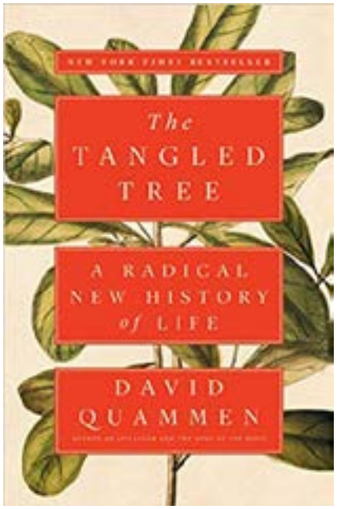
The story had a happy ending. Their son was fine and he is now a bright, healthy 5 year old with the sharp sense of humor of many 5 year olds, telling jokes that usually include poop.

Her reflections on her experience at the end of her story are heartfelt and left the audience with a powerful example of resilience, hope, and joy. You can read her story here.

by Kenneth Noll

THE STORY COLLIDER
STORIES ABOUT SCIENCE

MCB Hosts One of the Four Horsemen of Molecular Evolution



David Quammen, in his latest book "The Tangled Tree," describes how recent discoveries have questioned the usual depiction of evolution as a tree. One of the important contributors to this new view of evolution, as indicated by Quammen, is Professor **J. Peter Gogarten** of MCB. Along with Gogarten, Professors W. Ford Doolittle of Dalhousie University, Jeffrey Lawrence of the University of Pittsburgh, and William Martin of the Univeristy of Düsseldorf found evidence to show that genes had been widely shared among microorganisms through evolutionary time. Quammen points out the importance of Gogarten's contributions and how his work, and that of these three other investigators, advanced the field. Doolittle, the most senior scientist of this group, called these investigators "the four horsemen."

To illustrate the principle of sharing genes across evolutionary lineages, Quammen describes a real instance of the intermingling of branches of trees. In 1915, Wisconsin farmer/banker John Krubsack displayed his chair, made by intertwining and grafting box elder trees, at the World's Fair in San Francisco. Quammen uses Krubsack's fused branches to illustrate how tree branches can fuse if they rub against one another allowing their inner cells to grow together. This intermingling of branches is also found in modern depictions of the "Tree of Life," an illustration of the evolutionary progression of all life through time. Charles Darwin was the first to suggest that species can split into different lineages and evolve separately, creating a branching pattern through time, like the branches of a tree. Evidence provided by "the four horsemen" indicates that the Tree of Life is more like Krubsack's trees.

Krubsack sitting in his chair.

In 1989, shortly after his arrival at UConn, Gogarten published a paper that established the relationship between the three major evolutionary lineages of life: the bacteria, archaea (a group of bacteria-like organisms), and eukaryotes (organisms, including humans, with cells arranged unlike those of bacteria and archaea). Prior to this study, the relationship between these three groups was unknown. Gogarten's paper showed that the bacteria evolved away from the lineage that was the ancestor of the other two groups that subsequently diverged from one another. Life was thought to evolve in this vertical manner, with groups diverging from one another over time, as Darwin envisioned. In follow-up studies, published in 1993, Gogarten found that genes have been shared between the bacteria and archaea. Gogarten's work along with that of Doolittle, Townsend, Martin and others proved that horizontal gene transfer, that is inheritance of new genes from other, sometimes distantly related, lineages, has occurred since life emerged on Earth. The discovery of this phenomenon and the difficulties of its acceptance is the subject of Quammen's book.

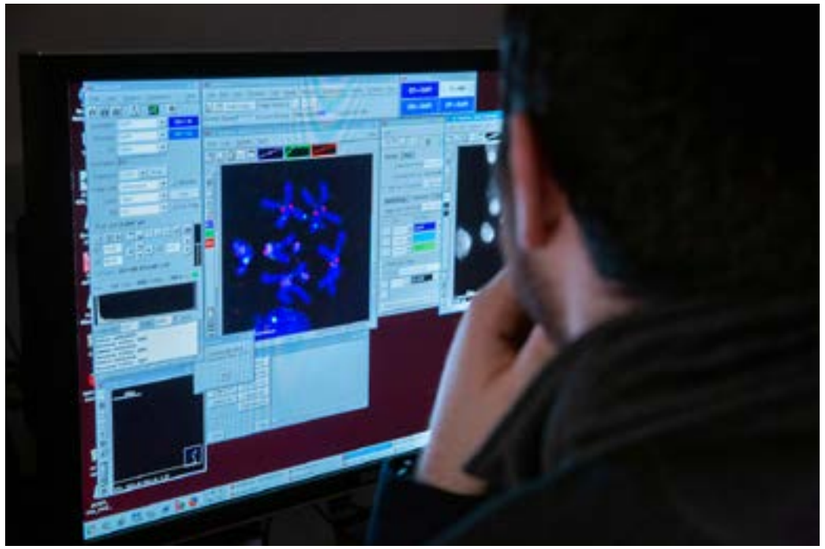
The four horsemen. L to R, Townsend, Gogarten, Doolittle and Martin. Doolittle is waving his illustration of the Tree of Life with horizontal gene transfer as the riders trample previously accepted versions of the Tree.

More recently Gogarten has characterized the evolution of life as like a "coral" rather than a tree. An image even Darwin suggested, indicating the complex interactions among the evolving lineages.

Gogarten has continued to work on questions about how molecular evolution operates and what impact horizontal gene transfer has had on the evolution of life. His work is highly respected in his field and he has received numerous awards for his contributions. His place is secure as one of the four horsemen of this new view of intermingled branches on the Tree of Life.

by Kenneth Noll

Study Unlocks Secrets of an Elusive Genome Compartment



Although much of the human genome has been sequenced and assembled, scientists have hit roadblocks trying to map unassembled regions of DNA that consist mostly of repetitive sequences, including the centromere.

Now, for the first time, researchers from the University of Connecticut and University of Rochester have sequenced all the centromeres in a multicellular organism.

Published in the journal PLOS Biology, the study on fruit flies sheds light on a fundamental aspect of biology, and shows that genetic elements may play a larger role in centromere function than researchers previously thought.

"Centromeres continue to be widely considered the 'black hole' of genomics," says **Barbara Mellone**, associate professor of molecular and cell biology at UConn and lead author on the study. "We break through these barriers and leverage the power of single molecule long-read sequencing and chromatin fiber imaging to discover the detailed organization of the centromeres."

The fruit fly, *Drosophila melanogaster*, is one of the most revered examples in biology of a model organism, or species that has been extensively studied for a long time in the lab in order to better understand its biology and to apply those lessons to human health. In the context of centromere biology, *Drosophila* is especially powerful because it only has four pairs of chromosomes as opposed to the 23 in humans, and the centromeres are smaller than those of humans and thus relatively easier to sequence and assemble.

If centromeres, vital for cell division, don't function properly, cells may divide with too few or too many chromosomes, which can result in aneuploidy disorders like Down syndrome or tumor progression.

In many species, including humans, centromeres are often found near the center of the chromosome, embedded in large blocks of repetitive DNA known as satellite DNA. Satellite DNA, and, in turn, centromeres, are challenging to sequence because of their repetitive nature: when mapping a genome, traditional sequencing methods chop up strands of DNA and read them, then try to infer the order of those sequences and assemble them back together. But the pieces of repetitive DNA all look the same, so assembling them is like trying to put together a puzzle with very similar pieces. To solve this long-standing puzzle, researchers joined their expertise in chromatin and repetitive DNA biology.

Contrary to previous thought, the fruit fly centromeres are in fact made up of "islands" of complex DNA enriched in retroelements. These complex islands are embedded deep in satellite arrays, which hampered their discovery for more than two decades, say the researchers.

Sequencing the most repetitive parts of genomes is one of the "last frontiers of genome assembly," says Amanda Larracuente, an assistant professor of biology at Rochester, and co-lead author.

Researchers recently presented their findings at the Centromere Biology Gordon Conference and the GSA Early Career Scientist Symposium "Cracking the Repetitive DNA Code."

"The approaches we describe will be foundational for the discovery of centromeres in other animals," says Mellone.

Other authors include Ankita Chavan, Jason Palladino, and Bryce Santinello, UConn; Ching-Ho Chang and Xiaolu Wei, University of Rochester; Nuno M.C. Martins, Jelena Erceg, and Chao-Ting Wu, Harvard University; Chin-Chi Chen, Johns Hopkins Medical Institutions; and Brian Beliveau, University of Washington.

The study was supported by grants from the National Institutes of Health; National Science Foundation; and a Damon Runyon Cancer Research Foundation Howard Hughes Medical Institute Fellowship.

by Combined Reports - UConn Communications

What's in a Name?

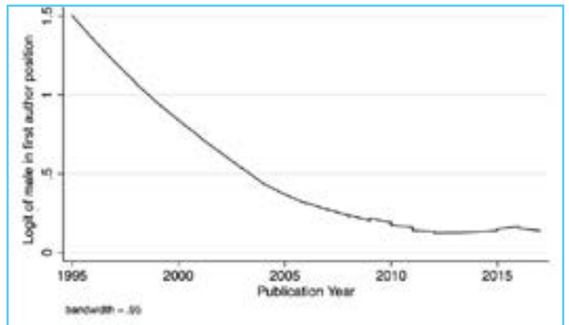
Professor **Nichole Broderick** was a guest on the Naked Scientists podcast "Weaponised Insulin" hosted by Managing Editor Chris Smith. The topic she discussed with him was the tradition of first authorship on published articles. Typically the first author on a paper is the lead author and the person who made the most significant intellectual contribution to the study, conducted the bulk of the research and analysis of the results that are reported in the paper. In some cases, two people made equal contributions, so an asterisk may be put by their names with a footnote explaining this. One of them, however, still appears first. What are the consequences of this? How is the decision made as to who goes first? Does it make a difference if they are different sexes? These were some of the topics that Prof. Broderick discussed with Smith.

