GLOUCESTER MARINE
GENOMICS INSTITUTE

2019 GMGI SCIENCE FORUM

SPEAKER ABSTACTS AND BIOGRAPHIES

KEYNOTE SPEAKER:

BARBARA BLOCK, PhD
Professor of Biology, Charles and Elizabeth Prothro Professor in Marine Sciences, Stanford University Hopkins Marine Lab, co-Director of the Tuna Research and Conservation Center

BIOGRAPHY:

Dr. Block's research is focused on how large pelagic fish utilize the open ocean using techniques spanning from genomics to biologging. She and her team have pioneered the successful development and deployment of electronic tags on tunas, billfishes and sharks. The combination of lab and field research has led to a rapid increase in the understanding of movement patterns, population structure, physiology and behaviors of pelagic fish. Dr. Block has built with the Monterey Bay aquarium the Tuna Research and Conservation Center, one of the only land based bluefin facilities in the world. She served as the Chief Scientist for the Tagging of Pacific Predators program (TOPP), organized under the Census of Marine Life. This international program, succeeded in placing 4,000 electronic tags on 23 predators in the North Pacific to understand how pelagic animals use the North Pacific ecosystem. Dr. Block founded the Tag-A-Giant program at The Ocean Foundation to elevate the science and conservation initiatives for bluefin tunas globally and together with her Stanford lab they have placed 2000 electronic tags in Northern bluefin tuna.

Dr. Block began her oceanographic career at Woods Hole Oceanographic Institution with Dr. Francis Carey. She earned a Ph.D. in 1986 at Duke University. She was an Assistant Professor at the University of Chicago before joining the faculty at Stanford University in 1994. Dr. Block has published over 200 peer-reviewed papers, edited two books on tunas, and has received numerous awards for her work including the NSF Young Investigator Award, a MacArthur Fellowship, a Pew Fellowship for Marine conservation, the Rolex Award for Enterprise, and a Benchley Award for Ocean Science. Dr. Block has helped produce multiple films and documentaries with Discovery, Disney and National Geographic, the most recent award-winning film on white sharks is called Blue Serengeti.

https://hopkinsmarinestation.stanford.edu/people/barbara-block

ABSTRACT:

Voyage to the White Shark Café: Using biologging and eDNA data to survey open ocean environs for predators

Apex predators are facing an unprecedented worldwide threat from climate change and overexploitation as these species are a source of protein for humans across the planet. Critical to protection of apex predators is an understanding of the oceanic habitats they occupy. The white shark Café expedition aboard the R/V Falkor (April–May 2018) explored a location far away from any land masses in the North Pacific Subtropical Gyre between the Hawaiian Islands and Baja California. While the region has no obvious surface signatures of elevated productivity, paradoxically it is place where white sharks spend up to 6 months per year. We used satellite tags deployed on sharks in the fall and winter months of 2017–2018, to detect their locations in the Café for an expedition in which real-time sampling was conducted within 24–48h of the presence of the sharks as indicated by the pop-up positions of satellite tags. We combined shipboard oceanographic and bio-acoustic surveys that sampled the epipelagic and mesopelagic ecosystems with eDNA, nets trawls, ROV, and autonomous vehicle (Saildrone and Slocum Glider) surveys. We also used high-resolution numerical simulations to interpret the observations in the context of the regional circulation and its variability. The data is still being processed but the talk will overview the expedition and what we have learned thus far.

AMY TEFFER, PhD
Smith Conservation Postdoctoral Fellow, Dept. of Environmental Conservation, UMass Amherst

BIOGRAPHY:

Amy Teffer is a David H. Smith Conservation Research Fellow based at the University of Massachusetts Amherst and the USGS Conte Anadromous Fish Research Laboratory in Turners Falls, MA. Her current postdoctoral research examines how improving watershed connectivity will affect the disease dynamics of wild brook trout populations in the context of climate change. She uses genetic tools to describe host-pathogen relationships at local and regional scales and inform management and conservation-based decisions. She also currently works with Fisheries and Oceans Canada and the University of British Columbia to study regional pathogen impacts on sockeye salmon productivity and health. She earned her PhD from the University of Victoria, BC and her BSc and MSc from UMass Amherst. Her graduate research investigated cumulative stressor effects on the health and migration success of adult Pacific salmon (PhD) and contaminant cycling in Southern New England marine food webs (MSc).

