**NRSP-8 Oyster Species Report for 2017**

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**Objective 1: To 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.**

* 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.

**Objective 2: To develop strategies to identify and exploit genes and allelic variation which contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.**

* Re-sequencing of 92 eastern oyster genomes at 20X coverage partially funded through NRSP8 Aquaculture program. PIs: M. Gomez-Chiarri, D. Proestou, H. Putnam.
* Expressed exome capture sequencing (EecSeq) method developed using the eastern oyster. NCBI Accession # PRJNA423022.
* 190K Affymetrix SNP array constructed for *Crassostrea gigas*.
* Medium-density Affymetrix SNP array containing ~27K *Crassostrea gigas* SNPs and ~11K *Ostrea edulis* SNPs has been developed.
* Significant QTL associated with *C. gigas* resistance to Ostreid herpes virus identified.
* Exon-level DNA methylation patterns across two tissues in *C. gigas* have been characterized.
* *C. virginica* histone variants and DNA methylation patterns characterized in response to Florida red tides.
* Transcripts and metabolites associated with glycogen content in *C. gigas* have been identified.

**Objective 3: To 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 will be held at the National Shellfisheries Association annual meeting in Seattle, WA, March 18-21. Workshop organizers: M. Gómez-Chiarri, S. Roberts, D. Proestou

**Publications:**

Puritz, J. B., & Lotterhos, K. E. (2017). Expressed Exome Capture Sequencing (EecSeq): a method for cost-effective exome sequencing for all organisms with or without genomic resources. *bioRxiv*, 223735.

Qi, H., Song, K., Li, C., Wang, W., Li, B., Li, L., Zhang, G. (2017) Construction and evaluation of a high-density SNP array for the Pacific oyster (Crassostrea gigas). *PLoS One*, *12(3)*, e0174007.

Bachère, E., Barranger, A., Bruno, R., Rouxel, J., Menard, D., Piquemal, D., & Akcha, F. (2017). Parental diuron-exposure alters offspring transcriptome and fitness in Pacific oyster Crassostrea gigas. *Ecotoxicology and Environmental Safety*, *142*, 51-58.

Gutierrez, A. P., Turner, F., Gharbi, K., Talbot, R., Lowe, N. R., Peñaloza, C., ... & Houston, R. D. (2017). Development of a medium density combined-species SNP Array for Pacific and European oysters (Crassostrea gigas and Ostrea edulis). *G3: Genes, Genomes, Genetics*, *7*(7), 2209-2218.

Gutierrez, A., Bean, T. P., Hooper, C., Stenton, C. A., Sanders, M. B., Paley, R. K., ... & Houston, R. D. (2017). A genome-wide association study for host resistance to Ostreid Herpesvirus in Pacific oysters (Crassostrea gigas). *bioRxiv*, 223032.

Song, K., Li, L., & Zhang, G. (2017). The association between DNA methylation and exon expression in the Pacific oyster Crassostrea gigas. *PloS one*, *12*(9), e0185224.

Gonzalez-Romero, R., Suarez-Ulloa, V., Rodriguez-Casariego, J., Garcia-Souto, D., Diaz, G., Smith, A., ... & Eirin-Lopez, J. M. (2017). Effects of Florida Red Tides on histone variant expression and DNA methylation in the Eastern oyster Crassostrea virginica. *Aquatic Toxicology*, *186*, 196-204.

Li, B., Song, K., Meng, J., Li, L., & Zhang, G. (2017). Integrated application of transcriptomics and metabolomics provides insights into glycogen content regulation in the Pacific oyster Crassostrea gigas. *BMC genomics*, *18*(1), 713.