Broderick noted that the first author "becomes part of our conversation and how we talk about the work." Consequently, the choice of first author has consequences for that person's reputation and career.

Broderick was interviewed because she published a study in the journal eLife with Arturo Casdevall of the Johns Hopkins School of Public Health in which they examined nearly 3,000 articles from primarily biomedical journals published between 1995 and 2017 that had two or more authors that shared first author position. For mixed-gender combinations of two-author combinations, males were more frequently the first author, though this disparity decreased over the time of the study. For studies with more than two "first author" listings, there were more males in the first position and more all-male than all-female combinations. Patterns of apparent male bias were similar for authors in North America, Europe, and Asia. Their analyses of the data indicated that these patterns were not consistent with their being the result of random or alphabetical ordering of authors.

So did the authors find out what was behind these patterns? Broderick was asked in the podcast and she said, "The one thing that we found was interesting was we only found about one or two papers that actually said, 'this order was decided by alphabetical order.'" They noted in their paper that journals generally do not require authors to state how author order was decided. "If you talk to scientists, anecdotally, I think they would tell you that sometimes that flipping of a coin and stuff happens less frequently than you might expect," Broderick said.

There is hope that the situation is changing. As their data show, it appears that the male-female authorship disparity is declining. Another study of this subject, cited in their paper, found no disparity when journals from a wider spectrum of scientific disciplines were examined. However, that study noted, as Broderick found, biomedical journals showed the largest disparity. Broderick has heard anecdotal evidence that journals are getting the word. "…people have told us that … editor in chiefs of journals …[are]… moving towards … having a very clear statement about how these decisions are made," she said.



Gender bias in the first author position over time. Temporal trend in gender bias among two equally contributing authors of different gender. From https://elifesciences.org/articles/36399#fig2.

Ironically, Broderick and Casdeval are listed as authors who contributed equally to the work. They take their own advice and indicate that "author order was determined both alphabetically and in order of increasing seniority." Broderick sees this sort of open expression as necessary and sees the situation improving. "It was very reassuring to see that there was a correction," Broderick said. "Who knows exactly why but it's wonderful to see and it's great to think that we're approaching equilibrium …."

by Kenneth Noll

Doctoral student travel awardees

Bryce Santinello (Genetics & Genomics, Mellone lab) was awarded the Spring 2019 MCB graduate travel award in recognition of his outstanding graduate seminar. **Cory Jubinville** (Genetics & Genomics, Goldhamer lab), **Corynne Dedeo** (Biochemistry, Teschke lab), and **Anthony Patelunas** (Cell & Developmental Biology, Goldhamer lab) were awarded Fall 2019 Doctoral Student Travel Fellowships by the Graduate School. Both these bi-annual awards provide support to students for conference attendance to enrich their graduate program study.

AN EVOLUTIONARY RESCUE IN POLLUTED WATERS

The combination of a big population, good genes, and luck helps explain how a species of fish in Texas' Houston Ship Channel was able to adapt to what would normally be lethal levels of toxins for most other species, according to a study published in the journal Science.

The exceptional survivor story of the Gulf killifish was one that intrigued scientists at the University of Connecticut, University of California-Davis, Baylor University, and Indiana University.

The minnow-like Gulf killifish are an important part of the food web for a number of larger fish species in coastal marsh habitats and they wanted to learn more about what other species may need to adapt to drastically changed environments.

"We know that rapid adaptive evolution can happen in response to human-caused environmental change but we don't have a great understanding of what factors facilitate it," says **Noah Reid**, UConn research assistant professor in molecular and cell biology and a co-author. "Learning the underlying genetic basis of adaptation in cases like this can help us make better predictions about how and when it will occur, and better plans to conserve species and mitigate the damage we are causing to the natural environment."

Surprise guest

The researchers sequenced the genomes of hundreds of Gulf killifish living across a spectrum of toxicity – including clean water, moderately polluted water, and very polluted water. They were searching for the footprints of natural selection that allowed the species to rapidly transition from a fish that is highly sensitive to pollution to one extremely resistant to it.

They were surprised to find that the adaptive DNA that rescued this Gulf Coast species came from an Atlantic Coast species of killifish, which has also been known to rapidly evolve high levels of pollution resistance. But Atlantic Coast killifish live at least 1,500 miles from their Houston brethren, leaving researchers to think their transport to the Gulf was likely an accident initiated by humans.

Nonnative species can wreak environmental havoc on native species and habitats. But in this case, their arrival in the 1970s – right at a moment when Gulf killifish were likely beginning to decline – amounted to an "evolutionary rescue" from pollution for the Gulf killifish.

"While the vast majority of research on invasive species rightly focuses on the environmental damage they can cause, this research shows that under rare circumstances they can also contribute valuable genetic variation to a closely related native species, thus acting as a mechanism of evolutionary rescue," says co-author Cole Matson, an associate professor at Baylor University.

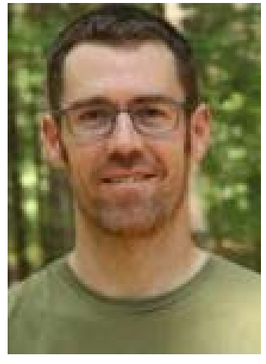
A cautionary tale

Gulf killifish began with many advantages other species do not have. Species with large populations can harbor high levels of genetic diversity that can help them adapt to rapid change. Gulf killifish already had among the highest levels of genetic diversity of any species with a backbone. Then, at the moment its population was beginning to decline, a long-distant relative – the Atlantic Coast killifish – came to visit, was able to successfully mate, and injected the Gulf species with genetic resources that helped it develop resilience and resistance to toxins. Whitehead is quick to note that not all species are so lucky.

"The adaptation of these killifish is a cautionary tale," says Andrew Whitehead, a UC Davis professor of environmental toxicology, and co-author. "It tells us what we need to do better for the vast majority of species that don't have access to the kind of genetic resources killifish have. If we care about preserving biodiversity, we can't expect evolution to be the solution. We need to reduce how much and how quickly we're changing the environment so that species can keep up."

Natural connections

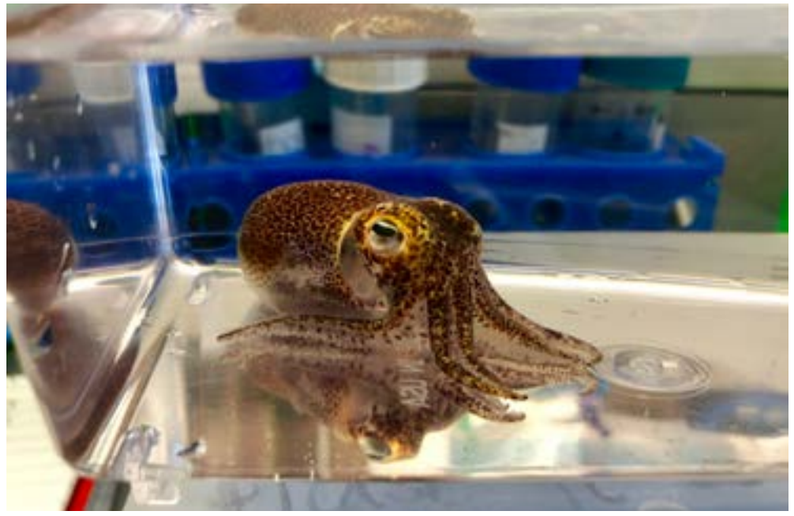
Humans are not only radically changing the environment, we are also fragmenting it, making it harder for animals to move throughout their range. Whitehead says a key lesson from killifish is the importance of keeping the doors to genetic diversity open. This includes connecting and preserving landscapes to allow for genetic variation to move more freely and naturally. That could help set the stage for more evolutionary "rescues" in the rapidly changing future.



From UConn Today; by Kat Kerlin, UC Davis

A Little Squid Sheds Light on Evolution with Bacteria

Bacteria, which are vital for the health of all animals, also played a major role in the evolution of animals and their tissues. In an effort to understand just how animals co-evolved with bacteria over time, researchers have turned to the Hawaiian bobtail squid, *Euprymna scolopes*.



Scientists led by UConn biologist Spencer Nyholm have found clues to the origin and evolution of symbiotic organs in animals from the genome of the Hawaiian bobtail squid. (Sarah McAnulty/UConn Photo)

In a new study published this week in the Proceedings of the National Academy of Sciences, an international team of researchers, led by UConn associate professor of molecular and cell biology **Spencer Nyholm**, sequenced the genome of this little squid to identify unique evolutionary footprints in symbiotic organs, yielding clues about how organs that house bacteria are especially suited for this partnership.

The first squid genome was sequenced by Nyholm, along with Jamie Foster of the University of Florida, Oleg Simakov of the University of Vienna, and Mahdi Belcaid of the University of Hawaii. The team found several surprises, for instance, that the Hawaiian bobtail squid's genome is 1.5 times the size of the human genome.

By comparing the genome of *E. scolopes* to its cousin, the octopus, the researchers show that the common ancestor of both the octopus and the Hawaiian bobtail squid went through a major genetic makeover, reorganizing and increasing the genome size. This "upgrade" likely gave the cephalopods opportunities for increased complexity, including new organs like the ones that house bacteria.

"The Hawaiian bobtail squid has served as a model organism for studying symbiosis for over 30 years," notes Nyholm. "Having the genome will help researchers who study these interactions, as well as those studying diverse areas of biology, such as animal development and comparative evolution."

Many animals have organs that house bacteria. The human gut houses trillions of bacteria that play important roles in digestion, immune function, and overall health. Understanding how these relationships are maintained by identifying genes that help animals cooperate with bacteria lays the groundwork for furthering knowledge of the human body. The Hawaiian bobtail squid is an excellent model for identifying these genes because of its symbiotic relationships with beneficial microbes, and its use by a number of scientists to study communication between bacteria and animals.

