



Dear Aquaculture Genomics Colleagues:

This Newsletter include the following topics:

- *A brief report of the Aquaculture Genome Workshop in San Diego during PAG XIII*
- *Great community efforts for the development of genome resources*
- *Great support of the Aquaculture Genomics/Genetics research community on the White Paper.*
- *Update on Genome Reagent & Tool Development Program*
- *Dr. Caird Rexroad and Dr. Dennis Hedgecock was elected as Chair and Chair-elect, respectively*
- *Shellfish Genome group meet in Philadelphia.*
- *Aquaculture Genomics web page has been re-organized*

1. **A success of the Aquaculture Genome Workshop in San Diego during PAG XIII** on January 15-16, 2005:

Gregory Warr was the organizer for Aquaculture Genomics sessions during PAG XIII. Greg has done a superb job. Please join me in congratulating Dr. Warr for the great success of the Workshop. In attendance were well over 100 in the morning, with 63 participants signed in from 14 countries or areas; USA, UK, , Canada, China, Belgium, France, Mexico, Australia, Japan, Singapore, Thailand, Sweden, Poland, Norway, Taiwan. 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 postdoctoral fellows, 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).**

On the second day of the Workshop (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.

2. **Great community efforts for the development of genome resources:** Several proposals have been submitted to the Joint Genome Institute (JGI) from Aquaculture Genome sector. These include submission of
  - a) A large-scale oyster EST sequencing project submitted by the Oyster Genome Consortium;
  - b) A whole genome sequencing project submitted by the Oyster Genome Consortium;
  - c) A BAC sequencing project of Atlantic salmon submitted by the Salmonids Genome Consortium;
  - d) A large-scale catfish EST sequencing project submitted by the Catfish Genome Consortium;
  - e) A whole genome sequencing project submitted by the tilapia Genome Consortium; etc.
  
3. **Great support of the Aquaculture Genomics/genetics research community on the White Paper entitled “GENOMIC ENABLEMENT OF AQUACULTURED**

**SPECIES”**. In order to advocate for research support for Aquaculture Genomics, a White Paper was prepared by a Steering Committee. We requested community support for this document and received over 300 signatures. Thank you all for supporting this White Paper. To date, the White Paper has been submitted to the officials of USDA, NSF, the National Human Genome Research Institute, and the Joint Genome Institute/Department of Energy. Submission to other agencies are to take place after proper agency and relevant officials are identified. I would like to extend my sincere appreciation, on behalf of the Aquaculture Genomics research community, to the steering committee, to all of you who supported the document, and particularly to Drs. Greg Warr and Paul Gross, who not only made the draft, but also spent numerous hours in revising the document. To see the White Paper, please visit <http://www.genome.iastate.edu/aquaculture/>

#### 4. **Update on Genome Reagent & Tool Development Program: Your Input Needed:**

As reported in the last Newsletter, our group strongly supports the continuation of the USDA Animal Genome Reagents and Tools Development Program. We submitted a White Paper January 2005 to USDA, followed by a White Paper from the National NRSP-8 Species Coordinators requesting the preservation of the program. Dr. Anna Palmisano, Deputy CSREES Administrator for Competitive Programs ([apalmisano@csrees.usda.gov](mailto:apalmisano@csrees.usda.gov)) responded (in an e-mail to Dr. Jerry Dodgson) to the NRSP-8 Species Coordinators request: "Many thanks for your detailed response to our request for input regarding the future of the NRI 43.1 Animal Genome Reagent and Tool Development competitive grants program. The program will continue to be offered (contingent upon the availability of funding). You will note, however, that the program description will be redesigned and refocused beginning with the FY 2006 NRI Request for Applications (RFA). ...” The NRSP-8 National Committee realizes that understanding of the various animal genomes is at a different level for each species. Therefore, for each species, we request the identification of top three priorities. Through communications with species coordinators, we have identified the following top three areas to be the top concern of Aquaculture Species:

1. BAC-based finger printing
2. Integration of linkage and physical maps involving BAC ends-sequencing, mapping of type I markers and BAC-tagged markers to linkage maps
3. Microarray development and application

In addition, several areas were also identified including large-scale EST sequencing and comparative maps and databases/browsers to relate maps and sequences to fully sequenced genomes of zebrafish, medaka, fugu, tetraodon.

Please send in to me ([zliu@acesag.auburn.edu](mailto:zliu@acesag.auburn.edu)) or to your species coordinators, your input for priority areas. To read the White Paper requesting continuation of the Grant Program, please visit <http://www.genome.iastate.edu/aquaculture/>

**5. Dr. Caird Rexroad and Dr. Dennis Hedgecock was elected as Chair and Chair-elect, respectively.** Dr. Caird Rexroad of the USDA ARS National Center for Cold and Cool Water Aquaculture was elected as our Chair for Aquaculture Genomics Workshop 2006 during PAG XIV. If you have any suggestions concerning the organization of Aquaculture Genomics Workshop, please send them to Dr. Rexroad ([CRexroad@ncccwa.ars.usda.gov](mailto:CRexroad@ncccwa.ars.usda.gov)). Dr. Dennis Hedgecock of University of Southern California was elected as the Chair-elect.

6. **Shellfish Genome group meet in Philadelphia.** A group of shellfish genomics researchers met in Philadelphia to communicate on research progress, research needs, and research planning.

7. **Our web page has been re-organized** (<http://www.genome.iastate.edu/aquaculture/>) . Dr. Caird Rexroad and Dr. Zhiliang Hu have done a great job on the web. Of particular attention is the addition of a [Group Discussion forum](#) that serves as a platform for communication within the research community. If you have any particular items to be put on the web or have any suggestions, please let Dr. Rexroad ([CRexroad@ncccwa.ars.usda.gov](mailto:CRexroad@ncccwa.ars.usda.gov)) or Dr. Hu ([zhu@iastate.edu](mailto:zhu@iastate.edu)) know.

*P.S. If you know someone who wishes to be on this mailing list, or if you wish to be removed from this mailing list, please send a note to John Liu ([zliu@acesag.auburn.edu](mailto:zliu@acesag.auburn.edu)).*