

## NRSP-8 Salmonids Aquaculture Research Progress Report for 2012

**Objective 1: Create shared genomic tools and reagents and sequence information to enhance the understanding and discovery of genetic mechanisms affecting traits of interest.**

### CATFISH

**Channel catfish genome sequencing:** To date 60X genome equivalent of Illumina sequences and mate paired reads of 3Kb, 8Kb, and 36 Kb with sequences equivalent to 3.1X, 0.5X, and 0.15X (clonal coverage of 47X, 21X and 27X), respectively have been generated. PacBio sequences equivalent to 9.5X genome coverage with an average length of 3.5 Kb have been generated. The channel catfish genome is under assembly.

**Blue catfish genome sequencing:** Doubled haploid blue catfish were produced and used as template for sequencing using Moleculo's Long Reads product to generate extremely long and accurate reads. A preliminary assembly with only the long reads using 99% sequence overlap identity produced 46,098 contigs with an N50 length of 12.9 kb and N80 length of 8.5 kb. A further 42,141 long reads remained singlets with an N80 length of 4.6kb and N50 length of 7.0kb.

**Transcriptome and annotation resources:** RNA-Seq of the doubled haploid catfish generated a transcriptome assembly including 25,144 unique protein encoding genes, with over 14,000 full-length transcripts. This resources has been used for expression profiling of mucosal surfaces for catfish challenged with the pathogen *Flavobacterium columnare*.

**Microarray development and use:** An Agilent 8x60K microarray is publicly available and has been utilized for profiling channel and blue catfish skin responses to *Aeromonas hydrophila* infection.

### OYSTER

**Oyster Genome Sequence:** International efforts to develop BAC physical maps, large volumes of SNPs and integrated cytogenetic maps culminated in the acquisition of an oyster genome sequence.

### SALMONIDS

**Rainbow Trout Reference Genome sequence:** A pooling and tagging scheme was used for sequencing of the ~15,000 clones of the BAC fingerprinting physical map minimal tiling path (MTP). Sequencing is complete and the assembly is underway. The current version of the assembly is estimated to cover 70% of the rainbow trout genome.

**Rainbow Trout SNP discovery from RADs:** We employed restriction-site associated DNA (RAD) technology to generate a large SNPs data set from deep sequencing of a panel of 11 homozygous lines. The dataset is composed of 145,168 high-quality putative SNPs that were genotyped in at least 9 of the 11 lines, of which 71,446 (49%) had minor allele frequencies (MAF) of at least 18%.

### SHRIMP

**Genome sequencing of Pacific White Shrimp, *Litopenaeus vannamei*:** Due to the high levels of heterozygosity and the complexity of the shrimp genome, it is very difficult to assemble the short reads generated by next-generation sequencing technologies. Efforts have been turned to finding shrimp inbred lines with relatively high homozygosity or sequencing BAC libraries.

**Development of a high-density SNP genotyping platform:** A deep sequencing of restriction-site associated DNA marker (RAD-Seq) method was used to find genetic markers involved in disease resistance in Pacific White Shrimp.

**RNA-seq:** A large scale RNA-seq project was initiated to characterize disease resistance mechanisms in shrimp.

### **STRIPED BASS**

**Striped Bass transcriptome:** A database (> 11,000 entries) for gene transcripts expressed by the striped bass ovary at all maturational stages was developed and published to provide a foundation for gene expression research on reproduction and breeding of the striped bass and its relatives.

**Striped Bass Genetic Map:** The first genetic map of the genome of the striped bass was developed and published. This medium-density linkage map is based on 298 microsatellite markers and is enabling detection of QTL affecting production traits.

**Objective 2: Facilitate the development and sharing of animal populations and the collection and analysis of new, unique and interesting phenotypes.**

### **CATFISH**

Selection for improved growth and filet yield in Year 1 of the Delta Select strain F2 Generation was completed. Channel, blue, and hybrid catfish were raised in intensive raceway environments and phenotyped for selective breeding.

