GLOUCESTER MARINE
GENOMICS INSTITUTE

**GMGI Science Forum**
**Saturday, May 14, 2022**
**Speaker Biographies and Abstracts**

## Christopher J. Gobler, PhD

*Endowed Chair and Professor, School of Marine and Atmospheric Sciences, Stony Brook University, Director of the New York State Center for Clean Water Technology*

Christopher J. Gobler is an Endowed Chair and Professor within the School of Marine and Atmospheric Sciences (SoMAS) at Stony Brook University. He received his M.S. and Ph.D. from Stony Brook University in the 1990s. He began his academic career as a professor at Long Island University (LIU) in 1999. In 2005, he joined Stony Brook University as the Director of Academic Programs for SoMAS on the Stony Brook – Southampton campus. In 2015, he was named Director of the New York State Center for Clean Water Technology. He has been editor-in-chief of the in international, peer-reviewed scientific journal, Harmful Algae, since 2018. He has published more than 200 manuscripts in peer-reviewed journals that explore the linkages between anthropogenic activities and coastal ecosystems.

### Decoding harmful algal blooms using molecular tools

Harmful algal blooms (HABs) are a significant threat to coastal ecosystems, fisheries, and public health, and the fraction of the US coastline experiencing HABs significantly increased from 1990 to 2020. While the ecophysiology of HABs has been studied for decades, a comprehensive understanding of these events has been limited by their complex nature whereby the causative species exists within a diverse plankton community. While deciphering the response of an individual HAB, therefore, represents a 'needle in the haystack' problem, the use of molecular tools has facilitated a series of key discoveries regarding HABs during the past decade. Using the brown tide-causing picoplanktonic pelagophyte, *Aureococcus anophagefferens*, as a model HAB, genome sequencing and the use of transcriptomics has yielded a series of key insights regarding how this species interacts with its environment and other organisms to form HABs. This talk will highlight the dynamic nature of the transcriptional response of the brown tide alga over the course of HABs and how the environmental factors controlling blooms change during bloom initiation, peak, and decline. Observational and experimental data will also be presented regarding the manner in which specific gene sets may be activated to cause harm to predators, allowing blooms to further proliferate.

**Christopher Dupont, PhD**
*Associate Professor, J. Craig Venter Institute*

Chris Dupont is an Associate Professor in the Genomic Medicine, Environment & Sustainability, and Synthetic Biology groups at JCVI. His primary research focus is microbial physiology and the environmental and evolutionary influence on physiological variation. This involves work with model organisms in laboratory systems, domestication of wild microbes for model studies, and sequencing based profiling of microbial communities in a variety of environments, including organismal microbiomes. This includes metagenomic and metatranscriptomic studies of the microbiomes found in the human gut, respiratory pathways, skin, and oral surfaces. Dr. Dupont is also working on applying synthetic biology and machine learning techniques to solve unique problems in big datasets associated with the human microbiome and the environment. Dr. Dupont began his career at JCVI as a postdoctoral fellow. He received his PhD in oceanography from the Scripps Institution of Oceanography, as well as a bachelor's in natural resources and a master's of biological and environmental engineering from Cornell University.

**Genomic and synthetic biology toolkits in a model marine diatom**

Diatoms are phytoplankton with rapid growth rates, thus forming the base of some of the most productive aquatic ecosystems in the world. They are also oleaginous and form intricate biosilica “shells,” making them organisms of interest for the biological production of chemicals or materials. Despite being photosynthetic, the evolutionary history, and thus presumably metabolism, of diatoms diverges substantially from that of the classical algal or plant model systems. This presents both a challenge, in an inapplicable existing knowledge base, as well as an opportunity for novel metabolisms expanding the possibilities for engineering successful bioproduction pipelines. The combination of genomics and synthetic biology has resulted in the elucidation of multiple biochemical pathways that are chimeras of enzymes with plant, metazoan, and bacterial evolutionary histories, including a urea cycle, mitochondrial nitrogen assimilation, and stereo-promiscuous lysine biosynthesis. To jump start further discovery, artificial chromosome technology was developed and used to elucidate the diatom centromeres. To augment these chromosomes, a library of endogenous promoters was domesticated and characterized, providing valuable tools for future metabolic engineering or pathway introduction. Finally, we have assembled a genetics parts registry for diatoms in a recursive DNA fabrication system that allows for community dissemination, integration, and education.

