Marine invertebrate environmental memory

Implications, mechanisms, and opportunities

Steven Roberts - University of Washington

github.com/sr320/talk-duke-2024

Duke | NICHOLAS SCHOOL of the ENVIRONMENT

Duke University Marine Lab

FHL

FHL

FHL

Early-life Priming

Hardening

Transgenerational Plasticity

Carry-over effects

Early-life Priming

Hardening

Early-life Priming

Hardening

Trends in
Plant Science

Special issue: Climate change and sustainability I

Review

Priming crops for the future: rewiring stress memory

Haipei Liu [1], Amanda J. Able [1], and Jason A. Able [1,@,*]

Cross-stress priming success relies on synergistic stress signalling pathways being shared across stresses varying in nature and intensity.

Geoduck Clams

Repeat exposure to hypercapnic seawater modifies growth and oxidative status in a tolerant burrowing clam

Samuel J. Gurr[1,*], Shelly A. Wanamaker[2], Brent Vadopalas[3], Steven B. Roberts[2] and Hollie M. Putnam[1]

Geoduck Clams

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- Initial conditioning followed by second and third exposure to severe and moderate PCO2 stress increased respiration rate, organic biomass and shell size, suggesting a stress-intensity-dependent effect on energetics.

- Stress acclimated clams had lower antioxidant capacity compared with clams under ambient conditions, supporting the hypothesis that stress over postlarval-to-juvenile development affects oxidative status later in life.

Geoduck Clams

Acclimatory gene expression of primed clams enhances robustness to elevated pCO_2

Samuel J. Gurr[1,2] | Shelly A. Trigg[3,4] | Brent Vadopalas[5] | Steven B. Roberts[3]
Hollie M. Putnam[1]

GEODUCKS CLAMS

- Does conditioning to low pH confer tolerance within a generation?

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Transgenerational Plasticity

Carry-over effects

INFLUENCE OF PARENTAL CONDITIONS

- **Selection (various generations)**
- **Germ cells are present**
- **Maternal provisioning**
- **Paternal role?**
- **Beneficial** versus detrimental
- *Mechanisms at play*

Crassostrea hongkongensis

Transgenerational responses to seawater pH in the edible oyster, with implications for the mariculture of the species under future ocean acidification

Yong-Kian Lim [1], Xin Dang [1], Vengatesen Thiyagarajan

Crassostrea
hongkongensis

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EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

- Oysters were held at **two temperature regimes** (6°C and 10°C) for 60 days in December
- A differential pCO2 exposure was **carried out after the temperature treatment ended**. Held at ambient pCO2 (841 µatm) or high pCO2 (3045 µatm) for 52 days, during the Winter.

Carryover effects of temperature and pCO_2 across multiple Olympia oyster populations

Laura H. Spencer,[1] Yaamini R. Venkataraman,[1] Ryan Crim,[2] Stuart Ryan,[2] Micah J. Horwith,[3] and Steven B. Roberts[1,4]

TEXT

Jun 2013
F, D, and O-1 cohorts produced
Jun 2015
O-2 cohort produced from O-1
6 Dec 2016
Temperature exposure, 60 d
4 Feb 2017
Gonad sampled
16 Feb 2017
pCO2 exposure, 52 d
8 Apr 2017
Gonad sampled
11 Apr 2017
Adults conditioned, spawned, 90 d
11 May 2017
Larvae counted, 60 d
Subset reared
4 Oct 2017
6°C juveniles moved to Clam Bay for winter
12 Jun 2018
6°C juveniles deployed in 4 bays, 86 d
Environmental conditions
Cohorts in common conditions (Clam Bay) before exposures
6°C
10°C
841 µatm pCO2
3045 µatm pCO2
841 µatm pCO2
3045 µatm pCO2
Common conditions (hatchery)
1°C daily increase to 18°C to spawn
Larvae reared at 18°C
Common conditions (Clam Bay)
Fidalgo Bay
Port Gamble Bay
Skokomish River Delta
Case Inlet
Adults
Offspring

LAURA SPENCER

EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

EFFECTS OF TEMPERATURE AND OA IN OLYMPIA OYSTER POPULATIONS

- Larval release occurred earlier in warm-exposed oysters
- Winter warming conditions increased larval production
- No effects on larval survival were detected
- **Juveniles of parents exposed to elevated pCO_2 had higher survival rates in the natural environment**

EFFECTS OF OA IN OLYMPIA OYSTER POPULATIONS

Latent effects of winter warming on Olympia oyster reproduction and larval viability

Laura H. Spencer [a,*], Erin Horkan [b], Ryan Crim [b], Steven B. Roberts [a]

[a] University of Washington, School of Aquatic and Fishery Sciences, 1122 NE Boat St, Seattle, WA 98105, United States
[b] Puget Sound Restoration Fund, 8001 NE Day Rd W, Bainbridge Island, WA 98110, United States

Fig. 1. Experimental timeline. Cells/mL indicate the concentrations of live algae given to oysters at various stages.

Environmental Memory

CAN BE BENEFICIAL
STAGE DEPENDENT
ACROSS GENERATION
IMPLICATIONS . . .