### **SALMONIDS**

Multi-year pedigreed rainbow trout populations phenotyped for plasma cortisol in response to stress, resistance to bacterial cold water disease (BCWD), spleen size, or growth on fish meal free/plant based diets have been developed and propagated for release to industry and identification of biological mechanisms underlying these traits.

### **SHRIMP**

Most of the shrimp populations developed for research are from breeding companies, and mainly support disease resistance studies. Resource populations exist for public and collaborative research.

### **STRIPED BASS**

Broodstock populations have been established in support of genetic improvement programs for *Morone* species. An experimental method for accelerating puberty and maturation of *Morone* species based on administration of the neuropeptide kisspeptin was demonstrated, opening the door to development of practical methods for application to these late-maturing species and pinpointing the proximal signal for maturation of *Morone* species.

**Objective 3: Develop, integrate and implement bioinformatics resources to support the discovery of genetic mechanisms that underlie traits of interest.**

#### **CATFISH**

The catfish RNASeq, ESTs, and related SNP information has been disseminated through the Catfish Genome Database, cBARBEL, <http://www.catfishgenome.org/cbarbel/>, that has generated tens of thousands of hits from over 30 countries.

#### **SALMONIDS**

**QTL Database:** A rainbow trout QTL database is now available through the Animal Genome website of the NRSP-8 bioinformatics group (<http://www.animalgenome.org/cgi-bin/QTLdb/index>) and is being continually updated.

#### **SHRIMP**

A website for the shrimp genomics community will be established, and various kinds of genomics resources for shrimp research will be assembled in the database.

### CATFISH

Li C, Wang R, Su B, Luo Y, Terhune J, Beck B, Peatman E. Evasion of Mucosal Defenses During *Aeromonas hydrophila* Infection of Channel Catfish (*Ictalurus punctatus*) Skin. *Dev Comp Immunol* (in press; <http://dx.doi.org/10.1016/j.dci.2012.11.009>)

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## OYSTER

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### SALMONIDS

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### SHRIMP

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### **STRIPED BASS**

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# Workshop Report

## Theme

Linking Genomic Variation to Phenotype

## Attendees

Number = 83

Countries = 8 (US, Mexico, France, Spain, China, Japan, Canada, Finland)

## Invited Presentations (4)

NGS-Enabled Research Tools for Crops and Livestock

Patrick S. Schnable, Iowa State University

TALEN-mediated gene editing in terrestrial and aquatic species.

Daniel F. Carlson, Recombinetics, Inc.

Use of Single Nucleotide Polymorphisms (SNP) to Fine-Map Quantitative Trait Loci (QTL) in Swine

Gary A. Rohrer, USDA, ARS, USMARC; Amanda K. Lindholm-Perry, USDA-ARS, U.S. Meat Animal Research Center; Steven D. Shackelford, USDA, ARS, USMARC; D.A. King, USDA-ARS, U.S. Meat Animal Research Center; T.L. Wheeler, USDA-ARS, U.S. Meat Animal Research Center; Dan Nonneman, USDA, ARS, USMARC

Ruminations On Lessons To Be Hatched From Genomics Research In Cattle and Goats  
Tad Sonstegard and Curtis P. Van Tassell, USDA-ARS-BFGL

## Contributed Presentations (20)

Association Mapping Of Disease Resistance Traits In Rainbow Trout Using RAD Sequencing

Nathan Campbell, Columbia River Inter-Tribal Fish Commission; Ken Overturf, USDA-ARS; Scott LaPatra, Clear Springs Foods; Richard Towner, Gentec Consulting; Shawn Narum, Columbia River Inter-Tribal Fish Commission

Epigenetic Landscapes In A Marine Mollusc: What DNA Methylation Patterns Tell Us About Gene Regulation In The Pacific Oyster (*Crassostrea gigas*)

Mackenzie Gavery, University of Washington; Steven Roberts, University of Washington

RNA-Seq Analysis Of Stress Response In Rainbow Trout

Sixin Liu, USDA - ARS - NCCCWA; Guangtu Gao, USDA/ARS/NCCCWA; Yniv Palti, USDA-ARS-NCCCWA; Gregory Weber, National Center for Cool and Cold Water Aquaculture; Caird E. Rexroad III, USDA-ARS-NAA-NCCCWA