**Michael J. Metzger, PhD**
*Assistant Investigator, Pacific Northwest Research Institute*

Michael Metzger earned a master's degree in epidemiology and a PhD in molecular and cellular biology at the University of Washington. He completed a short postdoctoral fellowship in basic science at the Fred Hutchinson Cancer Research Center, followed by a postdoctoral fellowship in Dr. Stephan Goff's lab at Columbia University — where he first identified transmissible cancer in clams. Dr. Metzger has established a lab at the Pacific Northwest Research Institute (PNRI) in 2018 as an assistant investigator to investigate these transmissible cancers. He is an affiliate faculty member of the University of Washington's Molecular and Cellular Biology Graduate Program and the Department of Genome Sciences.

**Chromosome-scale assembly of the genome of the soft-shell clam (*Mya arenaria*) and genomic analysis of their contagious cancer**

Sam Hart[1,2], Marisa Yonemitsu[1], Brian Beal[3], Michael Metzger[1,2]
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Cancer is normally an evolutionary dead-end—neoplastic cells that arise and evolve within an organism either regress or they kill their host, and the death of the host marks the death of the cancer lineage. However, in some cases, neoplastic cells develop the ability to spread from individual to individual, turning from conventional cancers into clonal contagious cancer lineages. The natural transmission of cancer cells has been observed in two mammals (Tasmanian devils and dogs), and we have found that a leukemia-like disease in soft-shell clams (*Mya arenaria*) is due to the horizontal spread of a clonal transmissible cancer lineage. We have also found independent transmissible neoplasia lineages in other bivalve species, including other clams, mussels, and cockles. We have assembled a phased, chromosome-scale reference genome for *Mya arenaria* using PacBio sequencing scaffolded with HiC data. Using this reference genome, we are investigating genomic changes in the evolution of the unique *Mya* transmissible cancer lineage, including SNVs, structural variation, transposable element amplification, and copy number variation. In particular, we have found that the roughly tetraploid genome is not due to a simple genome duplication—instead, it is characterized by complex rearrangements with variable copy-number levels and translocations on a massive scale throughout the genome. We observe many copy-number changes between the USA and Canadian subgroups of this cancer lineage, although within each lineage, the copy number profile appears stable. We also have identified a unique mutational signature in the somatic SNVs in this cancer lineage, most closely related to a mutational signature found in human B cell cancers. These data show that the *Mya* transmissible cancer lineage is likely hundreds of years old and characterized by ongoing mutation through a variety of mechanisms, providing the raw materials for continued selection as these cells evolve as pathogens spreading through clam populations.

**Bassem Allam, PhD**
*Marinetics Endowed Professor, Stony Brook University, Director of the Marine Animal Disease Laboratory*

Bassem Allam is the Marinetics Endowed Professor at Stony Brook University and Director of the Marine Animal Disease Laboratory (MADL). He earned his PhD from the European Institute for Marine Studies in Brest, France, and performed his postdoc at Rutgers University in New Jersey before joining Stony Brook in 2003. His research centers on the physiology and host-microbe interactions in shellfish, the resistance of these animals to infectious diseases, and how the environment affects these interactions. These activities use a diverse range of experimental and technical approaches ranging from ecological physiology to modern "omics" tools and methods. His work resulted in the publication of over 100 peer-reviewed scientific papers and book chapters on various aspects of shellfish physiology and health (https://you.stonybrook.edu/madl/publications/). His current collaborative research includes the development of marker-assisted and genomic selection for bivalve resistance to disease and environmental stress. In parallel, his group has been developing functional genomics methods (e.g. gene silencing) to link bivalve traits to particular genomic features. Understanding how genotype-environment interactions affect shellfish performances has also been an area of interest to his group.

