2016 GMGI Science Forum Speakers

Titles, Abstracts, Bios

Listed in Speaking Order

Bryan Barney, PhDc
Stanford University, Stephen Palumbi Laboratory, Hopkins Marine Station

9:00am

Highly localized adaptive divergence within supergenes in Atlantic cod (Gadus morhua) within the Gulf of Maine

ABSTRACT

Background: Atlantic cod (Gadus morhua) is known to vary genetically across the North Atlantic and across decades of heavy fishing in Greenland and Newfoundland. Spatial and temporal genetic changes are concentrated in three linkage groups, previously defined by pedigreed linkage mapping analysis, at which gene frequencies correlate with seawater temperature. The full extent and nature of these linkage groups is important information for interpreting cod genetic structure as a tool for future fisheries management.

Results: We conducted whole genome sequencing for 31 individual cod from three sub-populations in the Gulf of Maine. Across all protein coding genes and their promoters, we found 43,553 high frequency Single Nucleotide Polymorphisms (SNPs). We show that pairwise linkage analysis among these SNPs is a powerful tool to detect linkage clusters by recovering the three previously detected linkage groups. We then extend the membership of genes in these linkage groups based on pairwise linkage patterns and differentiation patterns of genes compared among alternative linkage group homozygotes. We find a total of 312 genes in three clusters by combined linkage and FST analysis. Across these genes, we find significant population differentiation among spawning groups in the Gulf of Maine and between Georges Bank and Gulf of Maine. Coordinated divergence among these genes, and their differentiation at short and long spatial scales, suggests that they are acting as linked supergenes in local adaptation of cod populations.

Conclusions: Differentiation between SNPs in linked clusters is the major signal of genetic differentiation between all groups tested within the Gulf of Maine. Our data provide a map of

genes falling into these clusters, allowing an enhanced search for neutral genetic structure for demographic inference and fisheries modeling. Patterns of selection and the history of populations may be possible to identify in cod once larger data sets are available that robustly separate neutral and selected genetic markers.

Bryan's Bio:
Bryan is a Ph.D. candidate (5th year) in Dr. Stephen Palumbi's laboratory at Stanford University's Hopkins Marine Station. His main research focuses on patterns of highly local population adaptation that allow for the maintenance of genetic variation at small spatial scales in high gene-flow species. Using high-throughput DNA sequencing technologies, genome assembly, and genetic variant discovery techniques, he studies patterns of genetic diversity in both intertidal organisms (the California mussel, *Mytilus californianus*), and commercially important species (the Atlantic Cod, *Gadus morhua*) that diverge across highly local environmental mosaics. Understanding the processes and conditions whereby individuals within species may be adapted to different environments is critical both for the appropriate management of commercially important species, as well as for predicting which individuals species may be pre-adapted to human-induced environmental change.

Jeff Kneebone, PhD
Research Scientist
New England Aquarium

9:35am

The importance of spatial ecology in the management of threatened elasmobranch fishes

Jeff's Bio:
Dr. Kneebone, a research scientist in the Anderson Cabot Center for Ocean Life at the New England Aquarium, focuses on the life history, movement patterns, and ecology of large fishes as well as the physical and physiological stress that fish incur when captured during fishing activities. Much of Jeff's doctoral work was conducted in partnership with the Massachusetts Shark Research Program, studying the emergence of a seasonal population of juvenile sand tiger sharks within Plymouth, Kingston, and Duxbury Bay, Massachusetts. His present work focuses on spatial ecology and discard mortality in thorny skates, yellowfin and Bluefin tuna, thresher sharks, and black sea bass, to name a few.

