**NRSP-8 Salmonids Aquaculture Research Progress Report for CY 2017**

**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.**

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: GGDU00000000). 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. The assembly was annotated with deeply sequenced transcriptomes from eight tissues collected from the same individual fish and integrated with reference models to predict 44,446 gene models having homology with curated Swissprot proteins and 35,696 models that cover more than 50% of a curated Swissprot protein.

This study tested utility of RNA-Seq in assessing phenotype-associated allelic imbalances in pooled RNA-Seq samples. About 50 SNPs were identified in this study, most of them were included in a new SNP-Chip design (available from Affymetrix) for genomic and genetic analyses in rainbow trout.

**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.**

*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.

Identified genomic SNPs associated with thermal adaptation in redband trout (Chen et al. 2017).

Identified landscape features along migratory routes that influence adaptive genomic variation in steelhead (Micheletti et al. 2017).

Identified patterns of selection in natural populations of various salmonid species (coho salmon and Chinook salmon) and candidate genes under selection (Campbell et al. 2017; Narum et al. 2017).

Developed genetic tagging program to monitor anadromous salmonids (Keefer et al. 2017; Matala et al. 2017).

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.

**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.**

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.

Contributed to development of FishGen.net database for storage of large-scale genotypes for genetic tagging and monitoring studies.

The study identified 90 microRNAs with differential expression between families with divergent muscle traits and SNPs present in 3′ UTR of target genes either destroyed or created novel illegitimate microRNA target sites associated with the traits.

**Salmonids publications in 2017:**

The Aquaculture Genomics Genetics and Breeding Workshop, G., Abdelrahman, H., Elhady, M., Alcivar-Warren, A., Allen, S., Al-Tobasei, R., Bao, L., Beck, B., Blackburn, H., Bosworth, B., Buchanan, J., Chappell, J., Daniels, W., Dong, S., Dunham, R., Durland, E., Elaswad, A., Gomez-Chiarri, M., Gosh, K., Guo, X., Hackett, P., Hanson, T., Hedgecock, D., Howard, T., Holland, L., Jackson, M., Jin, Y., Kahlil, K., Kocher, T., Leeds, T., Li, N., Lindsey, L., Liu, S., Liu, Z., Martin, K., Novriadi, R., Odin, R., Palti, Y., Peatman, E., Proestou, D., Qin, G., Reading, B., Rexroad, C., Roberts, S., Salem, M., Severin, A., Shi, H., Shoemaker, C., Stiles, S., Tan, S., Tang, K.F.J., Thongda, W., Tiersch, T., Tomasso, J., Prabowo, W.T., Vallejo, R., Steen, H.V.D., Vo, K., Waldbieser, G., Wang, H., Wang, X., Xiang, J., Yang, Y., Yant, R., Yuan, Z., Zeng, Q. & Zhou, T. (2017). Aquaculture genomics, genetics and breeding in the United States: current status, challenges, and priorities for future research. *BMC Genomics,* 18**:** 191.

Al-Tobasei, R., Ali, A., Leeds, T.D., Liu, S., Palti, Y., Kenney, B. & Salem, M. (2017). Identification of SNPs associated with muscle yield and quality traits using allelic-imbalance analyses of pooled RNA-Seq samples in rainbow trout. *BMC Genomics,* 18**:** 582

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Koganti, P., Wang, J., Cleveland, B., Ma, H., Weber, G., and Yao, J. 2017. Estradiol regulates expression of miRNAs associated with myogenesis in rainbow trout. Molecular and Cellular Endocrinology, 443, 1-14.

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Leeds, T. D., R. L. Vallejo, G. M. Weber, D. Gonzalez-Pena, J. T. Silverstein. 2016. Response to five generations of selection for growth performance traits in rainbow trout (*Oncorhynchus mykiss*). Aquaculture 465:341-351.

Liu, S., Palti, Y., Martin, K.E., Parsons, J.E., Rexroad, III, C.E. 2017. Assessment of genetic differentiation and genetic assignment of commercial rainbow trout strains using a SNP panel. Aquaculture. 468(1)**:** 120-125.

Ma, H., G. M. Weber, H. Wei, J. Yao. 2016. Identification of mitochondrial genome-encoded small RNAs related to egg deterioration caused by postovulatory aging in rainbow trout. Mar. Biotechnol. 18:584-597.

Macqueen, D.J., Primmer, C.R., Houston, R.D., Nowak, B.F., Bernatchez, L., Bergseth, S., Davidson, W.S., Gallardo-Escárate, C., Goldammer, T., Guiguen, Y., Iturra, P., Kijas, J.W., Koop, B.F., Lien, S., Maass, A., Martin, S.a.M., Mcginnity, P., Montecino, M., Naish, K.A., Nichols, K.M., Ólafsson, K., Omholt, S.W., Palti, Y., Plastow, G.S., Rexroad, C.E., Rise, M.L., Ritchie, R.J., Sandve, S.R., Schulte, P.M., Tello, A., Vidal, R., Vik, J.O., Wargelius, A. & Yáñez, J.M. (2017). Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. *BMC Genomics,* 18**:** 484.

Matala, A.P., B. Allen, S.R. Narum, and E. Harvey. 2017. Restricted gene flow between resident Oncorhynchus mykiss and an admixed population of anadromous steelhead. Ecology and Evolution 7:8349-8362.

Narum, S.R., P. Gallardo, C. Correa, A. Matala, D. Hasselman, B.J.G. Sutherland, and L. Bernatchez. 2017. Genomic patterns of diversity and divergence of two introduced species in Patagonia, South America. Evolutionary Applications 10:402-416.

Paneru, B.D., Al-Tobasei, R., Kenney, B., Leeds, T.D. & Salem, M. (2017). RNA-Seq reveals MicroRNA expression signature and genetic polymorphism associated with growth and muscle quality traits in rainbow trout. *Scientific Reports,* 7**:** 9078.

Vallejo, R.L., Leeds, T.D., Gao, G., Parsons, J.E., Martin, K.E., Evenhuis, J., Fragomeni, B.O., Wiens, G.D., Palti, Y. 2017. Genomic selection models double the accuracy of predicted breeding values for bacterial cold water disease resistance compared to a traditional pedigree-based model in rainbow trout aquaculture. Genetics Selection Evolution. 49(17):1-33.

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