Environmental measurements and high throughput sequencing data from samples collected at Martha's Vineyard Coastal Observation (MVCO) from 2013-2017

Website: https://www.bco-dmo.org/dataset/814424
Data Type: Other Field Results, Cruise Results
Version: 1
Version Date: 2020-06-05

Project
» Dynamics of Protistan Grazers: Diversity, Abundance and Prey Relations (Staining IFCB)

Contributors	Affiliation	Role
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Abstract
This dataset contains environmental measurements from Martha's Vineyard Coastal Observatory (MVCO) made from 2013-2017. Related high throughput sequencing data are available from NCBI under project numbers PRJNA504617 and PRJNA626352.

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Coverage

Spatial Extent: **Lat**:41.325 **Lon**:-70.5667
Temporal Extent: 2013-02-14 - 2017-08-02

Dataset Description

This dataset contains environmental measurements from Martha's Vineyard Coastal Observatory (MVCO) made from 2013-2017. Related high throughput sequencing data are available from NCBI. These are described below and cited under "Related Datasets".

Acquisition Description

Surface water samples were collected at approximately 2m depth using a Niskin bottle or a bucket near

the Martha's Vineyard Coastal Observatory (MVCO) offshore tower (41 19.500' N, 70 34.0' W). Sampling was accomplished from February 2013 – August 2017 about every 1-2 months, and usually twice monthly April – November, for a total of 62 samples. Water was kept cool and in the dark for transport back to the laboratory (about 1.5 hours).

Environmental data:
Reported temperature data are from the CTD rosette aboard the R/V Tioga. Chlorophyll and phaeo were collected and analyzed in the Sosik lab at WHOI using a Turner Designs Aquafluor Handheld 800446 extracted in 90% acetone.

Nutrients were analyzed at WHOI's Nutrient Facility. The official protocol summary can be found in the NES-LTER EDI data submission: https://portal.edirepository.org/nis/mapbrowse?packageid=knb-lter-nes.1.2

HPLC were analyzed at Horn Point Lab, as per NASA protocol. The summary protocol for HPLC and chl is available from Seabass: https://seabass.gsfc.nasa.gov/archive/WHOI/MVCO/documents

Sequencing data:
Volumes of water ranging from 0.75 to 2.5L were filtered in duplicate onto 45mm 0.22 µm Durapore GV filters under gentle vacuum. Filters were cut in half, placed into sterile 1.5 ml microfuge tubes, and stored at -80C until extraction.

Nucleic acids were extracted using the Zymo Research Fungal/Bacterial DNA MicroPrep Kit (Zymo Research Products). One half filter for each sample was transferred to a 2 ml microcentrifuge tube with silica beads and lysis buffer, and then shaken using a vortex adapter for 5 minutes. The extraction was then processed following the kit instructions and the eluted DNA frozen at -20C.

The eukaryotic ribosomal RNA gene V4 region was targeted for amplification and sequencing using 574V4F (5' [TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG]CGGTAAYTCCAGCTCYV) and 1132V4R (5' [GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG]CCGTCAATTHCTTYAART), described in Hugerth et al. (2014) and modified to include 5' adapter sequences for Illumina MiSeq (in square brackets). PCR reactions were accomplished in triplicate for each sample using 1 µl template DNA, 1.25 units AmpliTaq GoldR 360 DNA polymerase, 2mM MgCl2, 2 µl 2.5 µM dNTPs, and 2.5 µl 10X reaction buffer (25 µl total volume) with the conditions: 95C for 8 minutes; 40 cycles of 95C for 30 seconds, 58C for 30 seconds, 72C for 90 seconds; 72C for 5 minutes; 4C hold. No template negative controls were included with every set of PCRs. Each sample reaction was examined to confirm the correct product size of approximately 500 bp. Triplicate reactions were pooled and purified using either DNA Clean and Concentrator – 5 kit (Zymo Research) or AMPure XP beads. The samples were sent to the University of Rhode Island Genomics and Sequencing Center for library preparation and Illumina MiSeq (250 bp paired end; 500 cycle kit V2) sequencing. Samples 1-27 and 28-62 were sequenced in separate runs about a year apart.

Ciliate-specific amplicons were generated by amplifying the region between 152-528 bp of the 18S ribosomal RNA gene. The primers used for amplification are from Doherty et al 2007 (Aquatic Microbial Ecology). Primers were modified to carry 5' adapter sequences as noted above. AmpliTaq Gold 360 was used for amplification, and triplicate reactions were accomplished for each sample. Replicates were combined and purified using Agencourt AMPure XP. Products were sent to URI Genomics and Sequencing Center for Illumina MiSeq.

V4 amplicon raw reads are available at NCBI SRA project PRJNA504617. Ciliate amplicon raw reads are available at NCBI SRA project PRJNA626352. The Imaging FlowCytobot Dashboard for shared access to image data and data products, including MVCO time series, is available at https://ifcb-data.whoi.edu/mvco and the WHOI dock time series is available at https://ifcb-data.whoi.edu/WHOI_dock.

Processing Description

BCO-DMO Processing:
- renamed fields;

- converted date to YYYY-MM-DD format;
- changed missing data identifiers from "NaN" to "nd".