The Hawaiian bobtail squid has two different symbiotic organs, and researchers were able to show that each of these took different paths in their evolution. This particular species of squid has a light organ that harbors a light-producing, or bioluminescent, bacterium that enables the squid to cloak itself from predators. At some point in the past, a major "duplication event" occurred that led to repeat copies of genes that normally exist in the eye. These genes allowed the squid to manipulate the light generated by the bacteria.

Another finding was that in the accessory nidamental gland, a female reproductive organ, there was an enrichment of genes that are "orphan genes" or genes that have only been found in the bobtail squid and not in other organisms.

"Squid and octopus showed very unique genome structure, unlike in any other animals," says Simakov, "corroborating previous reports of their unusual nature and complexity."

Foster notes that teasing out these unusual and complex details is directly applicable to the study of other bacteria/animal relationships.

Hawaiian bobtail squid. UConn researcher Spencer Nyholm and his colleagues were the first to sequence this squid's genome. (Mattias Ormestad, www.kahikai.com)

"Microbes are major drivers of the evolution of animals and their tissues," she says. "The results of our study have helped identify the 'origin story' of those tissues that house an animal's microbes, and will help tease apart the genetic processes by which these different types of innovation can happen in animals."

This work was supported by a National Science Foundation IOS grant and the UConn Office of the Vice President for Research.

Institutions also involved in this study include University of California, Santa Barbara, University of Lyon, Jackson Laboratory for Genomic Medicine, Washington University, and University of California at Berkeley.

by Combined Reports - UConn Communications

Related Note: Nidhi Vijayan, (PhD Microbiology, Nyholm lab), has her movie of baby bobtail squid posted as one of Scientific American's best science GIFs.

Sarah McAnulty achieves notice for both her science outreach efforts and her research

Sarah McAnulty, Microbiology PhD student in the lab of Prof. Spencer Nyholm, was interviewed in *Nature Careers* about her creation of the Skype a Scientist outreach program. In an article entitled "The squid biologist connecting schools and scientists worldwide," she describes her program that was designed to connect students, teachers and other groups around the world with scientists on every continent. The program has so far linked more than 9,600 classrooms with 4,600 scientists from 43 countries. In the interview she said that after she graduates she will probably look into a science-communication career. She is applying for funding to support her program into the future. She is passionate about helping scientists to make connections outside their academic communities.

McAnulty was also featured on National Public Radio in Connecticut about squid, the subject of her research project in Nyholm's lab. In a program entitled "Why are Squids so Smart? We ask a Squid Nerd," she described the lifestyle of squids and what her lab is learning through their studies of bobtail squids. She also exhibited the excitement of research.

PSM Student Makes Her Mark at Start-up

Dominique Carrillo's success as a summer 2018 intern at Shoreline Biome, a startup in the UConn-Technology Incubator Program (TIP), led the startup CEOs to hire an immigration lawyer so Dominique could be employed full-time after graduating with her M.S. Microbial Systems Analysis degree in fall 2018. They were so impressed with her skills they did not want to lose her and employed her as a Manufacturing and Quality Control Associate. She played a key role in moving the microbiome kits from product development to production. Dominique credits this to the training in the MCB Professional Science Master's (PSM) program.

"The PSM program was great!" Dominique says. "One of the founders of the startup where I did my internship was happy that I did not need extensive training to do what they hired me for--that they could just hand me a lab coat, show me the lab, and that I'd just be ready to work. It equipped me with the knowledge and skills that the job market in my field requires."

The MCB PSM program offers a myriad of professional development courses and practical laboratory modules. What Dominique found particularly useful were the communication skills courses, the weekly professional development seminars with industry leaders, and the advanced short intensive laboratory modules, such as the characterization of microbial communities by 16S rRNA sequencing.

"The modules offered by the program are relevant to current industry laboratory practice. Not only has the program helped to develop my practical lab skills, but because of its holistic design, I've also learned how to communicate effectively." Dominique continues," The program gives students the door to a network of startup founders, academic thought leaders, big pharma executives, and PSM alumni. The opportunity to interact and network with these individuals has been one of the most important pillars of the program. In fact, I obtained my internship and employment through these seminars!"

by Elain Mirkin, First published in the National Professional Science Master's Association PSM Alumni and Graduate Chronicle

Good Bacteria, Bad Bacteria: Uncovering How the Microbiome Supports Health

Sabrina Yum-Chan '19 (CLAS), left, and Nichole Broderick, MCB Assistant Professor, look over vials of flies in a microbiology lab at the Torrey Life Sciences Building on Nov. 10, 2015. (Peter Morenus/UConn Photo).

Inside our bodies, there is a microscopic world teeming with life known as the microbiome. From the moment we are born, we begin accumulating a collection of helpful bacteria, viruses and fungi that support our immune system and digestive health.

Nichole Broderick, an assistant professor in the Department of Molecular and Cell Biology at the University of Connecticut has received a five-year, $1.92 million grant from the National Institutes of General Medical Sciences to build up the knowledge base of how exactly the microbiome performs these functions.

"I'm thrilled to have the support of NIH to carry out this work. The support of the Maximizing Investigators' Research Award (MIRA) program for early-stage investigators like myself is a critical boost to my lab as we tackle important questions about the role of the microbiome in animal health."

Broderick will use fruit flies, which have remarkably similar internal pathways and diseases as humans, to study which mechanisms in the host contribute to the establishment of a normal microbiome. She will look at how signals from microbes cause physiological changes in the host and how the host regulates the microbiome in turn.

Understanding how a healthy microbiome is maintained is an essential step in developing therapies for microbiomes that have been disrupted or not established properly.

For example, when a person goes on antibiotics for an infection like strep throat or a urinary tract infection, the medication that kills the disease-causing bacteria can also disrupt the "good" bacteria in our microbiome.

One disease that has been treated with microbiome therapy is *Clostridium difficile* infection, an antibiotic-associated diarrhea. By transferring microbiome bacteria from the fecal matter of a healthy person to an infected patient, the patient's system is able to re-establish a normal balance of their own microbiome.

The success of this treatment has led researchers to wonder other ways that microbiome therapies could be applied to treat various ailments — a question that remains largely unanswered.

Broderick will address this challenge and look to develop strategies to manipulate the microbiome in order to restore normal animal (including human) physiology.

Broderick received her PhD from the University of Wisconsin and completed postdoctoral training at École Polytechnique Fédérale de Lausanne in Switzerland. Her research focuses on understanding the mechanisms that underlie animal's interactions with their microbiomes to illuminate how beneficial as well as pathogenic bacteria impact host development, physiology, and health.

by Anna Zarra Aldrich '20 (CLAS), Office of the Vice President for Research

Drug Discovery Partnership with AI Biotech Company Reaps Promising Early Results

A half dozen University of Connecticut researchers are now working to identify potential new drugs to treat a wide range of diseases and conditions through a unique partnership that offers access to cutting-edge artificial intelligence (AI) technology and screening compounds.

Through its Artificial Intelligence Molecular Screen (AIMS) Awards program, Atomwise, a biotech company, provides access to advanced screening technologies that will help expedite the research at no cost.

MCB Assistant Professor **Simon White** was one of these UConn researchers participating in this partnership. White studies hand-foot-and-mouth disease and the virus that causes it. The disease typically infects children and infants, a small number of whom require hospitalization. With large recurrent outbreaks in Asia and no specific treatments for the disease, White looked to Atomwise to help accelerate his efforts to develop drug candidates that specifically target the virus.

"We're very hopeful these results will help get us closer to the first ever treatment for this condition," says White.

"We are thrilled that our faculty members have been able to take advantage of this program, which leverages cutting-edge technology from industry with innovative research from one of the nation's top universities," says Radenka Maric, vice president for research at UConn and UConn Health.

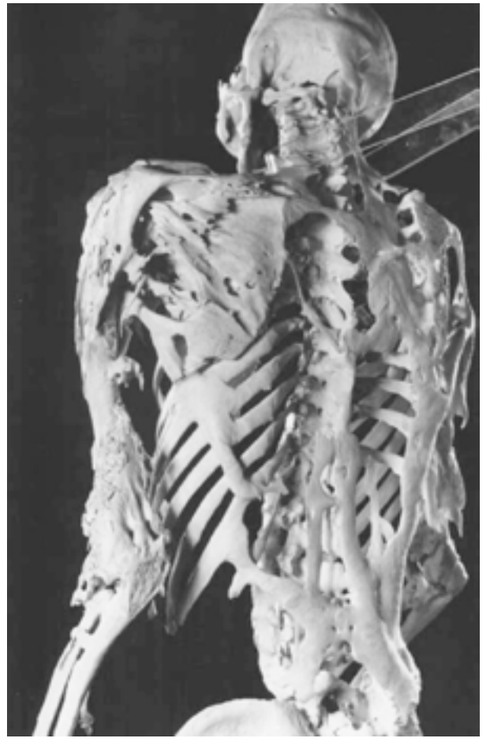
by Combined Reports - UConn Communications

Signals that Trigger Crippling Bone Disease Coming into View

Long bones normally grow longer at plates near their ends by first forming cartilage that then forms a matrix that then accumulates calcium to harden the bone. The whole bone is alive, so new bone can form elsewhere in the bone for repair of damage. Traumatic injury, or in some cases inherited disease, can cause abnormal bone growth called heterotopic ossification (HO) so that bone forms in places that it should not. One form of the condition, called endochondral HO, causes ossification, or calcium-based hardening, of muscle tissue or other soft tissues. Professor **David Goldhamer** studies this condition and a related debilitating, inherited, progressive disorder called fibrodysplasia ossificans progressiva (FOP). He recently wrote a review article describing research of these conditions and pointing out gaps that remain in our understanding, particularly knowledge of the mechanisms that direct the cells that initiate aberrant cartilage and bone formation.

