Eastern oyster gonad methylation patterns in response to experimental ocean acidification

Website: https://www.bco-dmo.org/dataset/785167
Data Type: Other Field Results
Version: 1
Version Date: 2019-12-30

Project
» Collaborative Research: Does ocean acidification induce a methylation response that affects the fitness of the next generation in oysters? (Epigenetics to Ocean)

Contributors	Affiliation	Role
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Abstract
Eastern oyster gonad methylation patterns in response to experimental ocean acidification at pCO2 levels 400 and 2800 ppm. Oysters were collected from an intertidal oyster reef in Plum Island Sound, MA, Gulf of Maine in mid-July 2016. This dataset includes GenBank BioProject PRJNA513384 metadata.

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Coverage

Spatial Extent: **Lat**:42.681764 **Lon**:-70.813498
Temporal Extent: 2016-07 - 2016-07

Dataset Description

Eastern oyster gonad methylation patterns in response to experimental ocean acidification at pCO2 levels 400 and 2800 ppm. Oysters were collected from an intertidal oyster reef in Plum Island Sound, MA, Gulf of Maine in mid-July 2016. This dataset includes GenBank BioProject PRJNA513384 metadata.

Acquisition Description

Adult *C. virginica* (9.55 cm ± 0.45) were collected from an intertidal oyster reef in Plum Island Sound, MA (42.681764, -70.813498) in mid-July 2016. The oysters were transported to the Marine Science Center at Northeastern University (Nahant, MA), where they were cleaned and randomly assigned to one of six flow-through tanks (50L) maintained at ambient seawater conditions. Oysters were acclimated for 14 days under ambient conditions, before initiating a 28-day experimental exposure. The oysters were exposed to either control (500 µatm) or elevated pCO_2 (2500 µatm; $\Omega_{calcite} < 1$).

DNA was isolated from ten gonad tissue samples using the E.Z.N.A. Mollusc Kit (Omega) according to the manufacturer's instructions. Isolated DNA was quantified using a Qubit dsDNA BR Kit (Invitrogen). DNA samples were sonicated for ten minutes at 4 ºC, on 30 second intervals periods at 25% intensity. Shearing size (350bp) was verified using a 2200 TapeStation System (Agilent Technologies). Samples (10) were enriched for methylated DNA using MethylMiner kit (Invitrogen). Libraries were prepared using Pico Methyl-Seq Library Prep Kit (Cat. #D5455).

Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names: filename3 to MBD_cv_id; filename4 to pCO2_treatment

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Parameters

Parameter	Description	Units
bioproject_accession	GenBank BioProject accession identifier	unitless
biosample_accession	GenBank BioSample accession identifier	unitless
library_ID	sample identifier used in library preparation	unitless
title	GenBank BioProject title	unitless
library_strategy	strategy used for sequencing: MBD-Seq = Direct sequencing of methylated fractions sequencing strategy	unitless
library_source	source material (genomic DNA)	unitless
library_selection	Method by which the material was selected: MBD2 protein methyl-CpG binding domain	unitless
library_layout	either a paired-end or single sequence run	unitless
platform	instrument type used to sequence DNA	unitless
instrument_model	DNA sequencing insturment model	unitless
design_description	method detail used in sequencing: whether run in Lane 1 or Lane 2	unitless
filetype	type of genomics file (fastq)	unitless
filename	filename of first paired-end sequencing file	unitless
filename2	filename of second paired-end sequencing file	unitless
MBD_cv_id	MBD Cv identifier	unitless
pCO2_treatment	pCO2 treatment	ppm

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq1500
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Paired-end 100bp DNA sequencing was performed on the Illumina HiSeq1500 system.
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

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Project Information

Collaborative Research: Does ocean acidification induce a methylation response that affects the fitness of the next generation in oysters? (Epigenetics to Ocean)

Coverage: Coastal Massachusetts near Nahant: 42°25'06"N 70°54'14"W

NSF Award Abstract: Marine ecosystems worldwide are threatened by ocean acidification, a process caused by the unprecedented rate at which carbon dioxide is increasing in the atmosphere. Since ocean change is predicted to be rapid, extreme, and widespread, marine species may face an "adapt-or-die" scenario. However, modifications to the DNA sequence may be induced in response to a stress like ocean acidification and then inherited. Such "epigenetic" modifications may hold the key to population viability under global climate change, but they have been understudied. The aim of this research is to characterize the role of DNA methylation, a heritable epigenetic system, in the response of Eastern oysters (Crassostrea virginica) to ocean acidification. The intellectual merit lies in the integrative

approach, which will characterize the role of DNA methylation in the intergenerational response of oysters to ocean acidification. These interdisciplinary data, spanning from molecular to organismal levels, will provide insight into mechanisms that underlie the capacity of marine invertebrates to respond to ocean acidification and lay the foundation for future transgenerational studies. Ocean acidification currently threatens marine species worldwide and has already caused significant losses in aquaculture, especially in Crassostrea species. This research has broader impacts for breeding, aquaculture, and the economy. Under the investigators' "Epigenetics to Ocean" (E2O) training program, the investigators will build STEM talent in bioinformatics and biogeochemistry, expose girls in low-income school districts to careers in genomics, and advance the field through open science and reproducibility. This research will specifically test if intermittent exposure to low pH induces a methylation response with downstream beneficial effects for biomineralization. These methylation states could be inherited and confer a fitness advantage to larvae that possess them. Phase 1 of the project will use an exposure experiment to determine the degree to which DNA methylation is altered and regulates the response to OA. Data from this experiment will be used to test the hypotheses that (i) DNA methylation, induced in the tissue of shell formation (i.e., mantle tissue), is correlated with changes in transcription and regulation of pallial fluid pH (calcifying fluid pH, measured by microelectrode), and (ii) that methylation changes induced in the mantle tissue are also induced in the germline --indicating that such changes are potentially heritable. Phase 2 of the project will use a pair-mated cross experiment to test the hypothesis that parental exposure to OA alters larval traits (calcification rate, shell structure, and polymorph mineralogy). Larvae will be generated from parents exposed to OA or control seawater, and then raised under control or OA conditions. Results will be used to (i) characterize inheritance of induced methylation states, (ii) estimate the variance in larval traits explained by genotype, non-genetic maternal/paternal effects, adult OA exposure, larval OA exposure, and parental methylome, and (iii) test the hypothesis that adult exposure alters the heritability (a quantity that predicts evolutionary response) of larval traits. Since the effects of epigenetic phenomena on estimates of heritability are highly debated, the results would advance understanding of this important issue. Because the investigators could discover that DNA methylation is a mechanism for heritable plastic responses to OA, knowledge of this mechanism would significantly improve and potentially transform predictive models for how organisms respond to global change.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1635423

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