**Multi-omic approaches to reveal interactions between the hard clam and its parasite QPX: from basic research to applications**

The hard clam or northern quahog, *Mercenaria mercenaria*, is one of the most valuable shellfish species along the east coast of the United States, representing the first marine resource in several states. In addition to their economic value, hard clams, like other suspension feeding bivalves, play an important ecological role in benthic-pelagic coupling. Since the 1990's, several Northeastern states have suffered severe losses in aquacultured and wild hard clam stocks due to a fatal disease caused by a protistan parasite called Quahog Parasite Unknown (QPX, recently described as *Mucochytrium quahogii* gen. nov., sp. nov.). In this framework, an understanding of host-parasite interactions and the development of disease mitigation strategies have become a primary research priority. This presentation will summarize our findings on host-parasite interactions using a complementary set of high-throughput genomic, transcriptomic and proteomic methods. Transcriptomic (RNASeq) profiling of infected clam tissues and parasite cultures allowed the identification of QPX transcripts produced in clams during infection. In parallel, these investigations allowed the identification of host factors and molecular pathways potentially involved in clam response to the infection. Proteomic methods allowed the identification of host factors that recognize and bind parasite cells in vitro. Finally, RADSeq methods contrasting allele frequencies between naïve clams and clams that survived QPX epizootics allowed the identification of genetic markers (SNPs) associated with disease resistance. Genomic resources generated throughout these investigations have been used to develop an efficient and cost-effective genotyping platform (SNP array) for *M. mercenaria.* This platform is being validated as a breeding tool to enable genomic selection for QPX disease resistance.

**Ahmed Zayed, PhD**
*Research Scientist, The Ohio State University*

Dr. Zayed's research spans environmental, medical, and pharmaceutical microbiology, and aims at understanding the interactions happening between microbes and their environments across different ecosystems. Employing cutting-edge bioinformatic and high-throughput tools, his research led to the discovery of hundreds of thousands of DNA/RNA viral sequences and thousands of microbes in the global ocean, human/animal bodies, and carbon-rich soils. He finished his Ph.D. in Microbiology in 2019 from the Ohio State University, where he is currently conducting his research on the ecology and evolution of RNA viruses. Dr. Zayed is also part of the leadership team of the EMERGE Biology Integration Institute which aims at understanding microbial acclimation, assembly, and adaptation processes in complex, dynamic ecosystems.

**Global marine genomics and biodiversity: the viral version**

Marine prokaryotic and eukaryotic planktons play a critical role in the functioning and overall health of the ocean and the entire planet. Viruses infect all forms of life and hence are key modulators of the roles played by the plankton community in the ocean. For example, viruses impact the community structure, evolution, and metabolic outputs of planktons through top-down control, gene flow, and metabolic reprogramming mechanisms, respectively. In this talk, I will present the insights gained from global expeditions such as the *Tara* Oceans and *Malaspina* expeditions on marine viral diversity in the open ocean from pole to pole and from the epipelagic to the bathypelagic layers. These viruses include DNA viruses from dedicated viral metagenomes as well as RNA viruses from prokaryotic and eukaryotic metatranscriptomes. The vast majority of these viruses were previously unknown to science, revealing untapped taxonomic and functional diversity in the ocean, and revising the evolutionary history for major viral groups as inferred from extant sequences. In addition, analyzing the ecological patterns of viral diversity and the potential physical, chemical, and biological drivers of these patterns provided new insights on the global marine zonation of plankton diversity and the potential determinants of this diversity. Even though viruses were sensitive sensors of plankton diversity in these global analyses, they still deviated from their hosts' patterns locally including in the climate-critical Arctic Ocean. Finally, network-guided, cross-validated statistical models applied on the abundances of these viruses across the ocean suggested new roles played by viruses in the export of carbon to the deep ocean.