Mark Gasser, MSc
Associate Scientist
Gloucester Marine Genomics Institute

10:10am

Survey in a cup: quantitative detection of jellyfish from environmental DNA

ABSTRACT
Public and scientific interest in jellyfish has grown in the last decade over concerns that anthropogenic pressures are increasing jellyfish populations. Jellyfish proliferations have impacted human industries and been observed overtaking some regional ecosystems. This issue has highlighted the lack of long-term data of jellyfish populations and current obstacles to monitoring: low densities or patchiness in distribution, and ineffectiveness of conventional sampling methodologies. Environmental DNA (eDNA) is a novel, molecular monitoring strategy that detects organisms from DNA (sloughed cells, saliva, gametes, etc.) shed in environmental samples (e.g. soil, water, air). This highly sensitive methodology can serve as an alternative or compliment traditional sampling strategies and is particularly useful for species that are difficult to detect as eDNA does not require targeted observation or capture. To test the feasibility of monitoring jellyfish using eDNA, DNA was extracted from seasonal water samples within the Belgian part of the North Sea (BPNS) and amplified using newly developed universal jellyfish and species-specific quantitative PCR (qPCR) primers to detect and quantify jellyfish eDNA. As proof-of-concept, density estimates from eDNA concentration were used to show the potential utility of eDNA as a quantitative sampling strategy for monitoring jellyfish populations.

Mark's Bio:
Mark is an Associate Scientist at Gloucester Marine Genomics Institute interested in how fisheries management can benefit from genomics and exploring marine organisms as a source of bioactive molecules. Mark received his B.S. in Biology from the University of Maryland, and M.Sc. from Universiteit Gent, Ghent, Belgium. His research thesis investigated the potential of environmental DNA as a marine monitoring tool and is the first documented detection of jellyfish environmental DNA. In addition, he assisted Greece's governmental research organization, Hellenic Centre for Marine Research, on comparing environmental DNA metabarcoding to traditional taxonomic identification for benthic invertebrate community analysis and environmental DNA degradation rates. Mark has been invited to speak on current and future uses of environmental DNA at an international research forum in Galway, Ireland.

Daniel L. Distel, PhD
Director
Ocean Genome Legacy Center of New England Biolabs
Marine Science Center, Northeastern University

11:00am

More than one way to eat a tree: genomics of wood digestion in shipworms.

ABSTRACT

Few animals can eat wood. In the terrestrial world, termites are the major consumers of wood. They get help in digesting wood from enzymes made by their gut microbes. In the ocean, shipworms (wood-eating clams) are the main wood consumers. In shipworms two distinct and surprising ways to live on a diet of wood have evolved, both of which are very different from anything found in the terrestrial world. I will discuss the genomics of wood consumption by shipworms and the surprising tale they tell.

Dan's Bio:

I received my B.S. in Biology from Cook College, Rutgers, University and my Ph.D. in Marine Biology from Scripps Institution of Oceanography, UCSD. I held postdoctoral appointments at Woods Hole Oceanographic Institute, MA at Scripps Institution of Oceanography, UCSD, and at Harvard University, Cambridge, MA. I held joint appointments, first as Assistant then as Associate Professor, in the School of Marine Science and the Department of Biochemistry, Microbiology and Molecular Biology at the University of Maine, Orono. Presently, I am the Director of the Ocean Genome Legacy Center of New England Biolabs at Northeastern University and a professor in the Department of Marine and Environmental Science. I am generally interested in marine biodiversity and specifically in how intracellular bacterial endosymbioses function and drive evolution in marine bivalves. I am also, strangely enough, a leading authority on the biology and systematics of the wood-boring bivalve family Teredinidae (shipworms).

Prarthana Khanna, PhDc
Tufts University, Dept. of Genetics, Sackler School of Graduate Biomedical Sciences

11:40am

Cracking the Lobster Genome: De novo sequencing, annotation and characterization of the Homarus americanus genome and transcriptome

ABSTRACT

We have successfully sequenced, assembled, and annotated the genome and transcriptome for *Homarus americanus*—the North American lobster. The completion and existence of the lobster genome will provide a scientific foundation for all crustacean species. With our collaborators at Gloucester Marine Genomics Institute, Dovetail Genomics, and the University of Prince Edward Island, we have finally solved the large polyploid genome of *Homarus americanus*. The MAKER2 and TRINOTATE pipelines were used to annotate the genome and transcriptome, respectively. Approximately 37,000 genes were identified from the genome and 24,000 from the transcriptome with a 70% to 80% concordance between the genome and transcriptome. We are currently in the process of characterizing the genome and transcriptome, especially in relation to immune system function and the unusual longevity of lobsters.

