Initial field conditions at Kane‘ohe Bay, Oahu, Hawaii and abundances of Parvocalanus crassirostris and Bestilina similis nauplii, May/June 2013 (EAGER: Copepod nauplii project)

Website: https://www.bco-dmo.org/dataset/712344
Data Type: experimental
Version: 1
Version Date: 2017-08-07

Project
» EAGER: New molecular methods for studying copepod nauplii in the field (EAGER: Copepod nauplii)

Contributors	Affiliation	Role
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Abstract
This dataset reports initial community conditions in Kane'ohe Bay including temperature, salinity, chlorophyll and naupliar abundance of two species of calanoid copepods, Parvocalanus crassirostris and Bestiolina similis as measured by microscopic counts and qPCR. These data are published in MEPS (2017) and are the result of M. Jungbluth's Ph.D. thesis work.

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Coverage

Spatial Extent: **Lat**:21.432 **Lon**:-157.78
Temporal Extent: 2013-05-27 - 2013-06-05

Methods & Sampling

From Jungbluth et al. 2017 – MEPS:

Estimates of in situ naupliar abundance

Naupliar abundances of the 2 target species in situ were estimated using a quantitative polymerase chain reaction (qPCR)-based method (Jungbluth et al. 2013), as well as microscopic counts of calanoid and cyclopoid nauplii. The qPCR-based method allows application of individual species grazing rates to in situ abundances to estimate the total potential grazing impact of each species. Samples were collected by duplicate vertical microplankton net tows (0.5 m diameter ring net, 63 µm mesh) from near bottom (10 m depth) to the surface with a low speed flow meter (General Oceanics). The contents of each net were split quantitatively. One half

was size-fractionated through a series of 5 Nitex sieves (63, 75, 80, 100, and 123 µm) to separate size groups of nauplii from later developmental stages, and each was preserved in 95% non-denatured ethyl alcohol (EtOH). The second half of the sample was preserved immediately in 95% EtOH for counts of total calanoid and total cyclopoid nauplii, which were used for comparison to the qPCR-based results of the abundance of each calanoid species. All samples were stored on ice in the field until being transferred to a -20°C freezer in the laboratory. EtOH in the sample bottles was replaced with fresh EtOH within 12 to 24 h of collection to ensure high-quality DNA for analysis (Bucklin 2000).

The 3 smallest plankton size fractions from the net collection were analyzed with qPCR to enumerate *P. crassirostris* and *B. similis* nauplius abundances (Jungbluth et al. 2013). In brief, DNA was extracted from 3 plankton size fractions (63, 75, and 80 µm) using a modified QIAamp Mini Kit procedure (Qiagen). The total number of DNA copies in each sample was then measured using species-specific DNA primers and qPCR protocols (Jungbluth et al. 2013). On each qPCR plate, 4 to 5 standards spanning 4 to 5 orders of magnitude in DNA copy number were run along with the 2 biological replicates of a size fraction for each sampling date along with a no template control (NTC), all in triplicate. A range of 0.04 to 1 ng µl-1 of total DNA per sample was measured on each plate ensuring that the range of standards encompassed the amplification range of samples, with equal total DNA concentrations run in each well on individual plates. In all cases, amplification efficiencies ranged from 92 to 102%, and melt-curves indicated amplification of only the target species. The qPCR estimate of each species' mitochondrial cytochrome oxidase c subunit I (COI) DNA copy number was converted to an estimate of nauplius abundance using methods described in Jungbluth et al. (2013).

Conditions

Salinity and temperature in the field were measured using a YSI 6600V2 sonde prior to collecting water for bottle incubations. For chl a, triplicate 305 ml samples were filtered onto GF/Fs (Whatman), flash-frozen (LN2), and kept at -80°C freezer until measurements were made 4 mo later. Chl a (and phaeopigment) was measured using a Turner Designs (model 10AU) fluorometer, using the standard extraction and acidification technique (Yentsch & Menzel 1963, Strickland & Parsons 1972).

For complete methodology, see the Supplemental Files section.

