

NRSP-8 Aquaculture 2017 Annual Report

Leadership

Coordinator: Steven Roberts, Washington State University

Co-coordinator: Eric Patman, Auburn University, Alabama

Species Leaders:

Catfish: Sylvie Quiniou, ARS Stoneville, Mississippi

Oyster: Dina Proestou, ARS University of Rhode Island, Rhode Island

Salmonids: Yniv Palti, ARS Leetown, West Virginia

Striped Bass: Ben Reading, North Carolina State University, North Carolina

2018 Aquaculture Workshop Report

Workshop Chair: Geoffrey Waldbieser, USDA ARS

Chair elect: Catherine Purcell

Theme

Genome Assembly and Application of Genomic Selection in Aquaculture

Attendees

Number = 50+

Number of institutes: 42

Invited Presentations (4)

- 1. Assembly and Computational Use of Aquatic Genome Models** Wesley Warren, McDonnell Genome Institute at Washington University, St. Louis,
- 2. A Strategy to Assemble High-Quality Reference Genomes for All Vertebrate Orders**, Adam M. Phillippy, National Human Genome Research Institute, National Institutes of Health, Bethesda,
- 3. Assembly and Computational Use of Aquatic Genome Models**, Nuala O'Leary, NIH/NCBI, "The National Center for Biotechnology (NCBI)
- 4. Applied Genomics for Conservation of Distinct Stocks and Phenotypic Diversity in Chinook Salmon**, Shawn Narum, Columbia River Inter-Tribal Fish Commission,

Contributed Presentations (15)

Poster Session Participants (30)

Business Meeting Minutes

Time: Saturday January 13, 2018, 5:30-6:00 pm

Place: Pacific Salon 3/4, Town and Country Hotel, San Diego, CA

1. Call to order. Dr. Steven Roberts called the business meeting to order at 5:30 pm, following the Aquaculture Workshop.
2. Dr. John Liu has stepped down for his role as chair of the NRSP-8 Aquaculture section; he was thanked for his dedicated service in this role. For now, Dr. Eric Peatman will be stepping into that role in Dr. John Liu's place.
3. The Species Coordinator reports have been submitted electronically.
4. FAASG (Functional Annotation of All Salmonid Genomes) initiative kicked off with a meeting in Victoria, B.C., Canada and a white paper (Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture; BMC Genomics. 2017 Jun 27;18(1):484. doi: 10.1186/s12864-017-3862-8.). They will be seeing what will happen with the E.U. efforts with annotation, and they are soliciting ideas for funding projects.
5. RFP Announcements: there will be small funding amounts available from NRSP-8 research grants (these would be in the range of ~\$10k).
6. PAG Aquaculture Workshop Chairs:
 - a. Dr. Geoff Waldbieser was thanked for the wonderful job he did as chair of the 2018 Aquaculture session.
 - b. Dr. Catherine Purcell will be chairing next year's Aquaculture session.
 - c. Dr. Tiago Hori (Center for Aquaculture Technologies) and Dr. Louis Plough (University of Maryland – Center for Environmental Science) were nominated to serve as Secretary (Chair-elect) for the 2019 workshop. As both Tiago and Louis were willing to serve in this role, the positions were decided for the following two years, as follows:
 - i. Tiago Hori: Secretary (Chair-elect) 2019, Chair of the workshop in 2020
 - ii. Louis Plough: Secretary (Chair-elect) 2020, Chair of the workshop in 2021
7. Dr. Caird Rexroad III: Gave updates on the report-in-progress, Genomes to Phenomes: USDA Blueprint for Animal Production. He is trying to ensure that aquaculture is well represented in this report; if anyone would like to contribute to the draft, please contact him. In addition, anyone who wishes to be more involved in this report was invited to the writing workshop for this report on Sunday (January 14th) morning.

8. Discussion on funding priorities: there is a need for groups to get together to collaborate and communicate, and start discussions with the NIFA leaders; aquaculture needs to speak up more to get funding and compete for larger funding amounts. Please share any feedback/experiences about what has/has not been successful.
9. The names of the six travel award recipients were announced [*most not present at the meeting*]: André L. S. Garcia, University of Georgia; Erin M. Roberts, University of Rhode Island; Huitong Shi, Auburn University; Melissa K. Holborn – University of Guelph; Rafael M.O. Silva, University of Georgia; Yujia Yang, Auburn University.
10. Meeting was adjourned.

Objective 1: Advance the status of reference genomes for all species, including basic annotation of worldwide genetic variation, by broad sequencing among different lines and breeds of animals.

Sequenced the YY genome of channel catfish using a YY sequencing template that avoid any X chromosome sequences in the assembly. The genome assembly was validated through linkage mapping of more than 250,000 SNP markers.

Eastern oyster (*Crassostrea virginica*) genome assembly v. 3.0 completed; 99% of sequences are assembled into the known number of chromosomes (10). Gene annotation completed using the automated NCBI pipeline.

The new version of the rainbow trout genome was annotated and released by the NIH-NCBI (GenBank assembly Accession GCA_002163495). Approximately 88% of the new assembly sequences are aligned within chromosomes to generate contiguous chromosome sequences.

A draft genome for Chinook salmon was assembled and submitted to NCBI which was released publicly on December 11, 2017 (accession #s: project: PRJNA402052; genome assembly: PIPH000000000; transcriptome assembly: GGDU000000000). The assembly was produced from a diploid wild male collected in the interior Columbia River (Johnson Creek). We produced a 2.36 Gb genome assembly with 72.2% (1.70 Gb) of the de novo assembly anchored to 34 chromosomes, with contig N50 of 19.1Kb, scaffold N50 of 153.3Kb (prior to chromosome placement), and anchored chromosome N50 of 45.4Mb.

