Depth distribution of mussel larvae in eastern Gulf of Maine from R/V C-Hawk day cruises in the Eastern Gulf of Maine from 2012 to 2014

Website: https://www.bco-dmo.org/dataset/783755
Data Type: Cruise Results
Version: 1
Version Date: 2019-12-20

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

Contributors	Affiliation	Role
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Abstract
Depth distribution of mussel larvae in eastern Gulf of Maine from R/V C-Hawk day cruises in the Eastern Gulf of Maine from 2012 to 2014

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Coverage

Spatial Extent: **N**:44.657059 **E**:-67.340914 **S**:44.4091939 **W**:-67.6526958
Temporal Extent: 2012-08-01 - 2014-08-07

Dataset Description

Depth distribution of mussel larvae in eastern Gulf of Maine from R/V C-Hawk day cruises in the Eastern Gulf of Maine from 2012 to 2014. These data were published in Weinstock et al., 2018 (see Fig 1, 2, 3, and 5).

Related Datasets: CTD casts were conducted immediately before and after the associated larval vertical distribution sampling and on both flood and ebb tides.
* CTD data for mussel study: https://www.bco-dmo.org/dataset/783736
* CTD cast log for mussel study: https://www.bco-dmo.org/dataset/783749

Methods & Sampling

Samples were collected by pumping 100L of water from specific depths and filtering the water through a 50 µm plankton net. Samples were preserved in ethanol. Bivalve veligers were sorted from other plankton and

enumerated under a microscope. A random subset of approximately 33 veligers per sample were prepared for SEM and viewed. Veligers were identified to the family level based on previously published criteria for hinge tooth morphology and all veligers classified as mytillids were measured. Mytilus sp. veligers were distinguished from the much rarer Modiolus by established relationships between shell length and the number of hinge teeth. The total number of bivalve veligers was multiplied by the fraction identified as Mytilus sp. to yield the estimated number of Mytilus sp. larvae in each sample. This method did not allow us to distinguish Mytilus edulis larvae from Mytilus trossulus larvae, but the later species is rare in the bays that we sampled.

For more information see Weinstock et al. 2018.

Data Processing Description

BCO-DMO Data Manager Processing Notes:
* exported data from excel to csv file
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions (spaces, +, and - changed to underscores). Units in parentheses removed and added to the Parameter Description metadata section.
* blank values in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system.
* Start and end timestamp columns added (UTC) in ISO 8601 format.
* Date column converted to ISO 8601 format

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Data Files

File
larvae.csv (Comma Separated Values (.csv), 22.92 KB) MD5:202c67719b441a1d3991564467ccd991 Primary data file for dataset ID 783755

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Related Publications

Weinstock, J. B., Morello, S. L., Conlon, L. M., Xue, H., & Yund, P. O. (2018). Tidal shifts in the vertical distribution of bivalve larvae: Vertical advection vs. active behavior. Limnology and Oceanography, 63(6), 2681–2694. doi:10.1002/lno.10968
Results

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Parameters

Parameter	Description	Units
Sample_Date	Sample date in ISO 8601 format yyyy-mm-dd	unitless
Site_name	Site name. Matches Fig. 1 in Weinstock et al. 2018	unitless
Latitude	Sample latitude	decimal degrees
Longitude	Sample longitude	decimal degrees
Start_time	Sample start time (UTC) in HH:MM	unitless
End_time	Sample end time (UTC) in ISO 8601 format HH:MM	unitless
Tidal_Phase	Tidal phase (Ebb or Flood tide)	unitless
Depth	Sample depth	meters
num_Mytilus_sp	The number of Mytilus larvae as calculated by the methods of Weinstock et al. 2018. The total number of bivalve larvae in the sample was multiplied by the fraction determined to be Mytilus edulis or Mytilus trossulus (the two species could not be distinguished) based on scanning electron microscope (SEM) analysis of larval hinge teeth. These are the raw data used for analysis.	per individual
percent_of_Water_column_total	The percent of water column total is number of Mytilus sp. divided by the sum of the number of Mytilus sp. at that location, date, and tidal phase for samples collected in 2014, and 1/3 of that same sum for samples collected in 2012 and 2013 to remove the effect of triplicate samples at each depth. These data remove the effect of variation in total abundance among sampling dates/sites and are presented in Fig. 2 of Weinstock et al., 2018.	percent
Start_DateTime_UTC	Sample start datetime (UTC) in ISO 8601 format YYYY-mm-ddTHH:MMZ	unitless
End_DateTime_UTC	Sample end datetime (UTC) in ISO 8601 format YYYY-mm-ddTHH:MMZ	unitless

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Deployments

Yund_GoME

Website	https://www.bco-dmo.org/deployment/699509
Platform	R/V C-HAWK
Start Date	2012-08-01
End Date	2016-07-29
Description	The C-Hawk is a 22 ft. fiberglass modified V-hull. These were multiple single-day deployments for GOMEPRO project. Eastern Gulf of Maine Sampled with single-day cruises on: 8/1/12 8/16/12 8/22/12 7/31/13 7/22/14 8/5/14 8/6/14 8/7/14 **Methods & Sampling** Date Site 8/1/12 MB1 8/16/12 MB1 & MB2 8/22/12 WB1 7/31/13 WB2 7/22/14 WB3 8/5/14 WB3 8/6/14 WB3 8/7/14 WB3

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Project Information

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.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1458188

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