

PAG XIII Aquaculture Workshop Report, January 15-16, 2005

In attendance were well over 100 in the morning, with 63 participants signed in from 14 countries; USA, UK, Taiwan, Canada, Belgium, France, Mexico, Australia, Japan, Singapore, Thailand, Sweden, Poland, Norway.

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The workshop was organized to provide an opportunity for invited speakers to present recent developments in comparative genomics, and for members of the aquaculture species group, especially students and postdocs, present an update of their research.

The first speaker, Chris Amemiya, presented an overview of comparative genomics from the perspective of control regions; how to detect them by bioinformatic analysis, how to test for their function, and how they are likely responsible for many QTLs.

Dan Rokhsar presented an overview of the Phycogenomics program at JGI, and how genomic sequencing was enhancing our understanding of the diversity and evolution of life forms. He also reviewed how genomics of algae contributed to our understanding of the carbon cycle, and provided opportunities for the development of silicon-based nanotechnologies. He also explained the JGI Community Sequencing program and gave much helpful advice on how the aquaculture community could approach the issue of requesting funding from this program.

Ben Koop provided an overview of the Canadian Salmon Genomics program (GRASP) and how it was providing insight into the evolution of the salmonids, as well as providing tools for the genetic and functional genomic analysis of multiple salmonid species.

Jonas Almeida provided an overview of the bioinformatic methods by which maximum information could be extracted from sequence collections and from microarray data, and the value of machine-learning approaches to developing models of organism/environment interaction.

Lena Gerwick compared the OSU long-mer array to the GRASP cDNA array as a tool to measure inflammatory responses in trout liver, and documented their comparable performance.

Marta Gomez-Chiarri presented the results of studies showing that Cavortin and histone H4 of oysters are regulated by infection with *Perkinsus*.

Jason Curole discussed the degree of polymorphism in the oyster genome, documenting a high level (up to 3%) of SNPs.

Leslie Mitchell, using the metallothionein genes of Atlantic Salmon, showed that these genes are the products of the ancient salmonid whole duplication genome, and that this event occurred 80-120 Mya.

Eric Peatman presented data that completely revised our ideas of the number of chemokines in fish, showing that their abundance in catfish is similar to that found in mammals.

Javier Robalino showed that shrimp have an innate immune response to viruses inducible non-specifically by dsRNA. When this response was evoked by long dsRNA that was virus specific, essentially complete protection against viral infection could be obtained.

Carlo Artieri showed convincingly that the sex-determining locus of Atlantic Salmon was on Chromosome 2.

Fernanda Rodriguez characterized the TLR3 of rainbow trout and showed that it was inducible by viral infection and challenge with virus (IHNV).

16 January 2005.

Species progress reports were presented (see ANNUAL REPORT) and then each species group went into informal session to plan collaborations and initiatives to advance the genomics of aquaculture species in 2005.