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Related Publications

Hugerth, L. W., Muller, E. E. L., Hu, Y. O. O., Lebrun, L. A. M., Roume, H., Lundin, D., … Andersson, A. F. (2014). Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. PLoS ONE, 9(4), e95567. doi:10.1371/journal.pone.0095567
Methods

Sosik, H. MVCO. SeaWiFS Bio-optical Archive and Storage System (SeaBASS), NASA. https://seabass.gsfc.nasa.gov/archive/WHOI/MVCO/documents
Methods

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Related Datasets

References

Woods Hole Oceanographic Institution (2018). MVCO V4 time series. National Library of Medicine (US), National Center for Biotechnology Information. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA504617. NCBI:BioProject: PRJNA504617. https://www.ncbi.nlm.nih.gov/bioproject/PRJNA504617/

Northeast U.S. Shelf LTER, & Sosik, H. (2018). Dissolved inorganic nutrients from NES-LTER cruises, including 4 macro-nutrients from water column bottle samples, ongoing since 2006 [Data set]. Environmental Data Initiative. https://doi.org/10.6073/PASTA/F7204A847A1D71FCE18ED880363E62F8 https://doi.org/10.6073/pasta/f7204a847a1d71fce18ed880363e62f8

Woods Hole Oceanographic Institution (2020). MVCO Ciliate amplicon diversity. National Library of Medicine (US), National Center for Biotechnology Information. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA626352. NCBI:BioProject: PRJNA626352. https://www.ncbi.nlm.nih.gov/bioproject/PRJNA626352/

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Parameters

Parameter	Description	Units
Start_Date	Date sampled; format: yyyy-mm-dd	unitless
Event_Number	MVCO event number	unitless
Temperature	water temperature	degress Celsius
Chl	total chlorophyll	micrograms per liter (ug per liter)
Phaeo	total phaeo pigment	ug per liter
NO2_NO3	nitrate and nitrite	micromolar
NH4	ammonia	micromolar
SiO2	silicate	micromolar
PO43	phosphate	micromolar
HPLC_Total_Chl_a	HPLC determined chlorophyll a	ug per liter
HPLC_Total_Chl_b	HPLC determined chlorophyll b	ug per liter
HPLC_Total_Chl_c	HPLC determined chlorophyll c	ug per liter
HPLC_Carotene	HPLC determined carotene	ug per liter
HPLC_But_Fucoxanthin	HPLC determined 19'-butanolyloxyfucoxanthin	ug per liter
HPLC_Hex_Fucoxanthin	HPLC determined 19'-hexanoyloxyfucoxanthin	ug per liter
HPLC_Alloxanthin	HPLC determined alloxanthin	ug per liter
HPLC_Diadinoxanthin	HPLC determined Diadinoxanthin	ug per liter
HPLC_Diatoxanthin	HPLC determined Diatoxanthin	ug per liter
HPLC_Fucoxanthin	HPLC determined Fucoxanthin	ug per liter
HPLC_Peridinin	HPLC determined Peridinin	ug per liter
HPLC_Zeaxanthin	HPLC determined Zeaxanthin	ug per liter

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Niskin bottle
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	CTD
Generic Instrument Name	CTD Sea-Bird
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	Turner Designs Aquafluor Handheld 800446
Generic Instrument Name	Fluorometer
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

Dataset-specific Instrument Name	bucket
Generic Instrument Name	bucket
Generic Instrument Description	A bucket used to collect surface sea water samples.

Dataset-specific Instrument Name	
Generic Instrument Name	PCR Thermal Cycler
Generic Instrument Description	General term for a laboratory apparatus commonly used for performing polymerase chain reaction (PCR). The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

MVCO

Website	https://www.bco-dmo.org/deployment/814458
Platform	Martha's Vineyard Coastal Observatory
Description	The Martha's Vineyard Coastal Observatory (MVCO) is a fixed, cabled observatory located in Edgartown, Massachusetts and the waters south of Martha's Vineyard. For more information, see https://mvco.whoi.edu/.

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Project Information

Dynamics of Protistan Grazers: Diversity, Abundance and Prey Relations (Staining IFCB)

Coverage: Martha's Vineyard Coastal Observatory, WHOI Dock

Description from NSF award abstract: Some of the most important primary producers and consumers in aquatic ecosystems are protists, or single-celled eukaryotes. It is well established that protistan predation can be a significant source of mortality for bacteria and phytoplankton. Grazing protists in turn serve as prey for zooplankton (copepods), and through the excretion of nitrogen and phosphorus compounds, they play a major role in the release of regenerated nutrients. Despite decades of studies on protistan grazing, knowledge gaps still exist with respect to their abundance, distribution, seasonality, prey selectivity, and co-occurrence patterns. The results from this project will advance the understanding of grazing communities in situ and how they respond to environmental conditions and prey communities. This will be one of very few studies of grazers that is unbiased by artificial prey and containment, and will yield both morphologic and genetic information about the organisms present and the distribution patterns of particular grazer populations. This project examines whether the persistence of a group of protistan grazers is determined by its feeding strategy (grazers with specialist feeding strategies are more ephemeral than generalists), and whether certain morphotypes exhibiting generalist feeding strategies have underlying genotypic diversity that maps to specialist feeding strategies. It builds upon an ongoing time series (with hourly resolution since 2006) of automated, high-resolution, measurements of the phytoplankton community by the Imaging FlowCytobot at the Martha's Vineyard Coastal Observatory. These measurements have led to the observation that, in addition to shifts from pico- and small nanoplankton during the summer to larger microplankton in the fall and winter, particular species (especially among the diatoms) exhibit distinct and recurring seasonal patterns. The instrument will be modified to also conduct automated measurements of grazer communities in situ. Links between selected grazer taxa (chosen based on the image time series) and phytoplankton prey will be provided through genetic analyses of individual cells (with their ingested prey). These cells will be obtained by use of a recently developed cell sorter that also captures an image of each sorted cell. In addition to providing predator/prey links, the genetic information will allow the investigators to determine whether a grazer morphotype represents multiple species. A third approach, high throughput sequencing and quantitative PCR analysis of whole water samples, will be applied to investigate abundance patterns of species whose morphology does not reliably map to genotype.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1434440

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