SEPTEMBER 12 2015 GMGI SCIENCE FORUM

SPEAKER ABSTRACTS AND BIOS

MORNING SESSION

9:00 am
Overview of genomic trends in marine science

Cindy Lawley, PhD
Sr. Manager Market Development, Illumina

Abstract:

Illumina's goal is to apply innovative technologies to the analysis of genetic variation and function. We place high value on collaborative interactions and this has been critical to our mission in providing scalable flexible solutions to unlock the power of the genome across a variety of markets including what I call "aquagenomics". In this presentation, I will provide an overview of the current needs and future potential needs within aquaculture, fisheries and water sampling through a market development lens.

Biography:

Cindy Lawley has a PhD in Biological Oceanography (UCSD), a master's in Evolutionary Biology (SDSU), and a Bachelor's in Biopsychology (UCSB). She also holds a Single Subject Teaching Credential and taught high school science in northern California before doing her graduate work. At Scripps Institution of Oceanography she used genetic methods as tools to study marine fish populations among the Channel Islands in southern California. She joined Illumina in 2004 and has coordinated the development of over 400 custom Genotyping and Sequencing projects through a variety of roles supporting instrument and reagent sales. She is particularly passionate about lowering the barrier of entry for customers interested in advancing agrigenomic and aquagenomic applications.

9:30 am

Whole genome resequencing reveals the potential for spatio-temporal population structure in Atlantic cod (*Gadus morhua*) in the Gulf of Maine.

Bryan Barney, PhD Candidate
Stanford University

Abstract:

Spatiotemporal patterns of population structure are important factors when implementing fisheries management policies. Historically, subpopulation structure patterns in both time and space have been demonstrated in the Atlantic cod (*Gadus morhua*) throughout the North Atlantic. To aid in cod fisheries management in Massachussetts, we performed whole-genome resequencing on cod samples taken from Georges Bank as well as summer and winter spawners within the Gulf of Maine. We identified 43,553 single nucleotide polymorphisms (SNPs) that were used to assess spatiotemporal population structure between these potential cohorts. Initial clustering analysis shows the potential for population structure, though 2 out of the 11 summer spawning cod were not clustering within their main group. Follow-up analyses of genetic differentiation and linkage disequilibrium patterns show population structure between summer and winter spawning cod, but only when the 2 unusual individuals are removed from the analysis. These patterns of structure between summer and winter spawning cod are tenuous, as no statistical support is provided due to the low sampling size (10 individuals per group). Determining the reason for observing the 2 unusual summer cod is essential for our understanding of structure in this system. As a result of this analysis, we have identified the need to sample several more cod from these cohorts to understand the degree of spatiotemporal structure in this management region.

10:00 am

Genomic analysis reveals new insights on cod population structure around Greenland

Nina Overgaard Therkildsen, PhD
Stanford University

Abstract:

Rapid advances in genomic analysis methods have recently opened completely new opportunities for detecting population structure and local adaptation in marine organisms. I will describe how we have taken advantage of these new tools to improve our understanding of fluctuations in cod abundance around Greenland over the past century. We genotyped a panel

of >900 gene-associated markers in 847 individuals collected over a 78-year period spanning major demographic changes. These data revealed the existence of four genetically distinct populations and showed that the spatial distribution of each of these populations had varied considerably over time. The genetic composition had remained stable over decades at some spawning grounds, whereas complete population replacement was evident at others. We have now developed a cost-effective genetic assay that can be used to assign individual cod to their population of origin. This type of assignment is useful both for further retrospective analysis of historical patterns and for prospective monitoring to promote more sustainable fisheries management. We have therefore optimized a pipeline for efficient low coverage genome sequencing, which will facilitate development of similar tools for other fish stock complexes.

Biography:

Nina Overgaard Therkildsen is currently a postdoctoral researcher in the laboratory of Professor Stephen R. Palumbi at Stanford University, but will join the Department of Natural Resources at Cornell University as an Assistant Professor in January 2016. She is keenly interested in developing ways to leverage genomic analysis to improve fisheries management. Using both contemporary and historical DNA samples, her research aims to characterize population structure in exploited species and shed light on how different populations respond to fishing pressure and other human-induced impacts. She holds a PhD in fish population genetics from the Technical University of Denmark, an MSc in biology from the University of Copenhagen, Denmark and a BA in human ecology from College of the Atlantic, ME.