Prarthana's Bio:

Prarthana is a Genetics PhD candidate in the Sackler School of Graduate Biomedical Sciences at Tufts University where she is co-mentored by Dr. David Walt, University Professor and Professor of Chemistry and Genetics, and Dr. Jill Maron, a leading neonatologist and interim Director of the Mother and Infant Research Institute at Tufts Medical Center. Prarthana holds a Bachelors with Honors in Biomedical Sciences from the University of Western Australia. She has previously worked at Massachusetts Institute of Neurodegenerative Diseases to better understand the genetics behind Huntington's disease using patient samples and animal models. Currently, her research is focused on studying the genetics and proteomics of oral feeding in premature infants using saliva diagnostics and learning how to use bioinformatics to annotate and characterize the lobster genome and transcriptome.

David Wiley, PhD
Research Coordinator for the NOAA Stellwagen Bank National Marine Sanctuary

1:00pm

Conservation Research in the Stellwagen Bank National Marine sanctuary

Dave's Bio:

Dr. David Wiley is the Research Coordinator for the National Oceanic and Atmospheric Agency's (NOAA) Stellwagen Bank National Marine Sanctuary. He received his PhD in Environmental Studies from Antioch University with a focus on environmental decision-making and conservation biology. Dr. Wiley's research has ranged from studying the reproductive and foraging ecology of endangered whales to mapping marine toxic/hazardous dumpsites. He has worked with fishermen to redesign fishing gear to reduce the risk of whale entanglement and pioneered methods to successfully rescue mass stranded whales and dolphins. His research led to the shifting of shipping lanes into the port of Boston, MA as part of an international effort to reduce the risk of ship strike to endangered whales. Currently he is leading a multi-organizational study using advanced telemetry and novel visualization software to explore the underwater behavior of endangered whales and using satellite telemetry to understand the movements and foraging ecology of Great Shearwater seabirds. His results have appeared in numerous scientific journals ranging from Animal Behaviour to Conservation Biology. He is the recipient of numerous awards including a Switzer Environmental Leadership Award, Gulf of Maine Visionary Award, NextGov Bold Award for Scientific Innovation, and the Society for Marine Mammalogy's award for Excellence in Scientific Communication. He has been recognized as NOAA's Employee of the Year for science; Office of National Marine Sanctuary's Science Team of the Year and awarded the US Department of Commerce Individual Gold Medal for Scientific Leadership. He and his family spent much of 2011 in New Zealand conducting research on marine protected areas as part of an Ian Axford (Fulbright) Fellowship. His research has been featured on the Discovery Channel, BBC documentaries, National Geographic, and National Public Television and Radio. He was profiled in the recently published *WILDLIFE HEROES*, as one of the "top 40" wildlife conservationists. He is also adjunct faculty in the College of Science and Mathematics at the University of Massachusetts Boston and affiliate faculty in the Department of Fisheries and Wildlife at Oregon State University.

Walt Golet, PhD
Research Assistant Professor, School of Marine Sciences, University of Maine.

1:40pm

Mysteries of the Migrators Unlocking the Life History Secrets of Atlantic Bluefin Tuna

ABSTRACT

Atlantic bluefin tuna are a large highly migratory species that utilizes the north Atlantic basin to satisfy their foraging and reproductive requirements. Admired since before the time of Aristotle, they have appeared in cave drawings, been stamped into currency, and provided a source of food and commerce in and around the Atlantic for millennia. Specialized morphology and physiological adaptations make them one of the strongest, fastest, warmest and most desired fish in the world's oceans. Such a highly migratory lifestyle poses unique challenges for fisheries managers when one considers this species can cross the entire north Atlantic in under fifty days. Stock assessments, used to evaluate the status of the population, contain high levels of uncertainty due to deficiencies in our understanding of life history. Scientists have been studying bluefin tuna for over a century, but technological advances over the past 20 years have given us unprecedented insight into their life history which has in turn improved our ability to asses and manage the stocks. This presentation will explore some of those advancements, and the new insights they have given us on the life history secrets of the worlds most valuable and sought after fish.

Walt's Bio:

Walt Golet is a Research Assistant Professor in the School of Marine Sciences at the University of Maine, Orono. He holds a joint appointment with the Gulf of Maine Research Institute in Portland Maine. Walt received his B.S. in natural resources at the University of Maine (Orono), and his Masters and Ph.D. at the University of New Hampshire. Walt's lab studies the life history of highly migratory species (tunas, sharks, billfish) and the application of this information to reduced uncertainty in stock assessment models. Walt holds an academic position on NOAA's highly migratory species advisory panel and serves as a technical advisor on the International Commission for the Conservation of Atlantic Tunas (ICCAT) advisory committee and is a regular contributor to the Standing Committee on Research and Statistics at ICCAT.

