

Session title: Applying Biogenomics to Ecology: From the Molecular to the Ecosystem Level

When? Saturday, February 20, 2010: 8:30 AM-11:30 AM

Where? Room 6D (San Diego Convention Center)

Challenges and Successes of Molecular Biology over the Past 30 Years

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If I should give an "age" to the Molecular Biology Era, I would have to go back more than 30 years ago when researchers succeeded in cloning genes, sequencing them one at the time and expressing them in different organisms. From that time on, the pace of research escalated enormously and led to the sequencing of the genomes of several organisms in the late '90s and to the landmark achievement of sequencing the complete human genome in 2003. All these accomplishments have been translated into real applications in biomedicine, for example in prognosis of diseases and in more targeted therapeutic treatments. The application of Molecular Biology to Environmental Sciences is more recent partly due to more complex problems; however the benefits that such an approach will bring are already clear. The seminar will present successes, challenges and outlook of Molecular Biology starting from Life Sciences and ending in the relatively new field of Molecular Ecology. I will illustrate some key steps of this "evolution" with some examples from my own career, starting as an undergraduate student painstakingly sequencing a human gene promoter, one base at the time to the current transcriptome analysis of the marine diatom, *Thalassosira pseudonana*, an alga.

Molecular Biomarkers: Endocrine Disruptors and Environmental Health

Nancy Denslow , University of Florida, Gainesville, FL

Personal care products and human pharmaceuticals are widely used and have been found in surface waters around the world. These products have been designed to exert biological effects on target organisms, e.g., in the case of pharmaceuticals on humans, but when released into the environment they can also affect aquatic non-target organisms. New advances in next generation sequencing technology have catapulted the use of molecular tools, such as microarrays, to assess the effects of exposures on fish. Microarray technology is a relatively novel tool in ecotoxicology, but the ability to use a global analysis to understand the effects on fish of exposure to mixtures of anthropogenic chemicals has focused interest in this area. Fathead minnows (*Pimephales promelas*) were treated with 17 α -ethinylestradiol, the estrogen antagonist, ZM 189,154, 17 β -trenbolone (androgen) and the androgen antagonist, flutamide. For ethinylestradiol many genes were up regulated including those involved in the production of good quality eggs and sex hormone synthesis while other genes were down regulated by the exposures. Genes altered by trenbolone include those involved in signaling through G-protein receptors, cell cycling, cell adhesion, proteins involved in egg-sperm binding interactions, spermine/spermidine biosynthesis, among others. In the presence of excess antagonist, the gene expression is reversed, but only for some genes. We have identified unique gene expression fingerprints which are robust and clearly distinguish estrogenic from androgenic exposures. Using the validated microarrays we have tested effluents from water treatment plants and animal agricultural areas. Sites chosen were up- and down-stream from water treatment plants or sites receiving agricultural runoff. Expression profiles were unique at each of the locations, suggesting that they each vary in their composition and complexity. Expression changes in key genes such as steroidogenic acute regulatory protein (StAR), estrogen receptors, among others illustrate the presence of endocrine disrupting chemicals. Pathway analysis illustrates toxicity pathways that may be of importance for complex effluents.