11:00 am

New approaches to genome assembly through mapping 3D chromosome folding

Job Dekker, PhD
Howard Hughes Medical Institute, Program in Systems Biology, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School.

Abstract:

Despite advances in DNA sequencing technology, assembly of complex genomes remains a major challenge, particularly for genomes sequenced using short reads, which yield highly fragmented assemblies. Here we show that genome-wide in vivo chromatin interaction frequency data, which are measurable with chromosome conformation capture-based experiments, can be used as genomic distance proxies to accurately position individual contigs without requiring any sequence overlap. We also use these data to construct approximate

genome scaffolds de novo. Applying our approach to incomplete regions of the human genome, we predict the positions of 65 previously unplaced contigs, in agreement with alternative methods in 26/31 cases attempted in common. Our approach can theoretically bridge any gap size and should be applicable to any species for which global chromatin interaction data can be generated. We are in process to assemble the genome of several marine species. It can also be used to deconvolute complex metagenomic marine samples into gene sets and genome assemblies at the species level.

11:30 am

Tackling complex genomes with *in vitro* proximity ligation from Dovetail Genomics, LLC.

David Walt will provide overview of the "*In Vitro* Proximity Ligation" method to build genome assemblies, followed by a project update on the GMGI/Dovetail collaboration on the lobster genome assembly.

AFTERNOON SESSION

1:00 pm

Examining American Lobster Host-Pathogen-Environment Interactions Using Transcriptomic Approaches

K. Fraser Clark[1,2] and Spencer J. Greenwood[1,2]
[1]Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada.
[2]AVC Lobster Science Centre, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada.

Abstract:

The northwestern Atlantic lobster fishery is the key economic driver for hundreds of rural communities in Atlantic Canada and New England. This wild fishery represents more than $2 billion annually going directly into local economies. The AVC Lobster Science Centre in Charlottetown, Prince Edward Island, Canada has recently begun using transcriptomic

techniques such as oligonucleotide microarrays and RNA-Seq to address basic and applied research questions that are critical to ensuring the health and sustainability of the American lobster fishery. The focus of this presentation will be our recent achievements investigating lobster health, immunity and the effects of long-term live lobster storage and shipment. Highlights will include the lobster immune response to bacterial, parasitic and viral pathogens as well as the many biochemical and transcriptomic changes that occur in lobsters during live storage and shipment. Brief descriptions will also be provided on some of our current projects involving the effects of anthropogenic environmental contaminants on larval lobsters and the potential spread of parasitic pathogens through the recent use of alternative baits.

1:30 pm
Sea urchins as models for aging, tissue regeneration and resistance to cancer

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

Abstract:

The oceans are home to many of the earth's longest lived animals with several species of non-colonial marine invertebrates documented to live for more than 100 years. Many of these animals grow and reproduce throughout their lifespans with no apparent functional decline or increase in mortality rate with age. Sea urchins offer a tractable model to study the molecular and cellular mechanisms underlying both negligible aging and lifespan determination[1,2]. Sea urchins grow indeterminately and continually reproduce, and yet different species have very different reported lifespans ranging from 4 to more than 100 years. Studies to date have demonstrated maintenance of telomeres, maintenance of antioxidant and proteasome enzyme activities and little accumulation of oxidative cellular damage with age in tissues of sea urchin species with different lifespans[3,4]. Gene expression studies indicate that key cellular pathways involved in energy metabolism, protein homeostasis and tissue regeneration are maintained with age[5]. The ability to regenerate tissues, assessed by measuring the regrowth of amputated tube feet and spines, is also maintained with age. Localized expression of the stem cell marker Vasa in somatic tissues suggests that multipotent progenitor cells are present throughout adult sea urchins and may contribute to normal homeostasis in addition to regeneration[6]. Long-term maintenance of mechanisms that sustain tissue homeostasis and regenerative capacity may be essential for indeterminate growth and negligible senescence and understanding these mechanisms may reveal avenues to prevent or treat age-related degenerative diseases in humans. Maintenance of tissue homeostasis relies on the accurate regulation of somatic and stem cell activity to balance growth and repair of damage while at the same time avoiding overproliferation. As neoplasms are rarely seen in sea urchins, they provide an additional unique opportunity to understand the regulatory factors involved in long-term tissue homeostasis and regeneration without conferring predisposition to cancer development.

