Images and Image Analysis

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Project
» MCA: Utilizing high-throughput proteomics to build a conceptual model of the effects of environmental change on early life stages of genetically diverse herring populations (Herring Proteomics)

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Coverage

Spatial Extent: **Lat**:0 **Lon**:0

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Parameters

Parameters for this dataset have not yet been identified

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Project Information

MCA: Utilizing high-throughput proteomics to build a conceptual model of the effects of environmental change on early life stages of genetically diverse herring populations (Herring Proteomics)

Coverage: Salish Sea - NE Pacific

NSF Award Abstract:
Pacific Herring represent a critical link in marine food webs along the West Coast of the United States, connecting the plankton they eat with larger predators (fish, sea birds, and marine mammals). Temperature strongly influences the development and success of herring. This investigation targets the underlying pathways that drive their temperature response by examining seasonal differences in protein expression. The outcome will be a better understanding of the processes most influenced by temperature, such as specific metabolic processes or stress responses. The project supports training for the investigator in new proteomics techniques and for undergraduate students at a Primarily Undergraduate Institution. Outreach includes engagement with local stakeholders and coastal indigenous communities. Societal benefits include a better understanding of population differences to inform conservation and recovery efforts for a culturally, economically, and ecologically important species.

Pacific Herring are ecologically important forage fish; fluctuations in their biomass drive far reaching food web responses. Climate variability is suspected to be a major driver of population trends, but the underlying mechanisms driving physiological responses remain unknown. Protein expression is a sensitive indicator of sub-lethal differences in stress response and metabolic state; therefore, comparisons across seasons unveil the cellular processes driving organismal responses to climate factors. Project goals are 1) a deeper understanding of the mechanisms driving the response of a key forage fish species to temperature and 2) workforce development, bringing cutting-edge molecular capabilities to faculty and students at a primarily undergraduate institution. Through a comparison between the robust Semiahmoo Bay (SB) population and the genetically and behaviorally distinct, and much depleted, Cherry Point (CP) herring population, the research team is detecting biomarker molecules of key physiological differences. Investigators are profiling SB and CP embryos collected from January through June using proteomic analyses, then developing targeted assays for peptides of interest, with total lipids and relevant environmental variables (T, Salinity, pH) providing meaningful context. Cohorts of embryos are also being reared to hatch from each collection date for comparison of protein biomarkers associated with survival or morphometric differences in the hatched larvae. This project provides the first large-scale survey of proteins present in early life stage Pacific Herring under different temperature regimes, advancing our understanding of herring response to environmental conditions associated with global change and ocean/atmosphere cycles.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2219978

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