Characterization Of Specific miRNAs Involved In Maternal-Zygotic Transition In Rainbow Trout Embryos (*Oncorhynchus mykiss*)

Hao Ma, West Virginia University; Mark Hostuttler, National Center for Cool and Cold Water Aquaculture; Hairong Wei, Michigan Technological University; Caird E. Rexroad

III, USDA-ARS-NAA-NCCCWA; Jianbo Yao, West Virginia University

Whole Genome SNP Discovery and Analysis Of Catfish Genetic Diversity  
Luyang Sun, Auburn University; Shikai Liu, Auburn University; Yu Zhang, Auburn University; Jiaren Zhang, Auburn University; Jianbin Feng, Auburn University; Geoff Waldbieser, USDA-ARS; John Liu, Auburn University; Huseyin Kucuktas, Auburn University; Ludmilla Kaltenboeck, Auburn University

Pathgenomics of the Oyster and Transcriptomic Infection Responses Reveals a Highly Evolved Innate Immune System

Linlin Zhang, Institute of Oceanology, Chinese Academy of Sciences; Ximing Guo, Rutgers University; Li Li, Institute of Oceanology, Chinese Academy of Sciences; Guofan Zhang, Institute of Oceanology, Chinese Academy of Sciences

Development Of The Catfish 250K SNP Array

Shikai Liu, Auburn University; Luyang Sun, Auburn University; Fanyue Sun, Auburn University; Yanliang Jiang, Auburn University; Yu Zhang, Auburn University; Jiaren Zhang, Auburn University; Jianbin Feng, Auburn University; Ludmilla Kaltenboeck, Auburn University; Huseyin Kucuktas, Auburn University; John Liu, Auburn University

Genome and Sex Determination Mechanism In Half-Smooth Tongue Sole (*Cynoglossus semilaevis*)

Songlin Chen, Yellow Sea Fisheries Research Institute, CAFS; Guojie Zhang, Shenzhen Laboratory of Transomics Biotechnologies, BGI; Changwei Shao, Yellow Sea Fisheries Research Institute, CAFS; Jun Wang, BGI-Shenzen; Manfred Schartl, University of Wuerzburg; Qisheng Tang, Yellow Sea Fisheries Research Institute, CAFS; Wentao Song, Yellow Sea Fisheries Research Institute,

Production Of Long (1.5kb – 15.0kb), Accurate, DNA Sequencing Reads Using An Illumina HiSeq2000 To Support De Novo Assembly Of The Blue Catfish Genome  
Geoff Waldbieser, USDA-ARS; Michael Kertesz, Moleculo, Inc.; Dmitry Pushkarev, Moleculo, Inc.; Tim Blauwkamp, Moleculo, Inc.; John Liu, Auburn University

Chromosomal Rearrangements In The Genus Of *Salmo*

Song Lin, Simon Fraser University; Jieying Li, Simon Fraser University; William S. Davidson, Simon Fraser University

RNA-Seq Approaches to the Study of Early Interactions Between Catfish and *Flavobacterium columnare*

Eric Peatman, Auburn University

Three Sex Loci and An sdY In Tasmanian Atlantic Salmon

William D. Eisbrenner, Simon Fraser University; Natasha Botwright, CSIRO; Mathew Cook, CSIRO; Evelyn A. Davidson, Simon Fraser University; Sonja Dominik, CSIRO; John Henshall, CSIRO; Stacy L Jones, Simon Fraser University; Peter D. Kube, CSIRO; Krzysztof P. Lubieniecki, Simon Fraser University; Nick G. Elliott, CSIRO; Sophia Peng,

Simon Fraser University; William S. Davidson, Simon Fraser University

Cyberinfrastructure Initiatives for Biology and Opportunities to Involve Aquaculture  
Jeffrey T. Silverstein, USDA-Agricultural Research Service

The Organization Of The Atlantic Salmon (*Salmo salar*) sdY Gene and Its Potential Genomic Environments