**Rachel O'Neill, PhD**
*Board of Trustees Distinguished Professor, Department of Molecular and Cell Biology, Director of the Center for Genome Innovation at the Institute for Systems Genomics,*
*Co-Director of the iPS Cell and Chromosome Core, University of Connecticut*

Professor O'Neill received her BA with Highest Honors in Zoology from the University of Texas at Austin in 1992 and her PhD in Genetics and Human Variation from La Trobe University in 1997. Dr. O'Neill arrived at UConn in 1999 and is currently a Professor at the University of Connecticut in the Department of Molecular and Cell Biology, with a joint appointment in the Department of Genetics and Genome Sciences at UConn Health. Prof. O'Neill serves as Director of the cross-campus Institute for Systems Genomics and serves as Director of the Center for Genome Innovation within the Institute for Systems Genomics. Prof. O'Neill received the CT Woman of Innovation Award, the College of Liberal Arts and Sciences Excellence in Teaching Award, was a finalist for the CT Science Center STEM Achievement Award and was recently elected to the CT Academy of Science and Engineering. Prof. O'Neill's research programs employ molecular, cytological and computational approaches to study fundamental processes underlying genome function and evolution. Her comparative genomics approach encompasses several model and non-traditional systems, including human, non-human primates, rodents, marsupials, several marine species of relevance to environmental genomics, microbial communities, and infectious viral communities. She has generated and analyzed genomic sequence for several chromosome-level eukaryotic and prokaryotic genome assemblies and developed novel scripts for improving genome assemblies for organisms utilizing data from multiple next generation sequencing platforms and library types. Part of this effort includes involvement in several consortia, including lead PI on the TE and Repeat annotation for the T2T (Human Telomere to Telomere) Project, Executive Board Member for the Earth Biogenomes Project, and Director of the Deep Ocean Genomes project.

**Deep-Ocean Genomes Project: accelerating discovery of deep-sea adaptions and biodiversity**

The deep sea hosts a broad spectrum of habitats including hydrothermal vents, methane seeps, oxygen minimum zones, seamounts, canyons and trenches with evidence suggesting deep-ocean life is richly diverse and highly adapted. Deep-sea life has overcome unique environmental and biological challenges, including immense pressures (> 15,000 psi), near-freezing to near-boiling temperatures, absence of sunlight, toxic chemical conditions, and diverse energy sources demanding novel physiological and genetic adaptations. Though considered remote to humans, the deep ocean provides increasingly important ecosystem functions, including biogeochemical cycling, carbon sequestration, food supply biomass, bioprospecting and drug discovery, and vast energy and mineral reserves. At the same time, deep-ocean life is more vulnerable than ever given the anthropogenic impacts of increasing acidification, rapid ocean warming, expanding oxygen minimum zones, extractive industries and growing presence of chemical waste, including PCBs and microplastics. In partnership, Woods Hole Oceanographic Institution and the University of Connecticut have established the Deep-Ocean Genomes Project (DOG) as an Affiliate program for the global Earth Biogenome Project. DOG aims to implement genomics technologies and address diverse ecological and evolutionary hypotheses within and across a myriad of species found in deep-sea habitats. A cryo-repository containing > 500 species from > 17 phyla, spanning > 30 habitat types has been developed from > 80 deep-ocean expeditions. We have entered Phase 1 of a ten-year project that will expand through shared mission partnerships, develop technologies and applications for genome sequencing, generate reference genomes, and identify biological innovations for further development. Our EBP-standard genome sequencing and assembly workflow is based on long and short-read sequencing applications that support chromosome-level assemblies, epigenomic profiling, and exploration of gene, regulatory, and noncoding content. Species currently in the phase 1 pipeline include annelids from vents, fish from hadal regions and cnidarians from canyons and seamounts.

**Matthew Harke, PhD**
*Research Scientist, Gloucester Marine Genomics Institute*

Matt Harke is a Research Scientist at the Gloucester Marine Genomics Institute (GMGI) leading the Ecosystem Function and Health program. He is a biological oceanographer by training and his research focuses on understanding the diversity and function of microorganisms in the environment and how that relates to ecosystem function and resilience. Before joining GMGI, he was an Associate Research Scientist at Columbia University's Lamont-Doherty Earth Observatory where he used metatranscriptomics to characterize the distribution, composition, and function of microorganisms in situ and in response to physical and chemical changes. He completed his MS and PhD at Stony Brook University investigating a range of topics including harmful algal bloom ecology (both fresh and marine), benthic-pelagic coupling, and microbial ecology.

