Raw proteome mass spectrometry data (.mzML files) from pacific herring embryos sampled at Semiahmoo Bay between February and April 2022

Website: https://www.bco-dmo.org/dataset/938909
Data Type: Other Field Results
Version: 1
Version Date: 2024-11-12

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)

Contributors	Affiliation	Role
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Abstract
These are the raw data files from 5 cohorts of pacific herring embryos collected from Feb through April of 2022. Embryos were homogenized, and digested for proteomic analysis on a Lumos Orbitrap. Pooled samples were used with narrow window scans for library generation. The purpose of this data set is exploratory analysis for seasonal differences between early life stage proteome of pacific herring. All embryos are believed to be from the Semiahmoo Bay population since the Cherry Point population had no spawn detected in 2022.

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Coverage

Location: Semiahmoo Spit, WA
Spatial Extent: **Lat**:48.992824917812 **Lon**:-122.78378231373
Temporal Extent: 2022-02 - 2022-04

Methods & Sampling

Embryos collected with a rake from small boat on 5 dates across three months and kept in a cooler with ambient seawater for 1-5 hours until returned to the lab. 1-5 embryos flash frozen and stored cyogenically for 3-6 months until processing.

Data Processing Description

Embryos were physically broken with a micropestle in a microcentriguge tube, then processed 3x 30 seconds with stainless steel beads in a bullet blender. Homogenate was removed from the bead then sonicated 3x. and digested using trypsin and a standard s-trap protocol. Tubes were dried using a speed vap and reconstituted

in water/ACN.

Samples were spiked with Pierce retention time standards and with yeast enolase as a standard in some cases. A 90 minute gradient was run on the LC serving the Lumos.

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Data Files

File
938909_v1_orbitrap.csv (Comma Separated Values (.csv), 5.81 KB) MD5:fe97252b745ce72fd108016c244daa5e Primary data file for dataset ID 938909, version 1

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Supplemental Files

File
mzml_2023_herring.zip (ZIP Archive (ZIP), 26.46 GB) MD5:bab416f1568db295f90396c9a67483a8 Raw mass spectrometry data (.MzML) files. see inventory file for naming and sampling details of the files.

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Parameters

Parameter	Description	Units
Location	Sampling area: Semiahmoo Bay	unitless
Date_Sampling	Sampling date	unitless
Latitude	Approximate sample latitude	decimal degrees
Longitude	Approximate sample longitude	decimal degrees
Sample_ID	Sample ID: cohort + sampling id	unitless
Cohort	Cohorts of pacific herring embryos: 1 - 5	unitless
Replicate	Sample replicate	unitless
Mass_Spec_Run_Number	Mass spectrometry run number	unitless
Date_Mass_Spec	Date of spectrometry run	unitless
Sample_Type	Description of single sample vs pool samples.	unitless
Filename	Filename of .mzml file in supplemental files. File name convention: DateRun_Intrument_project_sampleID_RunNumber	unitless

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Instruments

Dataset-specific Instrument Name	Lumos Orbitrap
Generic Instrument Name	Mass Spectrometer
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

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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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