Soft tissue injury or inflammation typically triggers HO, though how they do so is a mystery. HO is especially a problem in cases of limb amputation and traumatic combat injuries. It can lead to significant pain and swelling, affect joint mobility, and impede functional recovery. FOP is a very rare condition that seems to arise from spontaneous appearance of HO of the muscular system at an early age and that progressively immobilizes the afflicted individual. Mild injuries can trigger HO in these individuals, necessitating extreme precautions to avoid even the mildest trauma.

Treatments for HO are very limited, so the research of investigators like Golhamer are essential to find how this phenomenon starts so that its progression can be prevented or limited. His research involves the use of mouse models to study the cellular mechanisms involved in HO and FOP. His lab has produced mutant mice, using gene-targeting technologies, that exhibit FOP so that its underlying causes can be studied in the laboratory. A critical gene involved in this is the same in mice and humans, giving hope that results in the lab can be translated for use in treating the human condition.



Skeleton of Harry Eastlack, an FOP vicitim, on display at the Mütter Museum of the College of Physicians of Philadelphia.

Goldhamer has also been able to use methods to selectively tag different kinds of cells that exist between muscle cells. A new kind of progenitor cell, one that gives rise to other kinds of cells, was found that plays a key role in injury-induced HO. Following injury, these cells proliferate and can cause the appearance of cartilage and bone. These cells also seem to play a similar role in FOP. His findings were published in a recent Nature Communications article.

Evidence is accumulating that other kinds of stem and progenitor cells are to be involved in the various manifestations of HO. Goldhamer's work along with that of other investigators has also revealed the role of a protein in initiation of FOP, so work on this is showing more promise for future advances. By contrast, determining the underlying activation of HO as the result of muscular and even some neurological damage is more difficult. Though these may share common factors in the activation of aberrant bone growth, each might also have unique factors that will require more difficult methods to discover. Molecular tools to investigate each of these situations are currently lacking in some cases, so efforts in that direction are needed.

Goldhamer points out in his article that advances are proceeding in our understanding of the offending cell populations both in terms of their normal functions and the signals that subvert these normal functions. Consequently, information is accumulating that might lead to cell-specific therapeutic strategies to prevent or treat HO caused by injury or disease. Goldhamer has published one such study that examined the effect of therapeutic agents on pathogenic progenitor cells.

by Kenneth Noll

UConn, Biohaven Pharmaceuticals Ink Licensing Deal for Investigational Agent for Inflammatory and Autoimmune Diseases

Molecular and cell biologist Michael Lynes and an international team of researchers have developed a novel antibody designed to prevent the patient's immune system from attacking its own body. Lynes is shown here with lab manager Clare Melchiorre. (Taylor Hudak '18 (CLAS, ED)/UConn Photo).

Biohaven Pharmaceutical Holding Company Ltd. (NYSE: BHVN) announced today that it signed an exclusive, worldwide option and license agreement with the University of Connecticut for the development and commercialization rights to UC1MT, a therapeutic antibody targeting extracellular metallothionein (MT). Extracellular MT has been implicated in the pathogenesis of autoimmune and inflammatory diseases. Under this agreement, Biohaven has the option to acquire an exclusive, worldwide license to UC1MT and its underlying patents to develop and commercialize throughout the world in all human indications.

The antibody was discovered in the laboratory of **Michael Lynes**, PhD, head of the Department of Molecular & Cell Biology at the University of Connecticut Storrs. Lynes is a world leader in the study of metallothioneins and their role in disease. Biohaven and the University of Connecticut also signed a Sponsored Research Collaboration Agreement to support the ongoing exploration of the role of MT in human disease.

The new antibody, co-invented by the UConn researchers together with a team from Ghent University in Belgium, is designed to prevent the patient's immune system from attacking its own body and potentially causing irreversible damage.

"We are very excited about this opportunity to potentially expand our portfolio with the addition of this novel antibody and assess its activity in a range of diseases, including neuro-inflammatory disorders," says Dr. Vlad Coric, CEO of Biohaven. "The pre-clinical discovery work by Lynes at the University of Connecticut, and his collaborators at the Ghent University and Joslin Diabetes Center, an affiliate of Harvard Medical School, suggests that metallothionein can have dramatic influences on the modulation of both innate and adaptive immunity. We look forward to further evaluating this antibody and potentially advancing it into the clinic."

"This agreement represents a critical next step for my research group, as it helps define the path for taking our basic research discoveries into the clinic. The expertise that Biohaven Pharmaceuticals brings to my research team has been invaluable in advancing this goal," says Lynes. I believe we have an exciting opportunity to develop this new approach to the management of important inflammatory and autoimmune diseases where metallothionein plays a significant role."

The pre-clinical discovery work by Lynes at the University of Connecticut, and his collaborators […] suggests that metallothionein can have dramatic influences on the modulation of both innate and adaptive immunity.—Vlad Coric

MTs are a family of low molecular weight, cysteine-rich, metal-binding proteins that have a wide range of functions in cellular homeostasis and immunity. MT has traditionally been considered to be an intracellular protein that can be found in both the cytoplasm and nucleus; however, MT also can be found in extracellular spaces, particularly in disease states involving chronic cellular stress where intracellular MT production is upregulated by inflammatory cytokines, and extracellular MT acts as a danger signal, attracting leukocytes and modulating the immune response. In pre-clinical studies, UC1MT has been observed to block this extracellular pool of MT and the resulting MT-mediated inflammation and immunomodulation.

"We are looking forward to this partnership as we see great potential for this novel mechanism in inflammation. We intend to capitalize on our strong development experience and the deep scientific expertise of Dr. Lynes' team to rapidly advance innovative therapies to patients," says Clifford Bechtold, chief operating officer and head of biologic development at Biohaven. Bechtold has previous pharmaceutical industry experience in optimizing biologics development and manufacturing capabilities.

This option builds upon Biohaven's portfolio of innovative, clinical-stage product candidates for the treatment of neurodegenerative, neurologic and neuropsychiatric disease indications. Under the terms of the agreement, Biohaven paid an upfront option fee and, if Biohaven exercises its option to in-license the program, the University of Connecticut will receive additional license fees and will be entitled to low single-digit percentage royalties based on net sales of any commercialized products as well as milestone payments based on the achievement of development, regulatory and commercial milestones.

by Jessica McBride - Office of the Vice President for Research

The Road to a New Antibody

More than a decade ago, Lynes, professor and head of the Department of Molecular and Cell Biology at UConn, and his research team discovered a novel and important role that a protein called metallothionein (MT) plays in influencing the body's immune function. The body produces MT when cells are under stress, and extended periods of stress cause MT to be released from the cells that produced it, Lynes says. MT is an unusual protein that holds onto chemicals in the body – both those that are beneficial, such as zinc and copper, and those that are harmful – such as cadmium and mercury.

While studying MT, Lynes and his research team noticed that MT released from cells could mimic some of the signals that the immune system uses as cues to tell cells to go to one place or another in the body. Under normal circumstances, immune cells use these signals to guide them to local infections or other tissue damage. When cells are stressed over prolonged periods, this can mean that there is persistent inflammation accompanied by damage to nearby healthy tissue.

About 50 million people, or 20 percent of the U.S. population, suffer from some form of autoimmune disease or chronic inflammation, according to the American Autoimmune Related Diseases Association. More than 80 autoimmune diseases have been identified, and autoimmune diseases are becoming increasingly prevalent, for reasons unknown, according to the National Institute of Environmental Health Sciences. While causes of autoimmune diseases also remain largely unknown, scientific consensus is that autoimmune diseases are probably triggered by a combination of genetic and environmental factors.

A team of Belgium doctors and scientists studying Inflammatory Bowel Disease (IBD) had published a paper saying that their sickest patients were those whose bodies produced the most MT. The MT protein, which serves as a normal part of the cell's internal machinery inside the cell, was getting outside the cell and causing damage. That paper by Dr. Martine DeVos, Debby Laukens, and Lindsey Devisscher led to a collaboration with Lynes.

Since the protein serves an essential purpose, researchers can't shut it off all together; so they had to find a way to stop MT from prolonging inflammation and damaging healthy cells. Lynes and his team produced an antibody protein that basically attaches itself to MT when it is outside the cell and inactivates it – preventing the body from attacking its intestinal system. This approach dramatically reduced inflammation in mouse models of the human disease.

"We've recently extended that work with our colleagues You-Hua Tseng and Matthew D. Lynes at Joslin Diabetes Center of Harvard Medical School to show that UC1MT also shows therapeutic promise in a mouse model of Type 1 diabetes," Lynes says."

Sparrows and their Microbes Evolve Together

The American Society for Microbiology launched its second annual issue of mSystems highlighting early-career scientitsts. The 2019 May/ June issue "Early-Career Scientists Shaping the World" featured an article by MCB Professor Sarah Hird. Hird's article, "Microbiomes, Community Ecology, and the Comparative Method" described how her work on avian microbiomes uses two complimentary views, the microbiome as a community and the microbiome as a trait of the host.

These special issues highlight and promote the diversity of scientific ideas and approaches within microbial systems biology and also the diversity of the authors themselves. The journal editors consider this an important part of their mission to counter implicit and explicit biases that affect authorship in STEM fields (see article on page 5).

HIrd points out that avian microbiomes, like all microbiomes, exhibit considerable variation in species composition and function. These populations evolve in response to Natural Selection directed at these features. Additionally, avian microbiomes can promote or deter the health, fitness, and proper development of their host, and so serve as a selective force of their own. They are, in effect, a trait of their host like other traits that are subject to Natural Selection.

Hird applies classical ecological and evolutionary theory to her research questions and utilizes sophisticated statistical models to examine her data.

It is not clear how individual kinds of microbes come together to form a community in a given environment. They may come together rather haphazardly so that any kind of community, that of the avian gut, for example, could have a collection of species rather different between two birds or two species of bird. Alternatively, a given environment might require the services of a given spectrum of functions so that the community that would form there will have the same kinds of species regardless of which bird or species is examined. Hird is exploring these different theories by sequencing DNA extracted from different microbiomes, called metagenomics, to identify the members of the community and reveal the genetic potential in that community. Her lab will also sequence all the messenger RNA transcripts present in these microbiome samples to show which genes are being expressed and so reflect the functions that are being employed in these environments. Each of these will give evidence of the extent and nature of the microbial diversity in the environments examined.