Andrea Bodnar, PhD
Bermuda Institute of Ocean Sciences, St. George's, Bermuda GE 01

2:20pm

Cancer resistance in marine invertebrates: insight from the sea urchin

ABSTRACT

There is a wide discrepancy in the occurrence of cancer across different animal groups, with high prevalence in some species while it is very rare in others[1,2]. Commercially fished marine animals provide an opportunity to explore this phenomenon because large numbers of animals are studied and the incidence of disease is well documented. It is often generalized that cancer is more frequent in vertebrates compared to invertebrates, and among the invertebrates, occurrence in mollusks is more frequent than in crustaceans and echinoderms[2]. Sea urchins have been noted for the absence of neoplastic disease[2,3], despite the observation that some species are very long-lived (living more than 100 years)[4], they possess high regenerative capabilities[5], and lack an adaptive immune system[6]. Initial studies have demonstrated that sea urchin coelomocytes (immune cells) are highly resistance to DNA damaging agents, invoke a robust DNA repair response and can effectively repair DNA damage[7,8]. Further studies have found varying interspecific natural resistance to DNA damaging agents with a general correlation of resistance to DNA damage and species longevity [7,9]. DNA damage, induced in somatic tissues *in vivo* is accompanied by increased expression of a number of innate immune genes. This suggests a link between the DNA damage response and activation of the innate immune system which may play an important role in the surveillance and removal of damaged cells[10]. Further studies of the molecular, cellular and systemic cancer protection mechanisms utilized by sea urchins may reveal novel strategies with wider implications for the prevention or treatment of cancer in higher animals.

1) McAloose D, Newton AL. 2009 Wildlife cancer: a conservation perspective. *Nat Rev Cancer* 9, 517-526.

2) Robert J. 2010 Comparative study of tumorigenesis and tumor immunity in invertebrates and nonmammalian vertebrates. *Dev Comp Immunol* 34, 915-925.

3) Jangoux M. 1987 Diseases of Echinodermata. 4. Structural abnormalities and general considerations on biotic diseases. *Dis Aquat Organ* 3, 221-229.

4) Ebert T, Southon J. 2003 Red sea urchins (*Strongylocentrotus franciscanus*) can live over 100 years: confirmation with A-bomb ^{14}carbon. *Fishery Bulletin* 101, 915-922.

5) Bodnar AG, Coffman JA. 2016 Maintenance of somatic regenerative capacity with age in short- and long-lived species of sea urchins. *Aging Cell* doi: 10.1111/acel.12487.

6) Hibino T, Loza-Coll M, Messier C, Majeske AJ, Cohen AH, Terwilliger DP, *et al*. 2006 The immune gene repertoire encoded in the purple sea urchin genome. *Dev Biol* 300, 349-65.

7) Loram J, Raudonis R, Chapman J, Lortie M, Bodnar A. 2012 Sea urchin coelomocytes are resistant to a variety of DNA damaging agents. *Aquat Toxicol* 124-125, 133-138.

8) Reinardy HC, Bodnar AG. 2015 Profiling DNA damage and repair capacity in sea urchin larvae and coelomocytes exposed to genotoxicants. *Mutagenesis* 30(6), 829-839

9) El-Bibany AH, Bodnar AG, Reinardy HC. 2014 Comparative DNA damage and repair in echinoderm coelomocytes exposed to genotoxicants. *PlosOne* 9, e107815.

10) Reinardy HC, Chapman J, Bodnar AG. 2016 Induction of innate immune gene expression following methyl methanesulfonate-induced DNA damage in sea urchins. *Biol Lett* 12, 20151057

Andrea's Bio:

Dr. Bodnar was awarded a Ph.D. in Biochemistry from McMaster University in Canada in 1991. Since then she has worked in academic labs (University of London and the University of Singapore), a biotech company (Geron Corporation) and a pharmaceutical company (Hoffmann-La Roche) mainly focused on problems relating to human aging and cancer cell biology. She joined the faculty of the Bermuda Institute of Ocean Sciences (BIOS) in Sept 2003. In the Molecular Biology Department at BIOS her lab is using sea urchins as models to understand the cellular and molecular mechanisms underlying extreme longevity, negligible senescence and resistance to neoplastic disease.