Gene Expression Profile Analysis and Environmental Contaminant Exposure

Kevin Chipman , University of Birmingham, Birmingham, United Kingdom

Carson's "Silent Spring" almost 50 years ago was a turning point in awareness of the need to protect the environment from chemicals that have the potential to cause ecological and human harm. However for many subsequent years the methods for assessing the impact of pollutants on organisms was limited to rather crude, insensitive end points. Over the last decade, the rapid expansion of knowledge about gene sequence and function, coupled with "omic" and associated mathematical modeling technologies has provided an unprecedented opportunity to transform environmental monitoring into mechanism-based and sensitive early-warning alerts that can be prognostic and diagnostic of adverse effects. It is the simultaneous monitoring of many of the activities of cells that will provide a more complete "systems" approach to toxicology and to help in understanding modes of toxic action. The focus is thus moving away from measurement of severe acute lethal effects which might leave uncovered detrimental effects on populations, to protecting against more subtle chronic disturbance of organismal function. Since many pollutants enter aquatic environments (see Halpern BS et. al. 2008, Science, 319, 948-952) much work has focussed on fish. Transcriptomic analyses and associated bioinformatic interrogation can reveal the complex responses (in addition to e.g. the expected oxidative stress) in fish exposed to metals. Copper exposure in fish, for example, can produce a gene expression profile that simulates Wilson's disease in humans indicating the relationship between pollutant exposure and known disease mechanisms. Fish from different environments clearly have different gene expression profiles for many reasons. However, we have found that a sub-group of stress-related genes (identified from gene expression analyses following treatment of fish with pollutants under laboratory conditions) can be predictive of the environmental source of fish depending upon their levels of pollution exposure in their environments (Falciani et. al. 2008, Aquatic Toxicology, 90, 92-101). Interrogation of gene expression networks can reveal associations between key nodes of the network with health-related parameters. Thus expression profiles have potential utilisation as complex monitoring biomarkers, more informative than conventional single gene product biomarkers which lack specificity. Collaboration between academia, government regulatory bodies and industry is now extensive internationally to ensure a coordinated development of these novel strategies to contribute to environmental safety.

Marine Diatoms and Their Role in the Ecosystem

Mark Hildebrand , University of California, San Diego, CA

Diatoms are unicellular eukaryotic microalgae that play important ecological roles on a global scale. Diatoms are responsible for 20% of global carbon fixation and 40% of marine primary productivity. Thus they are major contributors to climate change processes, and form a substantial basis of the marine food web. At the cellular level, diatoms are characterized by having cell walls made of silica, and as the largest class of silicifying organisms on the planet, also are major contributors to biogeochemical processes. Diatoms are subject to varying environmental conditions from which they cannot readily escape, and so they must deal with environmental changes by altering cellular metabolism. Although measurement of environmental variables is relatively straightforward, the response of the organism is the critical determinant of the outcome of an environmental change. The organismal response comes from factors at the cellular level, hence monitoring changes in cellular processes is a potentially valuable approach to understanding how environmental factors drive ecological changes. The simplest way to evaluate changes in cellular processes is to monitor changes in gene expression – more specifically, changes in mRNA transcript levels. Our laboratory has focused on examining transcript changes in diatom transport protein genes in response to changes in environmental conditions, and determined that the responses can be complicated, and don't strictly correlate with environmental changes. Two contributing factors to the lack of correlation are the interconnected nature of control mechanisms over different cellular processes, and the lack of correspondence between mRNA and protein levels resulting from translational regulation. There are several options to explore to improve the situation; 1) apply genome-wide surveys to attempt to identify genes that might serve as robust markers for environmental changes, 2) develop multi-gene evaluation approaches on model species with well established environmental responses, or 3) apply metagenomic approaches to environmental populations and determine whether correlation between expressed transcripts and environmental conditions occurs.

On the Verge of Creating Synthetic Life

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The genomics revolution has transformed biology from qualitative phenomenology to structured rigor in many subtle and also not so subtle ways. There are many examples of this transformation in medicine, including personalized medicine for diagnosis, prevention, and cure.

The genomics revolution also offers tremendous potential for game-changing applications for the environment. Environmental genomics has created an entirely new field of scientific exploration by expanding our ways of studying ecological systems. The discovery of a vastly complex microbial diversity is giving us new insights into the intricate machinery of ecological function. Moreover, the realization that ecological function can be viewed in the context of gene function rather than organism function offers intriguing new ways to understand ecological new systems and eventually new mechanisms for rehabilitation. Several game-changing solutions can be contemplated in such wide-ranging applications as bioremediation of mixed chemical-radioactive waste as well as in geo-engineering for climate change mitigation.