ABSTRACT:

Using genetics to expand the disease ecology toolbox for conservation science and action

Many of the challenges of characterizing the disease dynamics of wild animal populations can be overcome using genetic tools. For screening purposes, genetic tools can be used to detect and measure genetic material of pathogens in the environment (e.g. water) or host tissues. By complementing pathogen screening with immune-related host gene sequence diversity or expression profiling, shifts in host-pathogen relationships can be detected prior to disease outcomes. I have used genetic tools to improve our basic knowledge of infectious agents affecting wild fish populations and help predict how environmental stressors and host immunity affect disease development and survival. Through experimentation and field studies, I have investigated how cumulative stressors can decouple host-pathogen relationships and enhance pathogen influences on Pacific salmon migration success, survival, and population productivity. As a David H. Smith Conservation Research fellow, I am currently assessing how conservation efforts to improve watershed connectivity (e.g. dam removal) will affect pathogen transmission and disease outcomes in wild brook trout populations under various projected stream temperatures. These applied research projects use genetic information to inform fisheries management (adjusting bycatch limits) and habitat conservation (dam removal prioritization and timing). The field of disease ecology will continue to benefit from the application of novel genetic tools that describe host-pathogen relationships and disease processes to inform conservation efforts.

YUAN LIU, PhD
Biologist, NOAA Fisheries, Northeast Fisheries Science Center

BIOGRAPHY:

Yuan received her Ph.D. in marine science from Stony Brook University in 2013. She is interested in using DNA-based molecular techniques (DNA fingerprinting, Sanger Sequencing and Next Generation Sequencing) to examine community structure, biodiversity, and the interactions between aquatic organisms and their environment. Using high throughput sequencing on partial mitochondrial rDNA amplicons from aquatic environmental DNA (eDNA) samples, Yuan is investigating the finfish communities associated with different oyster farming techniques. This work will provide scientific evidence to evaluate the ecosystem services provided by aquaculture gear. This fall, Yuan will join other NOAA fisheries scientists on R/V Gunther to test how eDNA metabarcoding works in an open ocean environment.

ABSTRACT:

Surveying finfish communities in Long Island Sound using eDNA metabarcoding - where do we go from here?

Environmental DNA (eDNA) metabarcoding was used to characterize finfish communities in a nearshore estuarine environment in Long Island Sound. Monthly sampling was conducted June - August 2017 at two sites with structured habitats: a natural rock reef and a shellfish aquaculture farm about 2 km away from each other. Confidence in molecular identification was improved appreciably by the recent contribution of locally-relevant reference sequences into GenBank and through the use of publicly-available data obtained from local trawling and seining surveys. Comparison between eDNA metabarcoding and trawling surveys on 6/27/2017, the only day when both data types were available, revealed more finfish species detected by eDNA metabarcoding. The high sensitivity of eDNA metabarcoding detected finfish species rarely observed in traditional surveys and showed the potential for this methodology to augment existing literature for finfish species distribution patterns and invasive species detection. Non-metric multidimensional scaling (NMS) analysis of finfish communities achieved a low-stress, 2D solution, and revealed greater variation between samples collected from different months than samples collected from the two different habitats. Similarly, permutational analysis of variance (PERMANOVA) found both the month and the interaction term (month x site) significant, with the latter identifying site as significant only in July and August.