Hird also examines the function of microbiomes as traits of their host bird. Using methods to determine the evolutionary relationship among bird species or variants, she can then relate the pattern of these relationships to the kinds of microbial communities each species or variant hosts. She will look for any relationships between the functions contained in a community or the kinds of species in a community with the evolutionary trajectory of its host. Any selective pressures the host's evolutionary lineage has experienced may be able to be related to the kind or function of its resident microbiome. Thus the microbiome would act as another of the host's traits.

Hird is focusing her efforts on the Saltmarsh Sparrow, an endangered saltmarsh specialist species. Her lab is collecting data from 35 breeding populations across its breeding range. Given

Saltmarsh sparrow Photo credit Audubon Society.

that the sparrow faces extinction by 2050, there is some urgency to gather and analyze these data to see if their microbiomes may hold clues to the survivability or perhaps the rescue of this species. In such questions, life is interconnected with both its environment and its microbiomes, so the more we know about each, the better stewards we can be for such fragile life.

by Kenneth Noll

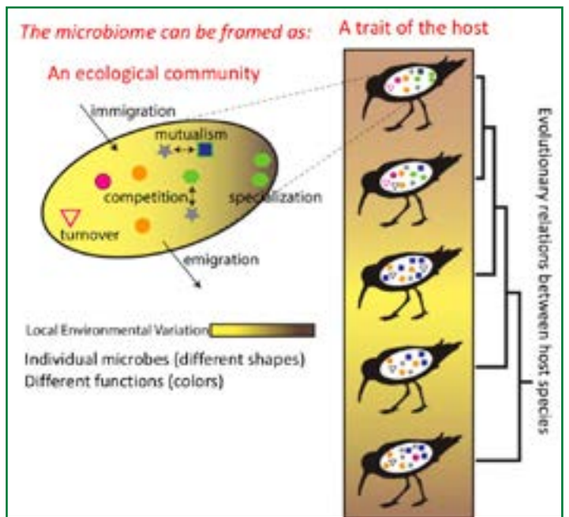


Figure from DOI: 10.1128/mSystems.00112-19

MCB Grad Students Win International Policy Competition

The team (l to r) Joshua Schreier ('19 MPP), Shankar Kumar ('19 MBA), Tony Patelunas ('19 MPP & '20 Ph.D. MCB), and Sneha Jayaraj ('19 MPP) with the final round judges (l) Prof. Jacqueline Klopp, Director of the Columbia University Earth Institute, and (r) Prof. Larry White, of the NYU Leonard N. Stern School of Business.

With over 500 students comprising 139 teams, the annual New York University Policy Case Competition (NYUPCC) came to a close on April 28, 2019. After reaching the final round, UConn students Shankar Kumar '19 (MBA), Tony Patelunas '19 (MPP), '20 (Ph.D.), Sneha Jayaraj '19 (MPP) and Joshua Schreier '19 (MPP) impressed the judges to become the 2019 champions. The team was awarded trophies, a $1000 prize, and a celebratory dinner with esteemed judges in New York City.

Teams from top schools around the world, including Canada, China, Pakistan, India, France, Spain, and across the US competed to produce the most innovative and effective policy proposals. In round one in early April, teams submitted a memo on an assigned topic in domestic, international, tech, or science policy. In round two on April 27, twenty qualifying teams presented their proposals before a panel of expert judges at NYU. The top five teams, with students from NYU, MIT, UPenn, Emory, the University of Washington and UConn, presented again in the final round on April 28. Assigned farm subsidies, UConn's winning presentation included proposals to cut federal crop insurance subsidies and create a targeted tax credit for small farmers.

Jacqueline Klopp, a Professor at Columbia University's Earth Institute and one of NYUPCC's final round judges stated that one of the reasons the UConn team won was its "holistic consideration of the interconnected effects of farm policies on human health, community, the environment, and the economy." Another judge, Lawrence White, the Robert Kavesh Professor of Economics at NYU Stern School of Business, complimented UConn students' "effective use of slides and clear communication skills." While the competition was close, judges said that the UConn team came out on top because of its nuanced considerations of political feasibility, effective and smooth teamwork, and careful quantification of costs and benefits.

"Basically we used the skills like memo writing, cost-benefit analysis, and public speaking we learned in our classes to win," Schreier said, "I'm so proud of what we accomplished together as a team."

The team focused its attention on full-time farmers with annual gross sales of less than $150,000 because this group has a median income less than that for US households overall and faces high farm land prices and other challenges. At the same time, small farmers provide many positive externalities not compensated by the market. "This proposal would decrease inequity in a system where government subsidies are currently highly skewed toward the largest and wealthiest farms. By providing support for small farmers who really need it, it makes our food system stronger," Patelunas explained.

An MBA student, Kumar joined the UConn team because of his interest in public policy and sustainability: "When you design public policies, all stakeholders need to be taken into account and that includes the well-being of the earth and everyone who depends on it."

The team donated the $1000 prize money to the Department of Public Policy's fund for students to participate in future professional development activities, conferences, and competitions like NYUPCC.

by Joshua Schreier '19 (MPP)

UConn Researcher Wins NASA Grant to Study Gene Transfer in Archaea

Colonies of *Haloferax volcanii* appear red due to carotenoid pigments. (Photo by Scott Chimileski Microbial Science Photography)

Human evolution is based on the premise of "survival of the fittest" where the organisms with the genetically encoded characteristics best suited to their environment survive to pass those genes on to their offspring who keep passing that trait on until all members of the population have it. But how do organisms that don't reproduce sexually evolve?

Archaea are a type of single-celled organism that can be found all over the globe, often in extreme environments. They help make up sea plankton which are the basis of all marine food chains, some live in hot springs and salt lakes, some even reside in the human gut and play an important role in digestion. But how this class of organisms, which may be the oldest on the planet, has evolved over billions of years largely remains a mystery.

The work of University of Connecticut Associate Professor **R. Thane Papke** may help illuminate part of this mystery. Papke has received a $989,000 grant from the National Aeronautics and Space Administration to study the role of horizontal gene transfer in archaeal evolution. MCB Assisstant Professor **Simon White** is a co-investigator and Uri Gophna from Tel-Aviv University in Israel is an international co-investigator for this grant.

Archaea and bacteria reproduce asexually. These organisms copy their DNA and make a perfect replica of themselves. This is why horizontal gene transfer is essential for the evolution of these organisms which otherwise would have no way to diversify their allele pool and ensure the survival of the species. If all members of a species have the same genetic profile, a single disease can wipe all members of that species out in one fell swoop.

Studies have shown archaea engage in a tremendous amount of horizontal gene transfer (HGT) and that they have acquired thousands of genes from bacterial sources. This has resulted in non-sexually reproducing organisms having the same amount of genetic diversity as sexually producing organisms, leaving evolutionary researchers scratching their heads.

"Sexual reproduction is thought to have arisen out of asexuality precisely because of the advantages of shuffling gene pools," Papke says. "However, it is clear that archaea and bacteria had solved that problem without sexual reproduction."

Previous studies have shown evidence of a cell-contact-dependent method of gene transfer in a type of archaea called *H. volcanii*, which is commonly found in the Dead Sea and other very salty environments.

Haloarchaea engage in a kind of horizontal gene transfer known as "mating" wherein two archaea swap genes through cell-to-cell contact without a clear donor/recipient dynamic which is seen in most other forms of HGT.

This archaeon's ability to survive in such environments makes it attractive to space researchers as these organisms could potentially live on Mars and offer insight into the evolution of extraterrestrial life there.

"I think NASA funds our work because we address fundamental questions that attempt to resolve where sexual reproduction comes from," Papke says. "NASA is interested in transitional states of biology, and sexual reproduction is a big one."

In this project, Papke hopes to identify and characterize the genes responsible for horizontal gene transfer in this particular archaeon. Papke and his team also hope to determine the rate of horizontal gene transfer between haloarchaeal species, the class to which *H. volcanii* belongs.

Papke will also study the role of the receiving organism's system for cutting non-self DNA in this process, which is how cells can be immune from virus or plasmid infection. Whenever organisms encounter foreign material, their immune systems naturally react and attempt to remove or destroy the invader. For a cell to take up a foreign gene successfully, its immune system must be overridden and signaled to stand down.

One of the features that makes *H. volcanii* an ideal model organism for this research because their method of horizontal gene transfer requires the membranes and cell walls of two or more cells to fuse, in a way that interestingly resembles the fusion of gametes to produce a zygote through sexual reproduction.

"This resembles what I would imagine as a primitive intermediate step towards sexual reproduction that demonstrates an expected cell contact mechanism for wholesale genetic flow, without having connected reproduction to the process yet, a kind of asexual reproduction sex," Papke says.

Papke received his Ph.D. in microbiology from Montana State University. He completed his postdoctoral training in the Department of Biochemistry and Molecular Biology at Dalhousie University in Halifax, Nova Scotia. His research interests include classifying and understanding the evolution of non-pathogenic prokaryotes.

by Anna Zarra Aldrich '20 (CLAS), Office of the Vice President for Research

Knecht receives research excellence award

David Knecht was awarded a College of Liberal Arts and Sciences Research Excellence Award in the Life and Behavioral Sciences division. Recipients are honored for a research program that has gained national and international distinction and impact in its field of study. The Award includes a medal and $1000 in support of the awardee's research.

From Lab Bench to Regulatory Affairs

In fall 2017, **Samantha Holmes** entered the M.S. Applied Genomics Professional Science Master's (PSM) program in the Department of Molecular and Cell Biology (MCB) at the University of Connecticut with the intent of enhancing her hands-on experiences in the laboratory. Exposure to different career opportunities in the program led her to an internship and a career in regulatory affairs. Even with the change in direction, Samantha knew that the technical skills and knowledge acquired through the program would prepare her, and set her apart, from other candidates in the job market.

