Elemental fingerprints of larval, juvenile, and settler Mytilus collected in the Gulf of Maine between 2015 and 2017

Website: https://www.bco-dmo.org/dataset/752530
Data Type: Other Field Results
Version: 2
Version Date: 2019-12-09

Project
» An integrated theoretical and empirical approach to across-shelf mixing and connectivity of mussel populations (MuLTI-2)
» Intertidal community assembly and dynamics: Integrating broad-scale regional variation in environmental forcing and benthic-pelagic coupling (GOMEPRO)

Contributors	Affiliation	Role
Etter, Ron J.	University of Massachusetts Boston (UMass Boston)	Principal Investigator
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Elemental fingerprints of larval, juvenile, and settler Mytilus collected in the Gulf of Maine between 2015 and 2017.

Table of Contents

Coverage

Spatial Extent: **N**:44.832368 **E**:-66.97212 **S**:42.31377 **W**:-71.04074
Temporal Extent: 2015-05-20 - 2017-10-02

Dataset Description

This dataset includes elemental fingerprints of larval, juvenile, and settler Mytilus collected in the Gulf of Maine between 2015 and 2017.

Methods & Sampling

We quantified larval fingerprints during spawning at each of the potential source populations to develop a reference map that will allow us to assign settled mussels to natal sites based on the elemental fingerprints of their larval shell. To develop a reference map of elemental signatures, we reared larvae in situ at each major mussel population (see sample locations data). After populations spawned in the field (based on our monitoring of gonad indices in each population) adult mussels from multiple sites were collected, spawned in the laboratory and the eggs fertilized. Within 24-48 hours (before shell formation begins) larvae were placed into small chambers and moored in situ at 3-5m depth. Because spawning varied among the populations, we staggered our deployment of larvae to coincide with our estimates of spawning times. After four weeks, larval

mussels were removed from in situ chambers, shells were rinsed in deionized water, dried and prepared for ICPMS. Settlers were collected from settlement plates deployed at each population.

Elemental concentrations were determined from single spot ablation in larval shells (85% energy, 10 hz, 200 shots, 25 µm spot diameter) for both larvae and settlers. Elemental compositions were quantified by external calibration (USGS MACS-3) and internal standardization. We quantified elemental compositions from count per second (cps) measurements of 24Mg, 55Mn, 59Co, 88Sr, 138Ba, 139La, 208Pb and 46Ca using laser ablation inductively coupled mass spectrometry (213 Nd:YAG laser coupled with Elan DRC II ICPMS) at the University of Massachusetts, Boston (LA-ICPMS). Elemental abundances were calculated as analyte cps/ 43Ca cps. We performed a one-point calibration using gas blank and MACS-3, and ran MACS-1 as a check standard every ten samples. Analytical accuracy and precision based on repeated check standard analyses was 96 + 4.4% (mean + sd). Each sample was analyzed in triplicate and mean concentrations normalized to calcium are reported.

Location:
Gulf of Maine: Frenchmen Bay (44 28.239 N -68 15.927 W) to Machais Bay (44 39.350 N -67 21.320 W).

Data Processing Description

Trace element concentrations relative to Ca (µmol element / mol Ca) were quantified using GeoPro(TM) software (Cetac Technologies). Concentrations were log transformed (log10 + 1), outliers were removed (identified as mean + 2*sd).

BCO-DMO Data Manager Processing Notes:
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* replaced character "" with an apostrophe in site name "Bailey s Island"
* Removed directionals from decimal degrees (negative longitudes are West; negative latitudes are South)
* Commas in location names changed to semicolons to support export as csv through the JGOFS system.
* Rounded lat/lons to 5 decimal places from 7.
* After communication with data submitter, Age value "Larval" changed to "Larvae" to be consistent with other values in the Age column. "Settlers" also changed to "Settler" to match other values of "Settler."

Data version 2 replaces data version 1:
* Data from 2017 added.
* 2017 data submitted as an excel file exported to csv.
* Date format changed to ISO yyyy-mm-dd
* " N" and " W" removed from decimal degrees. (It is accurately negative for W, positive for N)
* Date and lat/lon ranges updated in metadata text and geospatio-temporal bounds

[table of contents | back to top]

Data Files

File
mytilus_fingerprints.csv (Comma Separated Values (.csv), 361.90 KB) MD5:18890f73f354adf2220d498c6ce46c13 Primary data file for dataset ID 752530

[table of contents | back to top]

Parameters

Parameter	Description	Units
Site	Sample location	unitless
Site_Code	Sample location abbreviation	unitless
Age	Age (Larvae, Juvenile or Settler)	unitless
Latitude	Latitude	decimal degrees
Longitude	Longitude	decimal degrees
Date	Sample collection date (UTC) in ISO 8601 format yyyy-MM-dd	unitless
Sample_Number	Indicator to distinguish specific individuals	unitless
Mg	Magnesium concentration (umol Mg/mol Ca)	dimensionless
Mn	Manganese concentration (umol Mn/mol Ca)	dimensionless
Co	Cobalt concentration (umol Co/mol Ca)	dimensionless
Sr	Strontium concentration (umol Sr/mol Ca)	dimensionless
Ba	Barium concentration (umol Ba/mol Ca)	dimensionless
La	Lanthanum concentration (umol La/mol Ca)	dimensionless
Pb	Lead concentration (umol Pb/mol Ca)	dimensionless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	colonization substrata
Generic Instrument Description	Natural or artificial materials deployed in a marine or artificial environment for a given period to act as standardised, passive settlement sampling devices (e.g. settlement plates). They are used to determine the extent of colonization and/or the diversity of settled organisms.