BRIAN PETERSON, PhD
Research Leader and Center Director, USDA National Cold Water Marine Aquaculture Center

BIOGRAPHY

Dr. Peterson grew up in a small farming community in Gooding, Idaho. After earning his B.S. in Animal Science from the University of Idaho in 1992, he worked as a Veterinarian Technician for five years. He returned to the University of Idaho to earn a M.S. in Animal Science and a Ph.D. in Animal Physiology. His dissertation research focused on developing methods to control the endocrine system to make rainbow trout grow faster. In January of 2002, Dr. Peterson joined the USDA-ARS Warmwater Aquaculture Research Unit (WARU) in Stoneville, MS as a Research Physiologist. Dr. Peterson served as Acting Research Leader for the WARU from 2011-2012 and served as Lead Scientist on the project entitled “Improving Catfish Health and Production Performance” until late 2015. He then left MS to become Research Leader of an Atlantic salmon research facility (National Cold Water Marine Aquaculture Center) in Franklin, ME. Dr. Peterson’s interests include fish growth and nutrition, genetics, and disease resistance. Dr. Peterson has authored or coauthored over 60 peer-reviewed publications and has had formal

invitations to over 30 national and international meetings. He currently serves as Associate Editor for the North American Journal of Aquaculture and has adjunct faculty appointments at four universities.

ABSTRACT

Genetically Improved Atlantic Salmon at The National Cold Water Marine Aquaculture Center

Brian C. Peterson, Gary S. Burr, and Michael R. Pietrak.
National Cold Water Marine Aquaculture Center, USDA-ARS, Franklin, ME 04634.
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Atlantic salmon culture is one of the most successful aquaculture enterprises in the world. Production of Atlantic salmon in the U.S is primarily concentrated in the state of Maine. The USDA-ARS National Cold Water Marine Aquaculture Center in Franklin, ME has been developing a genetically improved North American Atlantic salmon. The St. John's River stock was chosen because of fast growth, certification of North American origin, and widespread utilization by industry. Objectives of the program have been to: 1) develop a selection index for carcass weight, fillet color, fat content, and sea lice resistance, 2) evaluate and validate the usefulness of incorporating genomic information into the salmon breeding program, and 3) evaluate the usefulness of a lumpfish (*Cyclopterus lumpus*) selective breeding program.

Our selected and unselected (control line) Atlantic salmon are evaluated with the assistance of industry partners in net pens to simulate commercial conditions. We have observed an increase in carcass growth by approximately 15% for each generation. Two of the most important traits for consumers are omega-3 fat content and color of fillet. We have observed increases in astaxanthin and canthaxanthin concentrations and omega-3 fatty acid content in every year class evaluated.

Selection for resistance to sea lice has been an important component of the breeding program since 2015. Evaluations of phenotypic family based resistance were standardized and conducted across all families in the breeding program. Evaluations are based on replicated small scale infections and the heritability seen across our populations is 0.20. In the fall of 2017, the first year class of families screened under the new program were spawned. The offspring of this spawning are currently being evaluated. In addition to the current challenged based screening, efforts are being made to develop genetic markers and tools to estimate genetic breeding values for all desirable traits.

DIANE KAPAREIKO
Microbiologist, NOAA Fisheries, Northeast Fisheries Science Center

BIOGRAPHY:

In 1980, Diane Kapareiko graduated with a Bachelor of Science degree in Biology from the University of Bridgeport. After participating in a cooperative internship semester at the NOAA Fisheries Milford Laboratory to complete her degree requirements, Diane graduated and was hired as a Biological Laboratory Technician in Microbiology. She has recently completed 35 years in federal service, all at NOAA's Milford laboratory. Diane is the principle investigator for researching and developing probiotics for oysters, beneficial bacterial strains which can prevent bacterial disease and improve hatchery production of Eastern oyster (*Crassostrea virginica*) seed for aquaculture and restoration. In 2016, Diane Kapareiko, Dorothy Jeffress and Gary Wikfors, all of the Aquaculture Sustainability Branch at NOAA's Milford Laboratory, were awarded the Department of Commerce Group Silver Medal for Scientific and Engineering Achievement for this probiotic research as well as negotiating a Cooperative Research and Development Agreement for commercialization.