Prior to entering the MCB PSM program, Samantha had an internship at Alnylam, where she was part of the RNAi research discovery team. This was followed by an internship at Merrimack Pharmaceuticals, where she created and evaluated mouse models for various cancer cell lines.

After graduating with a M.S. in Applied Genomics in the summer of 2018, Samantha went to work at Blueprint Medicines as a Regulatory Affairs Associate. As Samantha notes, it was the MCB PSM professional development seminars and courses that prepared her for her current job. "The program prepared me well for the job market. The networking from the professional development seminars was very useful as that is how I became familiar with Regulatory Affairs and their role in a pharmaceutical company. The coursework also gave me more advanced knowledge that is applicable to oncology and rare disease-based companies."

At Blueprint Medicines in Cambridge, MA, Samantha works in different parts of the regulatory arena, preparing and submitting new drug applications, working on global regulatory submissions, submitting FDA amendments, rolling out new protocols, and organizing ongoing clinical trials.

Based on her experiences in the MCB PSM program, Samantha says, "I recommend the program to other students as it is a lab driven and industry focused program. The program not only offers labs and coursework, but also professional development seminars, interview/resume practice, and strategies for managing people, which are all just as important."

by Elain Mirkin

Non-Coding Doesn't Mean Non-Functioning: Exploring the Role of Non-Coding RNA in Gene Expression and Evolution

Assistant Professor Leighton Core in the Engineering & Science Building. (Bri Diaz/UConn Photo)

University of Connecticut assistant professor of molecular and cell biology, **Leighton Core** hopes to answer new questions about RNA through a $2 million grant from the National Institute of General Medical Sciences.

Our bodies respond, on a cellular level, to environmental changes through a complicated process – turning on or off parts of our vast genome, expressing specific genes at specific levels to respond to specific situations.

However, experts are learning that this process may be even more complex than previously thought.

When our bodies need to produce proteins, necessary codes are found in our DNA. The process of transcription creates a messenger RNA that is an RNA copy of the DNA sequence. During translation, transport RNA then brings over the amino acids that correspond to the RNA code. These amino acids are joined together to create the protein. These proteins are responsible for everything that happens in our bodies from development, to immune responses, and healing.

But there are some segments of our DNA that make RNAs that don't code for any protein – so why do we have them?

This is the question Core hopes to answer.

Even though it is not translated into protein itself, noncoding RNA (ncRNA) plays a critical role in regulating transcription of protein-coding genes. ncRNA can recruit gene activators or suppressors to control where, when, and to what degree protein-coding RNAs are transcribed.

"These observations suggest that regulation of ncRNA biogenesis adds an intricate layer of control to overall gene expression levels," Core says.

Currently, a significant obstacle to studying and understanding the roles of ncRNAs is being able to identify and correctly classify them.

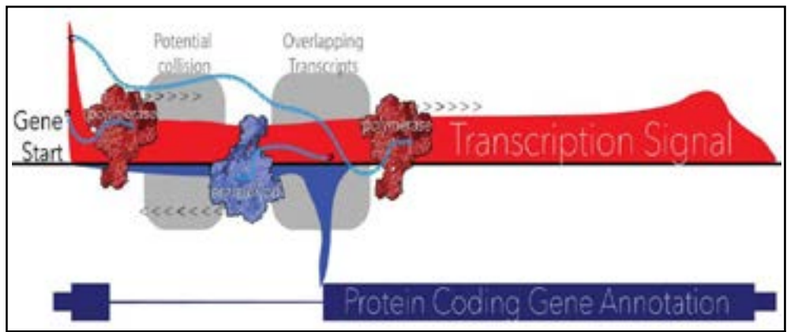
Core's project will develop new experimental and computational methods that can identify the transcripts of ncRNA that will also allow him to predict the function of these segments. He will then look to identify the mechanisms that regulate the production and destruction of ncRNA and determine the effect of ncRNA on the protein-coding gene transcription process of genes located near them on our genome.

"ncRNAs are involved in regulating every phase of gene expression from transcription factor recruitment to RNA transcription, processing, stability, and translation," Core says. "Intense efforts are still required to identify all species of ncRNAs and their diverse functions in regulating gene expression. These studies will generate important resources and represent foundational framework for studying ncRNA function."

Core is also investigating the capacity of ncRNA in the evolution of new genes. He will use an evolutionary genetic model to identify the nucleotide changes in our DNA associated with altered ncRNA transcripts. This aspect of the project will shed light on the mechanisms underlying acquisition of new phenotypes and inform future studies of evolution.

Core received his PhD in molecular biology and genetics from Cornell University where he also completed his postdoctoral training. Core's current research focuses on how changes in RNA transcription and processing drive changes or maintenance of cellular states during cellular responses such as development or disease progression.

by Anna Zarra Aldrich '20 (CLAS), Office of the Vice President for Research



Transcription maps generated by Leighton Core's Lab show non-coding RNAs that overlap and potentially regulate production of protein-coding genes. (Illustration by Geno Villafano)

Horseshoe Crabs: How Did They Get an Exception?

Every life form changes through the ages, and evolution is the only constant. Except for horseshoe crabs – which have stayed the same for 450 million years, keeping everything from the eyes on their tail to the antibacterial cells in their blood.

How they've managed to stay the same is a great mystery. Now, researchers at UConn's Institute for Systems Genomics are assembling a detailed map of the horseshoe crab's DNA. They hope the map will lead them to answers to the crabs' two great secrets: how their blood reacts to bacteria, and why the crabs seem frozen in time.

MCB Professor **Rachel O'Neill**, director of the Institute, is intrigued by horseshoe crabs (the native Connecticut species is *Limulus polyphemus*) because they're just so weird. They're members of Arthropoda, that vast phylum of life that includes insects, crustaceans, and spiders. But most of their relatives went extinct long, long ago, and horseshoe crabs' closest living relatives are ticks, spiders, and scorpions.

Horseshoe crabs are living fossils that look the same as they did 450 million years ago. How they have managed to stay the same is a great mystery. Now, Prof. Rachel O'Neill is heading a UConn team to create a detailed map of the horseshoe crab's DNA to learn why these "living fossils" seem frozen in time.

There aren't many detailed DNA maps of spiders or ticks to compare horseshoe crabs to. And even if there were, horseshoe crabs aren't exactly normal spiders. A map of their DNA is a window into the DNA of the Ordovician period of the Paleozoic, a time long before the dinosaurs, when mollusks and trilobites dominated the seas and the most complex lifeforms on land were plants similar to liverworts.

But even that long ago, bacteria were everywhere. And they were no friends to *Limulus polyphemus*. The crabs' blood contains roaming cells called amoebocytes that attack bacteria and coagulate like glue around them, instantly sealing off holes in the circulatory system.

That violent reaction to bacteria has made the horseshoe crab's blood extraordinarily valuable to the pharmaceutical and medical device industries, which use an extract from the blood to test for contaminants in every batch of vaccine, saline, or other injected drug, as well as every pacemaker, artificial hip, or other implanted device. Horseshoe crabs have to be captured and bled to provide the substance, and their declining numbers suggest the harvest is slowly killing them off.

Although there is a synthetic replacement available, it has been slow to catch on. O'Neill and her students think there is potential to expand its use, and perhaps design other, related proteins that detect other types of contaminants, not just bacteria.

"At this point it's science fiction. But this is a novel way of thinking about any contaminant detection," O'Neill says.

Graduate student Kate Castellano has raised the baby horseshoe crabs to watch how they grew from embryos to the inch-long three-year-olds shown in the video available at the UConn Today website. Part of it was to understand their basic biology – no one had even published a guide to the care and feeding of horseshoe crab embryos before – and part of it is public education. The little Limulus babies live in a 30-gallon tank in the common area of the Institute for Systems Genomics, and anyone can sit at the nearby table and watch them.

"The dinosaurs came and went, but the crabs stayed the same," O'Neill says. "We're exploring this fossil genome to understand the adaptations that let horseshoe crabs succeed for so long."

by Kim Krieger - UConn Communications, and Angelina Reyes - UConn Communications

Engaging Future Scientists

Prof. **Kenneth Noll** appeared as Charles Darwin and showed the children items from his Bag of Stories to illustrate Darwin's discoveries.

As part of Homecoming Weekend, on October 23 children ages 5 to 12 joined UConn faculty, staff, and students for an afternoon of STEM experiments.

The UConn Science Salon Jr. featured manipulations in chemistry, engineering creations, and environmental adventures. The event is an offshoot of the popular UConn Science Salon series, café events designed to encourage public discourse at the intersection of science and culture.

by Lucas Voghell '20 (CLAS)

Nature is a Rich Source of Medicine - If We can Protect It

Professor **John Malone** co-authored a recent article in The Conversation describing efforts, including his, to discover new medicines in Nature. From gila monsters to the Pacific yew, new classes of drugs have been discovered in the most unexpected places. Whether we will be able to continue such discoveries very much depends upon whether humans can more seriously assume the role of protectors of the environments in which potentially medically useful organisms live.

Harvesting chemicals useful as drugs from wild organisms can be very expensive and endanger the very creatures we come to depend on. A case in point is that of the Pacific yew, source of paclitaxel, the compound used to treat cancers that generates sales of about $80-100 million per year, as reported in Malone's article.

After its discovery in 1971, paclitaxel had to be extracted from the bark of yew trees, resulting in killing of these rare, slow-growing trees. Tree destruction continued until 1994 when chemists successfully synthesized the chemical. As new drug chemicals are discovered, more advanced chemical synthesis methods can be applied to perhaps obviate the need to harvest them from natural sources.

Of more concern to the survival of potential sources of new drugs is habitat destruction. Malone's article cites an estimate that one important drug is lost every two years from environment disruptions.