1) Bodnar, A.G. (2009) Marine invertebrates as models for aging research. Experimental Gerontology 44, 477-484.
2) Bodnar, A.G. (2014) Cellular and molecular mechanisms of negligible senescence: insight from the sea urchin. Invertebrate Reproduction & Development, 59:sup1, 23-27, DOI: 10.1080/07924259.2014.938195
3) Francis, N., Gregg, T., Owen, R., Ebert, T. and Bodnar, A. (2006) Lack of age-associated telomere shortening in long- and short-lived species of sea urchins. FEBS Letters 580, 4713-4717.
4) Du, C., Anderson, A., Lortie, M., Parsons, R. and Bodnar, A. (2013) Oxidative damage and cellular defense mechanisms in sea urchin models of aging. Free Radical Biology and Medicine 63, 254-263.
5) Loram, J. and Bodnar, A. (2012) Age-related changes in gene expression in tissues of the sea urchin *Strongylocentrotus purpuratus*. Mechanisms of Ageing and Development 133, 338-347.
6) Reinardy, H.C., Emerson, C.E., Manley, J.M. and Bodnar, A.G. (2015) Tissue regeneration and biomineralization in sea urchins: role of Notch signaling and presence of stem cell markers. PLoS ONE 10(8): e0133860. doi:10.1371/journal.pone.0133860

Biography:

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 and negligible senescence.

2:00 pm
Identification of Key Genes in Embryogenesis of Sea Lamprey

Ziping Zhang, PhD
SUNY Cobleskill

Abstract:

Lampreys are a group of jawless fishes that serve as an important model for studies of vertebrate evolution. The sea lamprey (*Petromyzon marinus*) is one of the most important invasive species in the Great Lakes as it was a major cause of the collapse of native fish populations in the Great Lakes. Genes that contribute to numerous vertebrate traits are activated or inactivated during embryonic development. Through an integrated approach

combining next-generation sequencing, in situ hybridization and other techniques, we profiled gene expression during sea lamprey embryogenesis. About 14,000 transcripts were found throughout the embryonic developmental stages. Statistical analysis of all the genes and embryonic stages were measured based on $\log_2$ calculations for the expressions fold of adjacent stages. After analysis of verifying genetic expression, function, and embryonic importance, several genes (e.g. *pxn, eef1a1, tgfbr1, traf6, smad2, slx4, pcna, exosc10*, *filip1a*, *vit*, *tgm2*, *prox1*, *crygn*, and *sox6*) were identified with statistical significance as well as importance of embryogenesis. In this study, we identified genes from the sea lamprey encoding an ancestral form of skin-predominant *cam* that bears two EF- hand domains. *In situ* hybridization reveals that the four-domain *cam*s are expressed in the nervous system and gut of embryo, similar to the homologous genes in other vertebrates and invertebrates. In contrast, the two-domain genes are expressed in embryonic skin cells. Skin- predominant *cam*s would be vertebrate-specific. Determining the stage- and tissue-specific patterns of gene expression shown by the embryo of sea lamprey in this project will provide information about the control of normal development, evolution of vertebrate traits, and potential targets for sea lamprey management.

Biography:

Dr. Zhang was awarded a PhD from the Department of Biology and Chemistry, City University of Hong Kong, Hong Kong, China and was a Post-doctoral research associate in the Department of Fisheries and Wildlife, Michigan State University. He is currently Assistant Professor, Program in Biotechnology, Department of Natural Sciences and Mathematics, SUNY Cobleskill. His research expertise includes marine biotechnology, recombinant DNA technique, genetics, functional genomics, molecular and cellular biology, environmental toxicology and aquatic model for human disease. Dr. Zhang is a frequently invited or keynote speaker at marine science and fisheries conferences.