ABSTRACT:

A New Probiotic Bacterium Improves Survival in Oyster Larviculture

Diane Kapareiko*, Dorothy Jeffress, Lisa Guy and Gary H. Wikfors.
USDOC/NOAA/NMFS/NEFSC, Milford Laboratory
212 Rogers Avenue, Milford, CT 06460. Diane.Kapareiko@noaa.gov

Hatchery production of shellfish seed is necessary for dependable aquaculture production. The livelihood of the U.S. seafood aquaculture industry, valued at $1.5 billion in 2016 (FAO), depends upon healthy larvae. Under intensive cultivation conditions, however, bacterial diseases are considered to be a major cause of mortality in commercial shellfish larviculture. In an effort to improve hatchery production of Eastern oyster (*Crassostrea virginica*) seed for aquaculture and restoration, NOAA's Milford Laboratory has isolated and evaluated a naturally-occurring beneficial bacterial isolate, probiotic strain OY15 (*Vibrio alginolyticus*) from the digestive gland of a healthy, adult Eastern oyster. This benign bacterial strain has shown significant, positive effects upon the survival and disease resistance of oyster larvae in experimental larval trials, improving survival by 20-35% when challenged with a known larval shellfish pathogen B183 (*Vibrio corallyliticus*). OY15 improves survival of oyster larvae by stimulating the immune defense functions of their white blood cells (hemocytes), critical in eliminating pathogens from shellfish and preventing bacteriosis and subsequent mortality. Advancing these efforts to transfer environmentally-compatible methods to prevent disease to commercial oyster aquaculture facilities has led NOAA's Milford Laboratory to partner with public and private companies through Material Transfer Agreements (MTA)

and Cooperative Research and Development Agreements (CRADA) to commercialize probiotic bacterial strain OY15 for use as an economic and stable feed supplement to prevent bacteriosis and improve survival of all life-stages of the Eastern oyster.

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JENNIFER BOWEN, PhD
Associate Professor, Marine and Environmental Sciences Center, Northeastern University

BIOGRAPHY:

Jennifer Bowen is an Associate Professor and Associate Chair of the Marine and Environmental Sciences Department at Northeastern University. Prior to joining Northeastern she was on the faculty at University of Massachusetts Boston. Jennifer did her PhD at the Boston University Marine Program when it was based at the Marine Biological Laboratory and she did post docs at The Ecosystems Center and at Princeton University. Her research program has been funded by numerous awards from the National Science Foundation, including an NSF CAREER award for young investigators.

ABSTRACT:

Not All Nitrogen is Created Equal: Genomic Insights into Salt Marsh Biogeochemistry

Nitrate concentrations in coastal and estuarine waters are increasing around the globe and much research has been done to understand the effects of nutrient enrichment on coastal ecosystems. Nitrate is unique, however, in that it can be used as a fertilizer to increase primary production in nitrogen limited coastal waters or as an important oxygen substitute to fuel microbial metabolisms under anoxic conditions. Determining which of these processes dominates is essential, as the former promotes carbon fixation and storage and the latter may decrease the carbon sink capacity of marshes. Meta-analysis results, as well as results from our own long-term nitrate enrichment experiments, suggest that the stimulation of primary production, measured as aboveground biomass accumulation, is lower when N is added in the form of nitrate. Further, when marsh sediment was exposed to dissolved nitrate we measured greater rates of microbial respiration than we measured under nitrate limiting conditions. Finally, metagenomic analysis, both via short read annotation and through genomic reconstruction, indicate the important shifts in the genomic capacity of the microbial community that results from nutrient addition. Taken together, our research suggests that the dissolved nitrate that continues to enrich our coastal waters may play an important role as an electron acceptor to fuel microbial decomposition of marsh carbon, which could ultimately affect the carbon storage capacity of these critical blue carbon habitats.

PAUL BERUBE, PhD
Research Scientist, Civil and Environmental Engineering, Massachusetts Institute of Technology

BIOGRAPHY:

Dr. Paul Berube is a microbial ecologist. He obtained his Ph.D. from the University of Washington where his doctoral work examined the physiological response of ammonia oxidizing bacteria to starvation. As a research scientist at the Massachusetts Institute of Technology, his work has explored nitrogen cycling processes through the lens of *Prochlorococcus*, an abundant marine cyanobacterium. Using genomics and physiology, his research aims to advance understanding of microbial evolution and ecological interactions between microorganisms.