Inexpensive and high-throughput DNA sequencing allows investigators to explore the biomedical potential of organisms without capturing or killing them. Small tissue samples can be taken to sequence the genomes of organisms or, in the case of microorganisms, to simply sample the waters or soils in which they live to sequence the DNA of billions of cells at once. As noted in Malone's publication, advanced chemical analysis tools, too, can detect and identify potential drug targets using very small environmental samples.

The subject of Malone's research, the African clawed frog, produces an anti-microbial protein in its skin secretions, the first such protein discovered. Researches noticed that surgical wounds on these frogs rarely became infected, despite the use of non-sterile procedures. The protein, called magainin, discovered in 1987, has yet to come to use in medicine.

Unfortunately well-intentioned international efforts to protect less-developed countries from being exploited for their natural sources of useful drugs has resulted in making international collaborations more difficult for academic researchers looking for potentially useful natural compounds. Malone and his co-authors recommend that governments team up to support international collaborative research efforts among different scientific disciplines to explore the natural potential for new discoveries. These collaborations would assure mutual sharing of any resulting benefits while taking steps to conserve natural resources. Such efforts would allow improved access to Nature's library of chemical books of beneficial information that is now restricted to those with the most resources to check out its books.

by Kenneth Noll

African clawed frog Photo from Australian ABC News.

Inaugural therapeutics awards announced

Recipients in the inaugural funding round for the UConn Program in Accelerated Therapeutics for Healthcare (PATH) were announced in Fall 2018. PATH accelerates the translational pathway for researchers to convert their discoveries to new medical therapeutics. PATH, funding is designed to quickly develop novel therapeutic approaches focusing on well-validated molecular targets for specific disease areas with an unmet treatment need in the current commercial marketplace. Seven PATH grants were awarded after a selective competition, and one was awarded to MCB Prof. **Simon White**. His project was entitled, *Screening for small molecule inhibitors against Enterovirus D68 2C helicase*.

MCB Graduate Students

Summer Fellowship Awards

Biohaven Internship
Ala Shaqra, SB3, Robinson Laboratory

Claire M. Berg Graduate Fellowship in Genetics
Katelyn DeNegre, Genetics and Genomics, M. O'Neill Laboratory
Gabrielle Hartley, Genetics and Genomics, R. O'Neill Laboratory

Arthur Chovnick Graduate Fellowship in Genetics
Kate Castellano, Genetics and Genomics, R. O'Neill Laboratory

Richard C. Crain, Jr. Memorial Fellowship
Melissa Skyork, SB3, Alder Laboratory
Aaron Feinstein, SB3, May Laboratory

Cross-Disciplinary Fellowships in MCB and Pharmaceutical Sciences
Sarah Goldstein, Microbiology, Klassen Laboratory

Jean Lucas-Lenard Special Summer Fellowship in Biochemistry
Matthew Kearney, Genetics and Genomics, M. O'Neill Laboratory
Anthony Patelunas, Cell and Developmental Biology, Goldhamer Laboratory

The Dr. Edward A. Khairallah and Dr. Lamia H. Khairallah Fellowships
Sarah McAnulty, Microbiology, Nyholm Laboratory
Rambon Shamilov, Pharmaceutical Sciences, Aneskievich Laboratory
Liming Chen, Pharmaceutical Sciences, Zhong Laboratory

Philip I. Marcus Graduate Student Fellowship in Virology
Corynne Dedeo, Biochemistry, Teschke Laboratory

Pfizer Summer Fellowships in Molecular and Cell Biology
Elizabeth Herder, Microbiology, Hird Laboratory
Virginia King, Cell and Developmental Biology, Campellone Laboratory

Antonio H. & Marjorie J. Romano Graduate Education Fellowship
Kevin Lee, Microbiology, Klassen Laboratory
Joshua Gil, Microbiology, Hird Laboratory

Sally Chamberland receives '18-'19 Outstanding Graduate Teaching Award

Sally Chamberland, MCB '19, Alder lab, was the Recipient of the 2018-2019 University Outstanding Graduate Teaching Award from the Center for Excellence in Training and Learning, The Outstanding Graduate Teaching Awards were established in 1999 to recognize teaching assistants who demonstrate excellence in the classroom or laboratory. The nominee for this award demonstrates effective instructional skills, possesses excellent interpersonal skills, provides practical feedback, and contributes to the development of the instructional program. Chamberland is now an Instructor of Biology at Springfield College teaching Microbiology, Virology, and Immunology.

Student Fellowships and Awards

DEMI-Pre Doc
Rebecca Newcomer, Matthew Ouellette, Jason Palladino, Rebecca Bova-Seliga, Ala Maher Shaqra, Shail Kabrawala

Doctoral Dissertation Fellowship
Kunica Asija, Kevin Boyd, Charles Bridges, Cory Jubinville, Shail Kabrawala, Danielle Lesperance, Ala Shaqra, Michael Stephens, Therese Tripler, Cassie Zerbe, Elizabeth Herder

Doctoral Student Travel Award
Cassie Zerbe, Elizabeth Herder, Charles Bridges, Therese Tripler, Rebecca Newcomer, Cassie Zerbe,

MCB Travel Award
Richard Whitehead (Fall), **Bryce Santinello** (Spring)

Outstanding TA Awards
Kevin Lee, Tony Petalunas

Microbiome Fellowships
Andrea Suria, Madison Condon, Yutian Feng, Katie Kyle, Todd Testerman

Graduate Degrees Conferred

August 2018
Aquino, Gabriela, PSM, Applied Genomics
Bolte, Elizabeth, PhD, Microbiology
Cordi (Pavanacherry), Sharon, PhD, Genetics
Daniel, Krista, MS, Cell Biology
Duda, Zachary, PhD, Genetics
Fullmer, Matthew, PhD, Microbiology
Han, Yueh-Chiang, PhD, Cell Biology
Henowitz, Liza, MS, Cell Biology
Holmes, Samantha, PSM, Applied Genomics
Leeser, Jacob, MS, Genetics
Mistretta, Meredith, MS, Microbiology

December 2018
McAnulty, Sarah, PhD, Cell and Developmental Biology
Stephens, Michael, PhD, Microbiology

May 2019
Adakole, Taiye, MS, Genetics and Genomics
Boonyavairoje, Chanon, MS, Genetics and Genomics
Chamberland, Sally, PhD, SB3
Deininger, Lee, MS, Microbiology
Kabrawala, Shail, PhD, Cell and Developmental Biology
Legendre, Nicholas, PhD, Genetics
Low (Bernardis), Sarah, PhD, SB3
Ma, Bowen, MS, Genetics and Genomics
Oliva, Courtney, MS, Genetics and Genomics
Ouyang, Luoxuan, PSM, Applied Microbial Systems Analysis
Richardson, Sasha, PSM, Applied Microbial Systems Analysis
Vasilenko, Marat, PSM, Applied Microbial Systems Analysis

August 2019
Asija, Kunica, PhD, Microbiology
Boyd, Kevin, NSF GRFP, PhD, SB3
Gagnon, Emily, PSM, Applied Microbial Systems Analysis
Kaplan, Anne, PhD, SB3
Liu, Alicia, PhD, Genetics and Genomics
McClure, Emily, PhD, Microbiology
Ouellette, Matthew, PhD, Genetics and Genomics
Suria, Andrea, PhD, Microbiology
Tripler, Therese, PhD, Biochemistry
Trusiak, Sarah, PhD, Genetics and Genomics

MCB PhD graduates, May 2019

Professional Science Masters Program News

MCB faculty provide two Professional Science Masters (PSM) degree programs, Microbial Systems Analysis (MSA) and Applied Genomics (AG), and a Professional Masters progam, Applied Biochemistry and Cell Biology. Each program offers cross-training for business, governmental or corporate environments. As part of their training in each program, students participate in internships, typically with partnering companies.

Recent internships

Applied Biochemistry and Cell Biology PM program

Incoming MCB Professional Science Master's (PSM) and Professional Master's (PM) students, Fall 2018.

Summer 2019

Brandon Wilkinson, Sarepta Therapeutic, Andover, MA, translational development team**.**

Maria Grishanina, Abbvie, Cambridge, MA, developing assays for tau tangle recognition used in the diagnosis of Alzheimer's disease**.**

James Gair Laucius, High Purity Extractions, Southbridge, MA, development initiatives for super critical CO2 extractions in CBD oil production from raw hemp flower.

Emily Poulin was awarded a Technology Incubator Program (TIP) Innovation Fellows Program Fellowship and worked with UConn TIP startup companies in Farmington, CT. Emily Poulin worked as a research assistant at CaroGen, Inc., investigating hybrid virus technology methods for disease treatment. Emily was selected to give a talk "PEGylation of Virus-Like Vesicles" on PIE Innovation Research Day and to present a poster, with the same title, during the TIP Entrepreneurship Showcase.

Microbial Systems Analysis program

Spring 2019

Marat Vasilenko, Biorasis, Advanced Technology Laboratory/Discover Drive Incubator facility, UConn, Storrs, worked on enzyme chemistry.

Summer 2019

Emily Gagnon was a PIE Fellow and worked with UConn TIP startup companies in Farmington, CT. Emily was chosen to present a pitch session "Enhancing the Gut Microbiome to Improve Companion Animal Health and Livestock Efficiency" during the TIP Entrepreneurship Showcase. Her pitch was based on the work she did at Bactana over the summer

Applied Genomics program

Spring 2019

Presley Galloway, Nemaha County Hospital, Nebraska, performed blood sample analysis and wrote an NIH instrument proposal grant.

Summer 2019

Hanshu Yuan, Xuejun Jiang lab, Memorial Sloan-Kettering Institute NYC, cell biology project

Maria del Carmen Heredia Chavez was a PIE Fellow working with Dr. Michael Blinov at UConn Health, where she worked on the annotation and visualization of small models in VCell. She presented her completed work in a poster "From a Complex Biological Model to Modelbricks: The Process of Construction of a New Biological Tool" during the PIE Innovation Research Day. **Elshaimaa Ali**, another PIE Fellow, a worked in Dr. Justin Cotney's lab at UConn Health. She also presented a poster on PIE Innovation Research Day, titled "Identification of Regulatory Elements Active During Eye Development of Mice". It should also be mentioned Elshaimaa is a Fulbright Scholar from Egypt.