Dataset-specific Instrument Name	Teledyne Cetac 213 G2+
Generic Instrument Name	Laser
Dataset-specific Description	Teledyne Cetac 213 G2+ laser coupled with a Perkin Elmer NexION 2000C mass spectrometer with autosampler and cross-flow nebulizer
Generic Instrument Description	A device that generates an intense beam of coherent monochromatic light (or other electromagnetic radiation) by stimulated emission of photons from excited atoms or molecules.

Dataset-specific Instrument Name	Perkin Elmer NexION 2000C
Generic Instrument Name	Mass Spectrometer
Dataset-specific Description	Teledyne Cetac 213 G2+ laser coupled with a Perkin Elmer NexION 2000C mass spectrometer with autosampler and cross-flow nebulizer.
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.

[table of contents | back to top]

Deployments

MuLTI-2_Mussel_Sampling

Website	https://www.bco-dmo.org/deployment/658775
Platform	Maine_Coast
Start Date	2014-04-24
Description	These locations were sampled using The Uglement, an automobile. Mussel Gonad Index (GI), size frequency, settlement, and density were surveyed.

[table of contents | back to top]

Project Information

An integrated theoretical and empirical approach to across-shelf mixing and connectivity of mussel populations (MuLTI-2)

Coverage: Gulf of Maine: Frenchmen Bay (44 28.239 N -68 15.927 W) to Machais Bay (44 39.350 N -67 21.320 W)

Acronym "MuLTI-2" (Mussel Larval Transport Initiative-2)

Extracted from the NSF award abstract:

Existing larval transport models focus mainly on along-shelf transport and have done little to explicitly incorporate the effects of cross-shelf mixing and transport processes. Yet cross-shelf transits (both outgoing and incoming legs) are critical components of the dispersal paths of coastal invertebrates. This project will explore the role of cross-shelf mixing in the connectivity of blue mussel populations in eastern Maine. Previous work has shown that the Eastern Maine Coastal Current (EMCC) begins to diverge from shore southwest of the Grand Manan Channel and creates a gradient in cross-shelf mixing and larval transport, with cross-shelf mixing being more common on the northeastern end, episodic in the transitional middle area, and then becoming rare in the southwestern half of the region of the Gulf of Maine. As a result, the investigators predict that northeastern populations of mussels are seeded mostly from up-stream sources, while a significant component of self-seeding (local retention) exists in southwestern populations. Larvae settling in the intervening bays are expected to be derived from a mixture of local and up-stream sources. Using a combined empirical and theoretical approach hydrographic, current profile, and larval vertical migration data will be collected and used to develop and validate a high-resolution coastal circulation model coupled to a model of larval behavior. The investigators will model simulations in different years using the empirical data from mussel

reproductive output and spawning times. Connectivity predicted from this model will be then tested against independent empirical estimates of connectivity based on trace element fingerprinting for larvae which can be connected to specific natal habitats. Regions of agreement and discrepancy in the model will be identified to guide additional data collection and model refinement. This iterative process will ensure an understanding of both larval transport patterns and processes, and provide estimates of inter-annual variability in connectivity for blue mussel populations in the Gulf of Maine.

Intertidal community assembly and dynamics: Integrating broad-scale regional variation in environmental forcing and benthic-pelagic coupling (GOMEPRO)

Coverage: Rocky intertidal shores and nearshore coastal waters throughout the Gulf of Maine

Rocky intertidal habitats in the Gulf of Maine (GoM) provide a model system to examine the structure and dynamics of natural communities. Throughout the Gulf of Maine, the same species are often found in these habitats but community structure, dynamics and productivity differ markedly among 3 distinct regions (southern, central and northern GoM). Past influential work, conducted primarily in the southern and central GoM, focused on the local processes driving intertidal community structure but produced very different conceptual models of how these communities are structured. This project examines whether regional differences in rocky shore community processes are driven by differences in recruitment that are shaped by regional variation in temperature and food availability and nearshore coastal oceanography. This project will improve the understanding of how large-scale environmental forces interact with local processes to control the distribution of species and the structure and dynamics of these communities. Understanding the interaction between processes operating at different scales is fundamentally important to developing more reliable models that can be used to predict community dynamics. In addition, data resulting from this project will have important implications for regional dynamics in commercially important species and for ecosystem and fisheries management within the GoM.

The overarching hypothesis of this project is that regional differences in community-level processes are driven by very different patterns of population connectivity and recruitment in a few key species, and that these differences are ultimately caused by regional variation in temperature and food availability and mediated by physical larval transport processes. Hence, the project will test the following hypotheses with manipulative field experiments, field sampling, connectivity estimates, and integrative modeling:
1) Locally-dispersing species dominate dynamics in regions with a net export of planktonic larvae (Northern GoM), while species with planktonic larvae dominate the dynamics in regions with high settlement and extensive connectivity among populations (Southern GoM).
2) Settlement density of species with planktonic larvae increases from northern to southern regions in accord with regional variation in food availability.
3) Population connectivity varies greatly among regions, with regions differing in the degree to which they are self-seeded or serve as larval sources vs. sinks; self-seeding leads to relatively localized population dynamics in the middle portion of the GoM.
4) Patterns of population connectivity are driven by physical transport processes and can be represented by coupling basic larval behavior models with circulation models.

At 18 different sites in the GoM across ~ 600 km, surveys will evaluate variation in recruitment, food availability and secondary productivity and experiments will assess community processes in wave-exposed and sheltered habitats. We will use hydrographic, current profile, and larval vertical distribution surveys to collect data for coupled larval/circulation models. Population connectivity will be both modeled and empirically evaluated (for one species) using elemental fingerprinting. A spatially explicit metacommunity model will integrate across all project components and test the relative importance of regional and local processes in controlling community organization and dynamics.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1334022
NSF Division of Ocean Sciences (NSF OCE)	OCE-1458154

[table of contents | back to top]