**Deep, dark, and diverse – an exploration of hydrothermal vent plume community composition and function**

Matthew Harke[1], Jennifer Polinski[1], Mattie Rodrigue[2], Jason Meyer[2]
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Deep under the surface of the ocean, beyond the reach of the sun, hydrothermal activity supports a vast diversity of organisms promoted by chemosynthetic primary production. These biological hot spots are still sparsely sampled, and our current knowledge is limited to snapshots in space in time. As such, it is still difficult to evaluate the role of isolation and dispersal in shaping the biogeography of deep-sea hydrothermal vents, particularly when considering microbial organisms. In July of 2021, as part of the OceanX Young Explorers Program, we set out to explore the Moytirra vent field along the Mid-Atlantic Ridge north of the Azores, with a goal of characterizing the diversity of organisms inhabiting vent plumes and how community composition and function changes with distance from the vent site. A transect was conducted within a plume collecting samples at 200m intervals across 2.4 km following the plume turbidity gradient. Samples were sequenced using both metabarcoding and metatranscriptome to assess the diversity and function of organisms within the plume and how it relates to biogeochemistry and distance from vent origin.

**Blair Bentley, PhD**
*Post-Doctoral Scientist, University of Massachusetts Amherst*

Blair Bentley is a postdoctoral research associate in the Department of Environmental Conservation at the University of Massachusetts, Amherst. His primary research focus is grounded in using molecular tools for marine conservation, with a strong focus on understanding the impacts of climatic change on sea turtle populations. This work includes the development of genomic resources, and their application to answer fundamental questions related to adaptation, resilience, and vulnerability. Dr Bentley completed his PhD in 2018 at the University of Western Australia, where his thesis addressed the impacts of rising temperatures on sex ratios and mortality in sea turtle embryos. He then completed a postdoctoral research fellowship at Florida Atlantic University in 2019 and subsequently returned to the US for his current research.

**Discovering the secrets of sea turtles with molecular tools to inform conservation**

Blair Bentley, Lisa Komoroske
University of Massachusetts Amherst, Amherst, MA, USA

The ecology, population dynamics, and evolutionary history of sensitive marine species is often poorly understood due to challenges in observing them in situ and limitations on using classic experimental approaches. This is especially true for long-lived, migratory species such as sea turtles with complex life histories that encounter a myriad of anthropogenic threats across large spatial and temporal spans. However, the rapid expansion of molecular technologies to non-model species applications has opened the door to addressing some of the most challenging mysteries in sea turtle biology, many of which have strong ties to the effective conservation of these threatened species. I will share some of our recent research developing and applying molecular tools in sea turtles, including determining relationships between population decline and genomic diversity, potential biomarkers for disease susceptibility, and understanding mating system dynamics to evaluate climate change resilience. I will also highlight what we have learned from recently assembling and analyzing high-quality reference genomes for the leatherback and green turtles, including genes underlying adaptation to life in the sea and divergent demographic histories.

**Sarah Davies, PhD**
*Assistant Professor, Boston University*

Dr. Davies earned her MSc in Biology from the University of Calgary in 2009 with Peter Vize and her PhD in Ecology, Evolution and Behavior from the University of Texas at Austin in 2014 with Mikhail Matz. In 2014, she worked as a postdoctoral researcher at the University of North Carolina at Chapel Hill with Karl Castillo (UNC-CH), Adrian Marchetti (UNC-CH) and Justin Ries (Northeastern University) and in 2016 she became a Simons Foundation Fellow of the Life Sciences Research Foundation. Davies is an integrative biologist and her expertise include ecological genomics, population genetics, physiology, and marine biology. Her research integrates field-based studies, controlled laboratory experiments and genomics to better understand how organisms respond to environmental change. She is specifically interested in understanding how the coral–algal symbiosis is maintained and potentially disrupted under climate change.