3:00 pm

From the deep-sea to Gloucester: Novel microbiome diversity in marine symbioses

Colleen M. Cavanaugh, PhD
Harvard University

Abstract:

Symbiosis is recognized as a dominant force shaping eukaryotic diversity; studies elucidating the nature and function of these interactions are critical for evaluating for the patterns we observe in extant life, from the population to ecosystem level. Partnering microbial genomic and metabolic functionality with eukaryotic structural complexity has enabled many taxa to colonize novel habitats and niches, necessitating reliable transmission strategies for symbionts

and hosts to find each other every generation. Traditionally, symbionts are characterized as being either transmitted vertically from the parental generation or horizontally through the environment. Symbiont evolution is strongly impacted as transmission mode affects gene flow between hosts and the external environment, with vertically transmitted symbiont genomes experiencing increased influence of genetic drift caused by small, regularly bottlenecked populations. However, evolutionary genomic trends in marine animal-bacteria associations are not as clear-cut. The medium may be the critical factor influencing transmission in these associations, as water is much easier to traverse than air. For example, though chemosynthetic bacteria – invertebrate associations are obligate in adults, symbionts of deep-sea hydrothermal vent tubeworms and Atlantic coast bivalves have been shown to experience horizontal transmission events. Using chemosynthetic symbioses as models, I will discuss the impact of vertical vs. horizontal transmission on symbiont genome evolution and on microbial diversity within the host animal and free-living in the marine environment.

Colleen M. Cavanaugh - Bio

Dr. Colleen M. Cavanaugh is the Edward C. Jeffrey Professor of Biology in the Department of Organismic and Evolutionary Biology and Co-Director and founder of the Microbial Sciences Initiative at Harvard University. Her research interests focus on microbial symbiosis and evolution with emphasis on bacteria-animal associations including diversity, transmission strategy, and host-symbiont co-evolution. She has participated in research cruises worldwide with deep-sea dives in the submersible Alvin. With expertise in the study of uncultured bacteria, her research has recently expanded from marine symbioses to the characterization of the microbiome of humans, human models, and wild animals and their role in health and disease. She received her B.G.S. from the University of Michigan, and her M.A. and Ph.D. from Harvard. She was a Junior Fellow at Harvard and currently is a Fellow of the American Association for the Advancement of Science and the American Academy of Microbiology. Dr. Cavanaugh is also a Visiting Investigator at the Woods Hole Oceanographic Institution, an adjunct scientist at the Marine Biological Laboratory, and Speaker for the MBL Society.

3:30 pm

Spatial balancing selection on thermal tolerance in a high-dispersal species: genetic variation in the mussel *Mytilus californianus* at microgeographic scales.

Bryan Barney, PhD Candidate
Stanford University

Abstract:

Understanding spatial balancing selection and the mechanisms through which environmental heterogeneity maintains genetic variation is an important path of research in our understanding

of basic evolutionary processes. While this is normally studied as "local adaptation" over a gradient of hundreds to thousands of kilometers, the spatial scale of environmental variability can be as small as the body size of the organism studied, representing a mosaic of environmental variability within one locality. Here we investigate the California mussel (*Mytilus californianus*) between neighboring mussel beds under potentially different thermal regimes in Pacific Grove, CA. We used RNA-Seq and transcriptomic techniques to discover single nucleotide polymorphisms within expressed mRNA transcripts from sun-exposed and shaded mussels and found signals of selection at a scale of a few meters. Of 173 high-F_{st} SNPs found to be under divergent selection using an outlier analysis, 12 were selected for further validation analysis. A total of 353 samples were genotyped at all 12 loci, and 9 of these were determined to be false-positives. From the three remaining loci, selection was significant between sun and shade mussel beds in the same two out of three paired sites tested, suggesting that selection may be variable even at these small scales. Further analysis of one of these loci evaluates the requirements for a stable polymorphism against the Levene model of balancing selection. Our results show that selection can act to maintain a balanced polymorphism at very small spatial scales in natural populations, though selection must be strong to overcome the homogenizing forces of high migration.