Emily I. Palibroda, Simon Fraser University; Krzysztof P. Lubieniecki, Simon Fraser University; Yvonne Y. Y. Lai, Simon Fraser University; William D. Eisbrenner, Simon Fraser University; William S. Davidson, Simon Fraser University

Genome-wide Genic SNPs Development and Association Analysis with Abiotic Stress in the Pacific Oyster *Crassostrea gigas*

Li Li, Institute of Oceanology, Chinese Academy of Sciences; Haigang Qi, Institute of Oceanology, Chinese Academy of Sciences; Jiafeng Wang, Institute of Oceanology, Chinese Academy of Sciences; Zhicai She, Institute of Oceanology, Chinese Academy of Sciences; Fei Xu, Institute of Oceanology, Chinese Academy of Sciences; Linlin Zhang, Institute of Oceanology, Chinese Academy of Sciences; Jinpeng Wang, Institute of Oceanology, Chinese Academy of Sciences; Guofan Zhang, Institute of Oceanology, Chinese Academy of Sciences

Genome-Wide SNP Association Analysis of Body Weight in Atlantic Salmon (*Salmo salar*)

Alejandro P. Gutierrez, Simon Fraser University; Krzysztof P. Lubieniecki, Simon Fraser University; Evelyn A. Davidson, Simon Fraser University; Steve Fukui, Mainstream Canada; Ruth E. Withler, Pacific Biological Station; Bruce Swift, TRI-GEN Fish Improvement Ltd.; Sigbjørn Lien, CIGENE, Norwegian University of Life Sciences; Matthew P. Kent, CIGENE, Norwegian University of Life Sciences; William S. Davidson, Simon Fraser University

Transcriptome and Expression Profiling Of Response To Acute Hypoxia In The Gill Of Adult Catfish

Jianbin Feng, Auburn University; Shikai Liu, Auburn University; Yu Zhang, Auburn University; Jiaren Zhang, Auburn University; Ludmilla Kaltenboeck, Auburn University; Huseyin Kucuktas, Auburn University; John Liu, Auburn University

The Transcriptome Of The Eastern Oyster *Crassostrea virginica* In Response To Bacterial Challenge

Marta Gomez-Chiarri, University of Rhode Island; Ian McDowell, University of Rhode Island; Chamilani Nikapitiya, University of Rhode Island; Saebom Sohn, University of Rhode Island

Diploid and Triploid Hybrids Derived from Female *Megalobrama amblycephala* Yih × Male *Xenocypris davidi* Bleeker

Jie Hu, DFO West Vancouver Lab

Gene Expression in Early Development of Rainbow Trout with Divergent Life Histories  
Garrett McKinney, Purdue University; Frank Thrower, NOAA; Krista Nichols, NOAA

**Poster Session Participants (30)**

## Business Meeting Minutes

Call to order (Liu)

Bioinformatics Update (Reecy) - Stated system open to help all systems. The AnGenMap subscription list is seeing growth. NRSP-8 community file sharing is available, this can be private and public. Animal Genome Tracks can be stored on the site. AnimalQTLdb also highlighted, 100 new papers last year. Future Developments: Helping the community deal with re-sequencing projects. Now available for fish community- correlation database (CorrDB). NRSP-8 Bioinformatics can host services. New effort to get information for aquaculture species gene ontology. Last year spending time with iPlant to develop pipelines for genome resequencing. iRODS overcomes large data transfer issues. iPlant collaborative is open to working with aquaculture community on pipelines.

Recognized and commended Peatman for organizing this year's workshop. Announced that persons should contact Roberts (sr320@uw.edu) with suggestions for next year's workshop speakers and themes.

Recognition of Travel Award Winners (10)

William Eisbrenner  
Song Lin  
Mackenzie Gavery  
Emily Palibroda  
Alejandro Gutierrez  
Luyang Sun  
Jianbin Feng  
Shikai Liu  
Garrett J McKinney  
Jie Hu

Nomination and election for chair-elect  
Nomination: Roger Vallejo  
Voted unanimously as new chair-elect

Request for community to contribute content to newsletter.

**Meeting adjourned 4:55**