ABSTRACT:

A Natural History of Prochlorococcus and its Role in Nitrogen Cycling

Prochlorococcus is an abundant marine cyanobacterium found throughout the nutrient poor subtropical ocean gyres. This microorganism harbors high degree of genomic diversity, with a pangenome that is estimated to exceed 80,000 unique genes. In the ocean provinces that *Prochlorococcus* dominates, nitrogen is often the proximal limiting nutrient controlling marine productivity. Understanding *Prochlorococcus'* nitrogen assimilation features can enhance our understanding the ocean carbon cycle and how it is coupled to marine nitrogen cycling. While most phytoplankton can use nitrate to satisfy their nitrogen demands, fewer than half of wild *Prochlorococcus* have the genetic capacity to assimilate nitrate. Overall, the diversity of nitrate assimilation genes in *Prochlorococcus* has been poorly characterized. How is the diversity of these genes, upon which selection ultimately acts, generated and maintained in wild *Prochlorococcus* populations? By examining over 300 culture and single cell genomes, it appears that nitrate assimilation genes have been present in *Prochlorococcus* genomes since they diverged from their closest relative, *Synechococcus*, approximately 650 million years ago. Over time, these genes have been lost from most low-light adapted clades of *Prochlorococcus*, but retained in more recently emerged lineages. Among these are the high-light adapted HLII clade, the most abundant group of *Prochlorococcus* in the global ocean, and the low-light adapted LLI clade. While high-light adapted cells with nitrate assimilation genes appear to be selected for in the surface waters of N-limited systems, the distribution of these genes in LLI *Prochlorococcus* is possibly governed by medium frequency dependent selection. New evidence indicates that a sizable fraction of nitrate transported into some LLI *Prochlorococcus* cells is partially reduced and excreted as nitrite, with the balance assimilated into biomass. Current research is aimed at assessing the potential for nitrite cross-feeding between cells within LLI *Prochlorococcus* populations and the role of emergent metabolic partnerships in facilitating population robustness.

MATTHEW HARKE, PhD
Research Scientist, Gloucester Marine Genomics Institute

BIOGRAPHY:

Matt Harke recently joined GMGI as a marine microbial research scientist. 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, including the influence of mesoscale eddies, volcanic interactions with seawater, artificial nutrient perturbation, diel periodicity, and host-microbiome interactions. He completed his masters and doctoral work at Stony Brook University investigating a range of topics including using filter feeding molluscs as top-down controls of the brown tide forming pelagophyte *Aureococcus anophagefferens* and using transcriptomics to understand how *Microcystis* (a common, often toxic, bloom-forming freshwater cyanobacterium) responds to various sources and concentrations of nutrients (nitrogen and phosphorus) and what factors may be most important in controlling toxin production.

ABSTRACT:

Biological Rhythms in a Diatom and its Symbiotic Partner

Diatom-diazotroph associations (DDA) are globally important microbial partnerships as they are sources of new nitrogen and can have an important influence on carbon export, particularly in oligotrophic waters such as the North Pacific Subtropical Gyre (NPSG). However, relatively little is known regarding the molecular underpinnings of this association or their ecology in situ. Here I present results from a metatranscriptomic study in the NPSG whereby Lagrangian sampling was conducted every four hours for four days. Metatranscriptomes were mined for signals of the diatom host *Rhizosolenia* sp. and its diazotroph symbiont *Richelia* sp. in order to explore possible mechanisms driving their coexistence. Analysis of periodic expression revealed broad diel patterns in the symbiont (25% of transcriptome) relative to the host (2%) as well as coordination in biological processes such as nitrogen fixation, energy acquisition, and carbon fixation. Analysis of co-expression between the host and symbiont highlighted potential mechanisms for exchange of resources such as nitrogen, carbon, and vitamins as well as maintenance of symbiosis. These data provide a first view into the daily rhythms in gene expression for a regionally important DDA. The timing of gene expression across the diel cycle for key metabolic components such as nitrogen and carbon fixation may help to inform models characterizing these components in the NPSG.