Efforts are ongoing to complete assembly of the striped bass (*Morone saxatilis*) and white bass (*M. chrysops*) genomes using Dovetail Hi-C and Chicago sequencing strategies.

Objective 2: Develop strategies to identify and exploit genes and allelic variation

that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.

Identified a candidate for sex determination gene in catfish through positional and functional evidence. Experimental knockout of the candidate gene converted genetic males (XY) to phenotypic females.

Medium-density Affymetrix SNP array containing ~27K *Crassostrea gigas* SNPs and ~11K *Ostrea edulis* SNPs has been developed.

Expressed exome capture sequencing (EecSeq) method developed using the eastern oyster. NCBI Accession # PRJNA423022.

A 50K transcribed gene Affymetrix chip was built. The chip contains ~21K transcribed SNPs with allelic-imbalances associated with important aquaculture production traits including WBW, muscle yield, and resistance/susceptibility to bacterial cold-water disease. The chip identified major QTL explaining genetic variance of body-weight-gain and muscle yield.

Columnaris disease (CD) is distributed around the world, and recently it has been identified as an emerging problem for the U.S. rainbow trout aquaculture industry. As a first step in developing selective breeding strategies for improving the resistance to CD, we scanned the genomes of two important domestic rainbow trout breeding populations for chromosome segments that contain genes that significantly affect resistance to CD. The research is conducted by scientists from USDA-ARS in collaboration with Troutlodge, Inc.

The striped bass genome sequence assembly was used to evaluate epigenetic markers of sperm quality (DNA methylation status) and gene pathways underlying male reproductive dysfunction.

Domestic white bass when crossed with domestic striped bass were shown to produce sunshine hybrid striped bass with 18% better growth to market size than wild-captured white bass from Lake Erie crossed with domestic striped bass in two independent replicate studies through time.

Objective 3: Facilitate analysis, curation, storage, distribution and application of the enormous datasets now being generated by next-generation sequencing and related "omics" technologies with regard to animal species of agricultural interest.

Hands-on comparative genomics workshop held at the National Shellfisheries Association annual meeting

NRSP-8 supported and facilitated a workshop of the Functional Annotation of All

Salmonid Genomes (FAASG) Consortium: an international initiative supporting future salmonid research, conservation and aquaculture.

A JBrowse integrated web portal of the draft striped bass genome resource is hosted online for use as an unrestricted public resource. Database URL:
<http://appliedecology.cals.ncsu.edu/striped-bass-genome-project/>.

Communication:

- NRSP-8 Aquaculture leaders participated in establishing the FAASG (Functional Annotation of All Salmonid Genomes) consortium. **Impact(s):** The consortium will allow coordinating data sharing and establish an infrastructure for providing high quality functional annotation of salmonid genomes.

Research support mini-grants (coordinator grants):

- Approximately 6 mini-grants (~\$10,000/each) supported projects that fall under all three primary objectives and include a variety of species. Awards listed:
 1. Evaluating the genetic potential for environmental adaptation in eastern oysters through resequencing Marta Gomez-Chiarri et al.
 2. Genetic Variation Related to Growth Performance in Domestic and Wild Striped Bass Benjamin J. Reading et al.
 3. Annotating the rainbow trout genome with Iso-seq technology for FAASG Moh Salem
 4. Target capture sequencing to map the genetic basis of salinity tolerance in *Crassostrea virginica* Morgan Kelly and Jerome La Peyre
 5. Outlining parent-of-origin effects in wild x domestic hybrid striped bass for eQTL potential Jason Abernathy and Adam Fuller
 6. Detection of candidate vAh resistance genes in channel catfish using RNA-seq Rex Dunham and John Liu

Travel support and opportunities for trainings:

- Travel of 6 students/postdocs was funded to attend the Aquaculture workshop at PAG meetings (2018). The purpose of the travel award program is to help graduate students and postdocs to travel to the annual PAG meeting to present their research.
- Awardees:
 - 1) André L. S. Garcia, University of Georgia, “Genomic Evaluation for Harvest Weight and Residual Carcass Weight in Channel Catfish Using Single-Step Genomic BLUP”;
 - 2) Melissa K. Holborn, University of Guelph, “Genome Wide Association Analysis for Resistance to the Causal Agent of Bacterial Kidney Disease in a North American Commercial Atlantic Salmon”;

- 3) Erin M. Roberts, University of Rhode Island, “Differential Expression of Apoptosis Pathway Gene Families in Response to Immune Challenge in *Crassostrea gigas* and *Crassostrea virginica*”;
- 4) Huitong Shi, Auburn University, "Identification of Resistance QTL and Candidate Genes Against Enteric Septicemia of Catfish";
- 5) Rafael M. O. Silva, University of Georgia, “GWAS for Detecting QTL Associated with Columnaris Disease in Two Rainbow Trout Breeding Populations”;
- 6) Yujia Yang, Auburn University, “Identification of Sexually Differentially Methylated Regions in Channel Catfish Provides Evidence of Epigenetic Control of Its Sex Determination”.

Leveraged funds and stakeholders’ use of project outputs

Leveraged funds from diverse projects totaling more than one million dollars from federal sources. Selected grants are highlighted below.

- The Genetic Basis of Low Salinity Tolerance in the Eastern Oyster: Baseline Data for Consistent Aquaculture Production in Coastal Areas, Plough, Louis, \$148,422.
- Sequencing of Y-chromosome and analysis of sex determination in catfish, Liu, John, \$500,000.

Major impact products (could be potential impact):

Draft genomes were assembled for Eastern oyster and Chinook salmon and an improved genome reference was reported for rainbow trout. The new genome references should help in identifying genes in control of economically important aquaculture production traits,

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