Environmental Memory

CAN BE BENEFICIAL STAGE DEPENDENT ACROSS GENERATION IMPLICATIONS . . .

Epigenetic Mechanisms

Epigenetics

ALTERS THE PHENOTYPE (WITHOUT CHANGING DNA CODE); HERITABLE

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CAN BE INDUCED WITH ENVIRONMENTAL MANIPULATION

ECOLOGICAL EPIGENETICS

Ecology Letters, (2008) 11: 106–115 doi: 10.1111/j.1461-0248.2007.01130.x

IDEA AND PERSPECTIVE

Epigenetics for ecologists

Affects

DESIRED TRAITS

mosaic

associated with gene bodies

METHYLATION LANDSCAPE IN MARINE INVERTEBRATES

Four Dimensionalities

Reliable Transcription	Spurious Transcription
Targeted Regulation	Stochastic Regulation

Four Dimensionalities

- Evolutionary
- Life History Driven
- Constitutive

Reliable Transcription	Spurious Transcription

- Distinct Lineage
- Experiential
- Inducible

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GEODUCKS AND OA

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GEODUCKS AND OA

DNA METHYLATION

GEODUCKS AND OA

GEODUCKS AND OA

GEODUCKS AND OA

GEODUCKS AND OA

New Results

Follow this preprint

Dynamic DNA methylation contributes to carryover effects and beneficial acclimatization in geoduck clams

Hollie M. Putnam, Shelly A. Trigg, Samuel J. White, Laura H. Spencer, Brent Vadopalas, Aparna Natarajan, Jonathan Hetzel, Erich Jaeger, Jonathan Soohoo, Cristian Gallardo-Escárate, Frederick W. Goetz, Steven B. Roberts

doi: https://doi.org/10.1101/2022.06.24.497506

GEODUCKS AND OA

Following four months of ambient common-garden conditions, **juveniles initially exposed to low pH compensatorily grew larger**, with DNA methylation indicative of these phenotypic differences, demonstrating epigenetic carryover effects persisted months after initial exposure.

GEODUCKS AND OA

Functional enrichment analysis of differentially methylated genes revealed regulation of signal transduction through widespread changes in the **Wnt signaling pathways that influence cell growth, proliferation, tissue and skeletal formation, and cytoskeletal change.**

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Can we see an imprint in parents transmitted to the offspring?

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Can we see an imprint in parents transmitted to the offspring?

NO

EXCITING?
COMPLEX
‘LAYER’ OF RESILIENCE

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COMPLEX
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Genetic Linkage

Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate

Katherine Silliman [1,†], Laura H. Spencer [2,†], Samuel J. White[2], and Steven B. Roberts [2,*]

First characterization of genome-wide DNA methylation patterns in the oyster genus *Ostrea*

Identified 3,963 differentially methylated loci between populations. Clear coupling between genetic and epigenetic patterns of variation, **with 27% of variation in inter-individual methylation differences explained by genotype**.

Underlying this association are both direct genetic changes in CpGs (CpG-SNPs) and genetic variation with indirect influence on methylation (mQTLs).

EPIGENETIC AND GENETIC POPULATION STRUCTURE

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Open Science

Bioinformatic Approaches in non-model species

marineomics.io

Received: 29 March 2023 | Accepted: 11 September 2023
DOI: 10.1111/2041-210X.14219

Methods in Ecology and Evolution

APPLICATION

A dynamic web resource for robust and reproducible genomics in nonmodel species: marineomics.io

Samuel N. Bogan[1] | Jason Johns[1] | Joanna S. Griffiths[2] | Danielle Davenport[3] | Sara J. Smith[4,5,6] | Sara M. Schaal[7] | Alan Downey-Wall[8] | Runyang Nicolas Lou[9,10] | Katie Lotterhos[11] | Megan E. Guidry[12] | Hanny E. Rivera[13] | Joseph A. McGirr[14] | Jonathan B. Puritz[12] | Steven B. Roberts[15] | Katherine Silliman[16,17]

Tabs for website topics

MarineOmics

Best Principles | Contributions | Population Genomics | Functional Genomics | Genome-Phenome | Panel Seminars | Discussion Forum

Topics covered within RADSeq tutorial

Setup for running code
Reduced Representation Sequencing (RADseq/GBS)
Considerations During Lab Work
Principles for Analyzing Your Data
Steps for a robust RAD analysis
First, look at the raw data!
Run an assembly pipeline
Evaluate potential sources of error
"Bad" samples
The power of PCA
Batch effects
Cryptic species/contamination/clones
Test a range of key parameters
Clustering threshold
Mapping parameters

RADseq

Katherine Silliman, Danielle Davenport

Description of tutorial steps

Setup for running code

If you would like to run the R code examples that are scattered throughout the guide (recommended but not required!), you will need to install some R packages. Only need to run this code once:

```
install.packages("tidyverse")
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install("SeqArray")
BiocManager::install("SNPRelate")
```

Example code to run using real data

Now load those packages, if using:

```
library(SeqArray) # efficient storage and filtering of genomic data
```

```
## Loading required package: gdsfmt
```

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