**NRSP-8 Salmonids Aquaculture Research Progress Report for 2016**

**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.**

A genome assembly project for Chinook salmon was imitated and several genome assembly approaches were evaluated (Narum and Campbell).

**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.**

A 50K cSNPs array was developed from allelic-imbalance analysis of pooled RNA-Seq samples that may be associated with muscle yield and fillet quality traits and also with bacterial cold water disease survival in rainbow trout.

Initial annotation of the new rainbow trout genome (reported last year) was submitted to NCBI for processing and evaluation. It is based on computer gene predictions and alignment of large transcriptome sequence data

Identified GREB1 gene associated with adult migration timing in anadromous steelhead (Hess et al. 2016).

Identified patterns of selection in natural populations of various salmonid species (steelhead, sockeye salmon, and cutthroat trout) and candidate genes under selection (Hand et al. 2016; Hess et al. 2016a; Kovach et al. 2016; Nichols et al. 2016).

Developed genetic tagging program to monitor stock-specific migration timing and abundance of anadromous salmonids (Hess et al. 2016a; Hess et al. 2016b; Matala et al. 2016).

The CRISPR targeted genome editing technique was successfully applied in rainbow trout to reduce and eliminate expression of a functional tyrosinase protein, which resulted in fish with variations in eye and skin pigmentation. This proof-of-concept study determined that the new technology is a viable approach to reduce or knockout gene expression in rainbow trout.

New RNA sequencing datasets were generated for egg quality and protein turnover studies in rainbow trout.

**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.**

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

The new rainbow trout reference genome including chromosome sequences and gene annotation was submitted to the NCBI.

**Salmonids publications in 2016:**

Danzmann, R.G., Kocmarek, A.L., Norman, J.D., Rexroad, C.E. & Palti, Y. (2016). Transcriptome profiling in fast versus slow-growing rainbow trout across seasonal gradients. *BMC Genomics,* 17**:** 1-18.

Gonzalez-Pena, D., Gao, G., Baranski, M., Moen, T., Cleveland, B.M., Kenney, P.B., Vallejo, R.L., Palti, Y. & Leeds, T.D. (2016). Genome-Wide Association Study for Identifying Loci that Affect Fillet Yield, Carcass, and Body Weight Traits in Rainbow Trout (Oncorhynchus mykiss). *Frontiers in Genetics,* 7**:** 203.

Hand, B.K., C.C. Muhlfeld, A.A. Wade, R.P. Kovach, D.C. Whited, S.R. Narum, A.P. Matala, M.W. Ackerman, B.A. Garner, J.S. Kimball, J.A. Stanford, and G.L. Luikart. 2016. Climate variables explain neutral and adaptive variation within salmonid metapopulations: the importance of replication in landscape genetics. Molecular Ecology 25:689-705.

Hess, J.E., J.S. Zendt, A.R. Matala, and S.R. Narum. 2016a. Genetic basis of adult migration timing in anadromous steelhead discovered through multivariate association testing. Proceedings of the Royal Society B 283:20153064.

Hess, M.A., J.E. Hess, A.P. Matala, R.A. French, C.A. Steele, J. Lovtang, and S.R. Narum. 2016b. Migrating adult steelhead utilize a thermal refuge during summer periods with high water temperatures. ICES Journal of Marine Science 73:2616-2624.

Hess, J.E., M.W. Ackerman, Jeffrey K. Fryer, D.J. Hasselman, C.A. Steele, J.J. Stephenson, J.M. Whiteaker, and S.R. Narum. 2016c. Differential adult migration-timing and stock-specific abundance of steelhead in mixed stock assemblages. ICES Journal of Marine Science 73:2606-2615.

Kovach, R.P., B.K. Hand, P.A. Hohenlohe, T.F. Cosart, M.C. Boyer, H.H. Neville, C.C. Muhlfeld, S.J. Amish, K. Carim, S.R. Narum, W.H. Lowe, F.W. Allendorf, and G. Luikart. 2016. Vive la resistance: genome-wide selection against introduced alleles in invasive hybrid zones. Proceedings of the Royal Society B 283:20161380.

Lien, S., Koop, B.F., Sandve, S.R., Miller, J.R., Kent, M.P., Nome, T., Hvidsten, T.R., Leong, J.S., Minkley, D.R., Zimin, A., Grammes, F., Grove, H., Gjuvsland, A., Walenz, B., Hermansen, R.A., Von Schalburg, K., Rondeau, E.B., Di Genova, A., Samy, J.K.A., Olav Vik, J., Vigeland, M.D., Caler, L., Grimholt, U., Jentoft, S., Inge Våge, D., De Jong, P., Moen, T., Baranski, M., Palti, Y., Smith, D.R., Yorke, J.A., Nederbragt, A.J., Tooming-Klunderud, A., Jakobsen, K.S., Jiang, X., Fan, D., Hu, Y., Liberles, D.A., Vidal, R., Iturra, P., Jones, S.J.M., Jonassen, I., Maass, A., Omholt, S.W. & Davidson, W.S. (2016). The Atlantic salmon genome provides insights into rediploidization. *Nature,* 533**:** 200-205.

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, Part 1**:** 120-125.

Matala, A.P., D.R. Hatch, S. Everett, M.W. Ackerman, B. Bowersox, M. Campbell, and S.R. Narum. In press. What goes up does not come down: compositional and demographic differences between steelhead returning to spawn and emigrating post-spawned kelts. ICES Journal of Marine Science 73:2595-2605.

Nichols, K.M., C.C. Kozfkay, S.R. Narum. 2016. Genomic signatures among *Oncorhynchus nerka* to inform conservation and management of endangered sockeye salmon. Evolutionary Applications 9:1203-1311.

Paneru, B., Al-Tobasei, R., Palti, Y., Wiens, G.D. & Salem, M. (2016). Differential expression of long non-coding RNAs in three genetic lines of rainbow trout in response to infection with Flavobacterium psychrophilum. *Scientific Reports,* 6**:** 36032.

Vallejo, R.L., Leeds, T.D., Fragomeni, B.O., Gao, G., Hernandez, A.G., Misztal, I., Welch, T.J., Wiens, G.D. & Palti, Y. (2016). Evaluation of genome-enabled selection for bacterial cold water disease resistance using progeny performance data in rainbow trout: Insights on genotyping methods and genomic prediction models. *Frontiers in Genetics,* 7**:** 96.