**Leveraging facultative symbioses and genomic tools to understand coral bleaching**

The symbiosis between corals and dinoflagellate algae is threatened by climate change, with increasing seawater temperatures resulting in dysbiosis, of this often obligate relationship, termed “coral bleaching”. The obligate nature of this relationship makes understanding the molecular underpinnings sustaining symbiosis challenging, as aposymbiosis is inherently coupled with stress. Facultatively symbiotic corals offer a unique opportunity to uncouple this relationship as they naturally exist in symbiotic and aposymbiotic states. We leveraged two species of facultatively symbiotic corals and their algal symbionts to disentangle how symbiosis is maintained under baseline conditions and perturbed under thermal challenges. We investigated gene expression differences between aposymbiotic and symbiotic host tissues under baseline conditions and identified nitrogen cycling, cell cycle control, and immune responses as key pathways maintaining symbiosis. We also compared responses of symbiotic and aposymbiotic fragments under hot and cold thermal challenges to investigate the role of symbiosis in governing the host's response. Cold stress elicited strong transcriptomic differences regardless of symbiotic state, while the response to heat stress was more muted and dependent on symbiotic state. We then characterized responses of both partners *in hospite* and *ex hospite* to these same thermal challenges and found that symbionts showed muted transcriptional responses in symbiosis suggestive of host buffering. Lastly, we explored the role of heterotrophy in the stress response and found that temperature elicits stronger transcriptomic responses than starvation. Our data highlight the strengths of studying facultatively symbiotic corals and offer key insights into the molecular mechanisms underlying symbiosis maintenance and loss in corals.

**Russell T. Hill, PhD**
*Executive Director and Professor, Institute of Marine and Environmental Technology, University of Maryland Center for Environmental Science*

Russell Hill has served as Director of the Institute of Marine and Environmental Technology (IMET) since 2012. He completed his Ph.D. at the University of Cape Town in 1988 and did postdoctoral studies with Rita Colwell at the Center of Marine Biotechnology (COMB), University of Maryland Biotechnology Institute. He then held a faculty position at COMB, worked for several years at the Australian Institute of Marine Science and returned to COMB where he served as Professor and Associate Director. He is a Fellow of the American Academy of Microbiology and of the Society for Industrial Microbiology and Biotechnology. He has served as President of the International Marine Biotechnology Association and on the Editorial Boards of “Applied and Environmental Microbiology”, “Frontiers in Microbiology“, and “Marine Biotechnology”. Research interests include the biodiversity and functions of marine symbiotic microbes associated with marine invertebrates, particularly sponges. He studies the potential of marine microbes as sources of new drugs. He has an interest in marine microalgae and associated bacteria as a source of biofuel and other products.

## Sponges and their symbionts-a key role in nutrient cycling in coral reefs

Sponges and their bacterial symbionts play important roles in cycling of carbon. Nitrogen and phosphorus in the coral reef environment, in which the surrounding water has very low concentrations of these nutrients. Sponges filter large volumes of water and feed on the bacteria, viruses and dissolved matter in this water, enabling them to concentrate nutrients and potentially provide these nutrients to other organisms in the reef ecosystem. Sponges also contain abundant bacterial symbionts, comprising up to 40% of the weight of the sponges. These symbionts are key in nutrient cycling, including the ability to fix and transform nitrogen. In recent work, we discovered that sponges growing in low-nutrient, coral reef environments contain abundant stores of phosphorus in the form of the energy- and phosphorus-storage compound polyphosphate. Microbial cells present in sponges were shown to contain polyphosphate granules that could comprise up to 40% of the total phosphorus present in the sponge tissue. A cyanobacterial symbiont cultured from sponges was shown to accumulate polyphosphate in culture. Genes implicated in polyphosphate formation were amplified from the sponge holobiont. We have used radiolabelled $^{32}P$ to study uptake of organic and inorganic forms of phosphorus by sponges. The evidence is building that sponges play a key role in concentrating essential nutrients and providing these nutrients to other organisms in reef ecosystems.