GARY M. WESSEL, PhD
Professor, Department of Molecular and Cellular Biology and Biochemistry, Brown University

BIOGRAPHY:

Gary Wessel is a Professor in the Department of Molecular and Cellular Biology and Biochemistry at Brown University. Dr. Wessel's research uses a variety of diverse organisms including sea urchins to understand reproduction, arguably the most important goal of any organism. Using a combination of experimental approaches and recent advances in technology, Dr. Wessel's team has uncovered key mechanisms underlying fertilization, primordial germ cell formation, oocyte development and quality. Dr. Wessel's lab is at the forefront of developing functional genomic tools for mechanistic studies in echinoderm model systems and was one of the first to introduce targeted modifications into the sea urchin genome using CRISPR/Cas gene editing.
https://vivo.brown.edu/display/gwessel

ABSTRACT:

How Do You Make a Germ Line, and How Do I Get One?

Eggs and sperm are the successful result of germ line development, and the primordial germ cells are the embryonic origin for these cells. The mechanism of primordial germ cell specification varies among animals but roughly clusters into inherited or inductive mechanisms. Mammals use inductive mechanisms, that is, cell fate determination based on secreted signaling molecules between cells, during gastrulation to craft their germ line. Tractable model systems to study inductive mechanisms of germ line formation though are limited, but recent progress points to sea star embryos as an important model for primordial germ cell formation. While not a common organism for biomedical research, the sea star has many experimental and strategic attractions especially for studies in development and in the biology of reproduction.
Here I will explain what we are learning in germ line formation by indicative interactions. The mRNAs for germ cell factors, e.g. the RNA-binding proteins Vasa and Nanos, in the sea star initially are present broadly in the embryo and then become restricted to the left side of the embryo where the germ cells form. This restricted retention is essential for successful germ line formation. We find that the TBF-beta signaling factor Nodal, present on the right side of the embryo is required for the restriction of the germ cell factors to the left side. We learned that Nodal specifically restricts germ cell factor accumulation by 1) inhibition of transcription, 2) degradation of mRNAs, and 3) inhibition of tissue morphogenesis. These inductive mechanisms in sea stars appear in sharp contrast to how it works in its near neighbor, the sea urchin. Sea urchins instead appear to use an inheritance of localized factors for germ line formation as seen in e.g. flies, roundworms. Thus, two closely related clades have distinct mechanisms of specifying the germ line and make a strong comparative approach to understand germ line specification.

JOSHUA ROSENTHAL, PhD
Senior Scientist, The Eugene Bell Center, The Marine Biological Laboratory

BIOGRAPHY:

Joshua Rosenthal is a Senior Scientist at the Marine Biological Laboratory (MBL) in Woods Hole, Massachusetts. He received his Ph.D. in Biology from Stanford University and completed his postdoctoral training in biophysics and physiology at UCLA. Before coming to the Marine Biological Laboratory, he rose from Assistant to Full Professor at the University of Puerto Rico's Medical Sciences Campus. Dr. Rosenthal's research focuses on the process of RNA editing from a variety of angles. His group has shown that mRNA recoding is unusually active in cephalopods. They are interested in what it's being used for and how the underlying machinery for RNA editing differs in this taxon. Other projects aim to use RNA editing as a vehicle for therapeutics. Finally, Rosenthal also leads an initiative at the MBL to create genetically tractable marine model organisms.

ABSTRACT:

Rewriting the Cephalopod Neural Transcriptome by Editing mRNAs

Genetic information is stored in DNA and realized in proteins after passing through RNA. Its transient residence in RNA provides a prime opportunity for modification. Changes in DNA are permanent and perilous-those in RNA go away and thus are safer. There are a variety of systems for altering RNA in cells. Alternative splicing, of course, is a well-studied example. My lab focuses on RNA editing through adenosine deamination, a system for introducing point mutations within RNA. All multicellular metazoans use this system, but cephalopods take it to a new level, particularly in their nervous system. I will discuss how cephalopods use RNA editing, the molecules it is targeting, where it is taking place both within and between cells, and how it can respond to changes in the environment. I will also discuss the trade-offs between evolution at the DNA and RNA levels.