

Functional Re-annotation of Oyster Genomes with Epigenetic Resources (FROGER)

Proposal to the Aquaculture Section - USDA-NIFA National Research Support Project 8 (NRSP8).

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With the recent release of the Eastern oyster genome and excellent resources from other oyster species (e.g. Pacific Oyster, Olympia oyster) a framework is in place to effectively assess how epigenetic variation influence commercially important traits. Currently there are several labs across the United States working on the role of the epigenome in improved performance. There is wealth of disparate information that we will integrate into platforms that will facilitate distribution and application of the datasets. These data include MBD-seq, bisulfite sequence data, MBD micro array, miRNA, lncRNA, and data sets associated with histone modification. Integration of these datasets will further facilitate the discovery of key mechanisms driving cultured oyster performance traits, thereby providing the knowledge that will enable precision oyster breeding and enhance productivity and profitability of this rapidly expanding industry. ***We are requesting funds to support a workshop for researchers to come together and advance the status of the oyster genomes.***

Potential for Epigenetic Variation to Inform Breeding Approaches: Oyster aquaculture occurs in biologically, chemically, and physically heterogeneous coastal environments. Evaluation of selected oyster lines grown in a range of environments underscore the importance of genotype x environment interactions on oyster performance which may seriously confound main effects in traditional family-based selection. Variable phenotypes in response to environmental cues may be explained by epigenetics, or dynamic and heritable post-synthesis modification of DNA or DNA-associated proteins. Epigenetic mechanisms include: DNA methylation, histone variants and their post-translational modifications, non coding RNAs, and transcription factor regulatory networks. Overall, epigenetics constitutes the next frontier for understanding how mechanisms of temporal and spatial control of gene activity work during transient responses and long-term adaptations. To this end, ***elucidation of epigenetic mechanisms provides critical capacity to establish fundamental cause-effect relationships between genotype, specific epigenetic marks and subsequent modifications in gene expression patterns, and the environmental factors triggering those epigenetic marks in the first place.***

Epigenetic mechanisms have the potential to be heritable and contribute to long-term performance changes in animals and plants. In marine invertebrates, offspring fitness is impacted by parent or grandparent exposure to stress. The transgenerational effects of parental exposure (TGP) to stress can depend on the degree and duration of adult exposure, the presence of other stressors, the offspring stage examined, and other life history traits. Direct examples of positive TGP are found in multiple shellfish species exposed to low pH including Manila clams and Sydney rock oysters. In Pacific oysters, observations that the methylome is heritable, persists through development and is linked to transcriptional regulation provide evidence that TGP can be accomplished epigenetically. The emerging knowledge about epigenetics in oysters and other molluscs provides a very powerful toolkit to investigate how these mechanisms contribute to the epigenetic determination of transgenerational phenotypes. ***Together these studies provide evidence for heritable epigenetic mechanisms playing a major role in oyster performance. Thus, a full functional annotation of oyster genomes must include epigenetic mechanisms.***

We request \$10,000 for travel and participant costs from NRSP-8 to conduct the FROGER Workshop. This proposed activity is consistent with NRSP8 Objectives as it will (Obj1) advance the reference genome status for multiple species and (Obj3) facilitate analysis, curation, storage, distribution and application of the numerous and large datasets associated with the oyster community sequencing efforts. Deliverables as part of this project will include numerous genome feature tracks and annotation tables that will be made immediately available to the community. In addition the protocols (i.e. code) will be available and provide framework for epigenetic characterization in other aquaculture species.

Small Funding Opportunities for US Aquaculture Groups: The Aquaculture Genome Co-Coordinator of USDA-NIFA National Research Support Project 8 (NRSP8) request proposals for activities that support community research efforts for US Aquaculture species; primarily catfish, oysters, salmon/rainbow trout, shrimps, striped bass and tilapia. Proposals should specifically address the current NRSP8 Objectives which are:

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;

Objective 2: Develop strategies to identify and exploit genes and allelic variations that contribute to economically relevant phenotypes and traits, in part through improving functional annotation of the genomes of our species.

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.

Investigators should be based at US institutions, proposals should be no more than 1 page in length, and funding requests should not exceed \$10,000. Proposals should identify the relevant research community and outline how funds will be used for research support activities. Such activities may include but are not limited to training, workshops, development of high throughput genotyping platforms, genome sequence assembly and annotation, developing and/or supporting community databases and web sites. Proposals should be sent to Steven Roberts (sr320@uw.edu) by May 31, 2018.