MCB Professional Science Master's laboratory module in molecular biology techniques, Fall 2018.

Recent employment

Applied Genomics graduates

Samantha Holmes was hired as a Regulatory Affairs Associate at Blueprint Medicines in Cambridge, MA immediately after her internship there.

Ryan Drennan was admitted to the MCB Ph.D. program**.**

Matthew Costello was admitted to the Pathobiology Ph.D. program.

Khalia Cain was admitted to the MCB Ph.D. program.

Affrin Ahmed was admitted to the Biomedical Ph.D. program at the UConn Health Center.

Ahmad Hassan was admitted the MCB Ph.D. program.

Microbial Systems Analysis graduates

Daniel Spitzer is now an Associate Translational Scientist at Enzo Life Sciences, Inc. in Stony Brook, NY.

Dominique Carrillo completed her internship at Shoreline Biome and was hired by this startup company as a Manufacturing and Quality Control Associate.

Luoxuan Ouyang continued her work at Genewiz in South Plainfield, NJ upon completion of her internship.

Marat Vasilenko will continue to work at Biorasis, based in the Advanced Technology Laboratory/ Discovery Drive incubator building, at UConn, where he did his internship.

Nahian Rahman is a QC Microbiology Technician at Medinstill Development LLC in New Milford CT. He was hired during his last semester in the M.S. Microbial Systems Analysis program.

Sasha Richardson recently accepted employment at the Yale School of Medicine as a Research Assistant in Regulatory Affairs.

PSM outreach

During summer 2019, the MCB Professional Science Master's (PSM) programs once again participated in the CTNext Partnership for Innovation and Education (PIE) Fellowship program, organizing workshops on molecular biology techniques and 16S rRNA gene sequencing for the student fellows in the program. This outreach activity involved student fellows from SCSU, CCSU, University of Hartford, Trinity College, University of St. Joseph, and Capital Community College, in addition to student fellows from UConn.

MCB Ph.D. and Professional Science Master's (PSM) Career Panel, Fall 2019.

MCB Undergraduates

Awards

University Scholars

The following MCB undergraduate majors were named 2019 University Scholars (of 20 total Scholars). University Scholars is a prestigious UConn undergraduate program in which students design and pursue an in-depth research project and craft individualized plans of study during their final 3 semesters.

Marlene Abouaassi, MCB and Sociology. “Study of Putative Niche Adapting Operon in Microbes Inhabiting the Gut of Blood Digesting Animals,” Committee: J. Peter Gogarten, MCB (chair); Joerg Graf, MCB; Simon Cheng, Sociology
Grace Nichols, MCB, “Understanding Tinnitus at the Electrophysiological Level,” Committee: Douglas Oliver, Neuroscience, UConn Health (chair); Monty Escabi, Electrical and Computer Engineering; Charles Giardina, MCB

Outstanding Senior in MCB Award

Awards presented for talks given during the 5th Annual Undergraduate Research Colloquium in Molecular and Cell Biology

Co-winners:

Brian Aguilera, MCB, “CD13 Regulates Integrin Recycling in the Formation of Tunneling Nanotubes ,” Thesis Advisors: Dr. Mallika Ghosh/Dr. Linda Shapiro

Jennifer Messina, MCB, “The Signaling Pathways of Metallothionein-Mediated Chemotaxis in Breast Cancer ,” Thesis Advisor: Dr. Michael Lynes

IDEA Grant Awardees

The UConn IDEA Grant program awards funding to support student-designed and student-led projects, including creative endeavors, community service initiatives, entrepreneurial ventures, research projects, and other original and innovative projects. Awards can be up to $4,000 per student.

Marlene Abouaassi ’20; MCB & Sociology, “Study of Putative Niche Adapting Operon in Microbes Inhabiting the Gut of Blood Digesting Animals,” Mentor: Peter Gogarten, Molecular and Cell Biology

Alyssa Addesso ’20; MCB, “Exploring the Relationship Between the Microbiome and Immune System in Zebrafish,” Mentor: Sarah Knutie, Ecology & Evolutionary Biology

Nathalia Hernandez ’20; MCB & Spanish, “Identifying Electrode Placement in the Hippocampus Using the Microorganism Bacillus subtilis,” Mentor: Etan Markus, Psychological Sciences

Amanda Pan ’20; Pharmacy Studies & MCB, “Formulation of Acetaminophen for Rapid Dissolution and Absorption Sublingually,” Mentor: Diane Burgess, Pharmaceutical Sciences

Valeria Sarmiento ’20; MCB & IMJR: Global Health & Nutrition, “Investigating the Mechanisms of Plastid Division in the Human Pathogen Toxoplasma gondii,”Mentor: Aoife Heaslip, Molecular and Cell Biology

Phi Beta Kappa Inductees

Congratulations go out to those of our majors in Molecular and Cell Biology, Structural Biology and Biophysics, and Biological Sciences for their election to Phi Beta Kappa in 2019!

Membership in Phi Beta Kappa is by invitation only and is nationally recognized as a rare and special distinction. Selection is conducted annually by the UConn faculty, staff, and administrators who comprise the UConn PBK Epsilon Chapter of Connecticut and is based on several factors, including a student’s excellent academic record and the depth and breadth of their coursework in the Liberal Arts and Sciences.

Ryan Kelly, Noelle Khalil, Sumanya Kumar, Anika Makol, Allyssa Matz, Akriti Mishra, Magda Mocarska, Nazli Morel, Shana Morel, Nehal Navali, Amy Nelson, Grace Nichols, Derek Pan, Natasha Patel, Radha Patel, Usra Qureshi, Twisha Shah, Gagganpreet Singh, Raven Vella, and Seungi Yu

Lt. Paul Drotch Memorial Scholarship

MCB majors **Emily Blackburn, Dylan Feldmeier,** and **Kanika Malani**

Todd M. Schuster Award

Liting Liu, MCB, Knecht Laboratory

SURF Awards

Summer Undergraduate Research Fund (SURF) Awards support University of Connecticut full-time undergraduate students in summer research or creative projects. SURF awards are available to students in all majors at all UConn campuses. SURF project proposals are reviewed by a faculty committee representing various Schools and Colleges, and SURF award recipients are chosen through a competitive process. The maximum total amount awarded for SURF awards is $4,000 ($3,500 stipend for the student researcher and up to $500 for consumables associated with the research project).

Lauren Alexandrescu ’20; MCB & Structural Biology and Biophysics, “Investigating the Roles of Long Non-Coding RNAs in Picornavirus Infections,” Mentor: Simon White, MCB

Halle Barber ’20; Chemistry & MCB “Development of a Novel DNA Crosslinked Nanocapsule for Diagnostic and Therapeutic Applications,”Mentor: Jessica Rouge, Chemistry

Helen Bian ’21; MCB & Spanish, “Functional Classification of Known and Novel Single Nucleotide Polymorphisms Associated with Chronic Lymphocytic Leukemia Predisposition,” Mentor: Dr. Leighton Core, MCB

Chenghong Deng ’20; MCB & Psychological Sciences, “The Genes Expressed in Frog Skin and their Role in Evolutionary Innovation ,” Mentor: John Malone, MCB

James He ’21; MCB, “LHX2 and LMX1B Regulation of Supratentorial Ependymoma Tumor Growth ,” Mentor: Joseph LoTurco, Physiology and Neurobiology

Kelsey Hebert ’20; MCB, “Investigating WDR73 and Fmn1 in the Microtubule Cytoskeleton and Disease,” Mentor: Kenneth Campellone, MCB

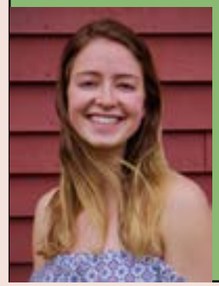
Timothy Mason ’20; MCB, “Investigating the Regulation of Centromere Size in *D. melanogaster*,” Mentor: Barbara Mellone, Molecular and Cell Biology

Grace Nichols ’20; MCB, “Evaluating the Effectivity of Tinnitus Induction in Mice through Behavioral Screenings,” Mentor: Douglas Oliver, Neuroscience

Fabio Saccomanno ’20; MCB, “Proving the Relationship between Wdr73 and Asymmetric Organogenesis in Zebrafish,” Mentor: David Daggett, MCB

Inglis Tucker ’20; MCB, “Characterizing the Virome of Two Species of Wild Migratory Birds,” Mentor:. Sarah Hird, MCB

Alyssa Mathiowetz, MCB `18, was awarded an NSF Graduate Fellowship. Mathiowetz is currently a PhD student in the Metabolic Biology program in the Department of Nutritional Sciences and Toxicology at the University of California - Berkeley.



MCB PSM/PM/PhD Career Panel

In fall 2018, the MCB PSM and PM programs, in conjunction with the GO:MCB graduate student organization, organized an MCB alumni career panel for the MCB PSM, PM, and Ph.D. students. This event was sponsored by MCB and the MCB PSM programs. The MCB PSM programs invited the following MCB Ph.D. and PSM alumni as panel participants: Dr. Lindsey Cambria (Ph.D. Microbiology), Senior Support Scientist, Roche; Matthew Capozziello (M.S. Applied Genomics), Lab Coordinator, Sema4; Courtney Gunter (M.S. Microbial Systems Analysis), Program Manager, The Jackson Laboratory for Genomic Medicine; and Brendan Tierney (M.S. Applied Genomics), Senior Associate Bioanalytical Scientist, Pfizer.

Your contributions to MCB are appreciated.
To give, visit https://mcb.uconn.edu/giving/

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Scenes from the 2019 MCB Retreat at Avery Point