José A. Fernández Robledo, PhD
Bigelow Laboratory for Ocean Sciences

3:15pm

Protozoan parasites of oysters in Maine: epizootiology and biotechnological applications

ABSTRACT

Mollusc bivalves are key components of marine and estuarine environments because, as filter feeders, they play a critical role in maintaining water quality and ecosystem integrity. Bivalves also are an abundant resource for the coastal inhabitants and in most places traditional local harvesting of the natural populations is being substituted worldwide by semi– intensive aquaculture initiatives. Concerns for developing oyster aquaculture include the presence of protozoan pathogens capable of producing significant production loses and, through filter feeding, the ability concentrate human pathogens that put at risk the consumers of raw oysters. *Perkinsus marinus* is a protozoan parasite of molluscs that can be propagated *in vitro* in a defined culture medium, in the absence of host cells. We previously reported that *P. marinus* trophozoites can be transfected with high efficiency by electroporation and proposed its potential use as a "pseudoparasite". We have reported that humanized HLA-DR4 mice fed *P. marinus* do not develop noticeable pathology but elicit systemic immunity support rationale grounds for using genetically engineered *P. marinus* as a new oral vaccine platform to induce systemic immunity against malaria; indeed, we have achi
eved transient expression of two *Plasmodium berghei* genes. Although this heterologous expression system will require optimization for integration and constitutive expression of *Plasmodium* genes, our results represent attainment of proof for the "pseudoparasite" concept we previously proposed, as we show that the engineered *P. marinus* system has the potential to become a surrogate system suitable for expression of *Plasmodium* spp. genes of interest, that could eventually be used as a malaria vaccine delivery platform.

Jose's current position:

Senior Research Scientist at Bigelow Laboratory for Ocean Sciences and Research Scientist at Colby College, Waterville, ME URL: http://www.bigelow.org/research/srs/jose-fernandez-robledo/

Research Gate (Link)

W. Kelley Thomas, PhD
Director, Hubbard Center for Genome Studies
University of New Hampshire

4:00 pm

Sequencing our way towards understanding global eukaryotic biodiversity

ABSTRACT
Abstract: One of the grand challenges is biology is to understand the patterns of evolutionary diversity and ecological roles for the vast unseen "creatures" that inhabit our planet. In the late 1980s the advent of the polymerase chain reaction (PCR) transformed molecular evolution. That methodology ultimately transformed population biology and gave rise to modern day meta-barcoding. In my group we have used these technologies to explore the patterns of diversity in the small eukaryotic phyla and most recently applied those approaches to investigate the consequences of the Deep Water Horizon Oil Spill in the Gulf of Mexico. We now have the opportunity to apply those same approaches coupled to Next Generation Sequencing in an attempt to test for the existence of ecologically meaningful patterns of biogeographic structure among these small organisms long thought to be largely unstructured.

5:00 Keynote Talk:

James J. Collins, PhD
Termeer Professor of Medical Engineering & Science and Professor of Biological Engineering, MIT; Member of the Harvard-MIT Health Sciences & Technology Faculty; Core Founding Faculty member of the Wyss Institute for Biologically Inspired Engineering at Harvard University; Institute Member of the Broad Institute of MIT and Harvard

Synthetic biology: life redesigned

Jim's Bio:
The Collins research group works in synthetic biology and systems biology, with a particular focus on using network biology approaches to study antibiotic action, bacterial defense mechanisms, and the emergence of resistance. Professor Collins' patented technologies have been licensed by over 25 biotech, pharma and medical devices companies, and he has helped to launch a number of companies, including Sample6 Technologies, Synlogic and EnBiotix. He

has received numerous awards and honors, including a Rhodes Scholarship, a MacArthur "Genius" Award, and NIH Director's Pioneer Award, as well as several teaching awards. Professor Collins is an elected member of all three national academies – the National Academy of Sciences, the National Academy of Engineering, and the National Academy of Medicine – as well as the American Academy of Arts & Sciences and the National Academy of Inventors.