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- reformatted date from d-Mon-yy to yyyy-mm-dd

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Data Files

File
physical_MEPS.csv (Comma Separated Values (.csv), 592 bytes) MD5:87e448a80d0674c8af90f6c9806eb04f Primary data file for dataset ID 712344

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Supplemental Files

File
Full Methodology - naupliar grazing expts. filename: Jungbluth_etal_MEPS_2017_Methodology.pdf (Portable Document Format (.pdf), 599.55 KB) MD5:12d9d0250b1a8a2e3bac5812c5dd2b6a Methodology for datasets from project “New molecular methods for studying copepod nauplii in the field” (EAGER: Copepod nauplii) https://www.bco-dmo.org/project/473049

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Related Publications

Jungbluth MJ (2016) Copepod nauplii and their roles in planktonic marine food webs. Oceanography Ph.D. Dissertation, University of Hawai'i at Manoa, Honolulu, Hawaii.
https://pqdtopen.proquest.com/pubnum/10587374.html
Results

Jungbluth, M., Selph, K., Lenz, P., & Goetze, E. (2017). Species-specific grazing and significant trophic impacts by two species of copepod nauplii, Parvocalanus crassirostris and Bestiolina similis. Marine Ecology Progress Series, 572, 57–76. doi:10.3354/meps12139
Results

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Related Datasets

IsRelatedTo

Goetze, E. (2021) **Copepods Parvocalanus crassirostris and Bestiolina similis naupliar ingestion and clearance rates on natural prey assemblages from Kaneohe Bay, Oahu, 2013 (MEPS 2017) (EAGER: Copepod nauplii project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2017-09-01 doi:10.26008/1912/bco-dmo.712293.1 [view at BCO-DMO]

IsReferencedBy

Goetze, E. (2021) **Initial prey abundances for copepod grazing experiments in the Kaneohe Bay, HI, May-June 2013 (MEPS 2017) (EAGER: Copepod nauplii project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2017-09-01 doi:10.26008/1912/bco-dmo.712626.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
experiment	experiment number	unitless
date_local	local date formatted as yyyy-mm-dd	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
sal	seawater salinity	ppt
temp	seawater temperature	degrees celcius
chl_a	chlorophyll-a concentration	micrograms/liter
chl_std_err	standard error of chl_a concentration	micrograms/liter
counted_total_nauplii	counted abundance of total nauplius population	nauplii/liter
counted_total_nauplii_se	standard error of counted_total_nauplii	nauplii/liter
qPCR_Parvocalanus	abundance of Parvocalanus crassirostris nauplii based on qPCR	nauplii/liter
qPCR_Parvocalanus_se	standard error of qPCR_Parvocalanus	nauplii/liter
qPCR_Bestiolina	abundance of Bestiolina similis nauplii based on qPCR	nauplii/liter
qPCR_Bestiolina_se	standard error fo qPCR_Bestiolina	nauplii/liter

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Instruments

Dataset-specific Instrument Name	General Oceanics Digital Flowmeter
Generic Instrument Name	Flow Meter
Dataset-specific Description	Low velocity rotor
Generic Instrument Description	General term for a sensor that quantifies the rate at which fluids (e.g. water or air) pass through sensor packages, instruments, or sampling devices. A flow meter may be mechanical, optical, electromagnetic, etc.

Dataset-specific Instrument Name	
Generic Instrument Name	Microscope - Optical
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

Dataset-specific Instrument Name	microplankton net
Generic Instrument Name	Plankton Net
Dataset-specific Description	0.5 m diameter ring net, 63 µm mesh
Generic Instrument Description	A Plankton Net is a generic term for a sampling net that is used to collect plankton. It is used only when detailed instrument documentation is not available.

Dataset-specific Instrument Name	Roche LC96 thermalcycler
Generic Instrument Name	qPCR Thermal Cycler
Generic Instrument Description	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).

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Deployments

Goetze_2012-2013

Website	https://www.bco-dmo.org/deployment/637678
Platform	lab UHawaii_SOEST
Start Date	2012-03-16
End Date	2013-06-05
Description	microzooplankton studies

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Project Information

EAGER: New molecular methods for studying copepod nauplii in the field (EAGER: Copepod nauplii)

Coverage: Kaneohe Bay, Oahu, Hawaii

Description from NSF Award Abstract:
The most abundant metazoans in the open sea are often the earliest developmental stages of copepods, their nauplii. Nauplii remain under-studied due to the limitations of conventional techniques and an historical emphasis on studying the larger mesozooplankton. However, there is increasing recognition that nauplii play important roles in food web dynamics, and considerable evidence that nauplii may be important trophic intermediaries between microbial and classical food webs due to their high abundance, high weight-specific ingestion rates, and ability to feed on relatively small particles. This team of investigators is developing a novel molecular approach to studying diverse populations of nauplii in mixed field samples based on quantitative Polymerase Chain Reaction (qPCR). They propose to complete development and validation of this qPCR-based technique for enumeration of nauplii, and evaluate its utility in the field. The specific objectives of this research are to identify and reduce technical and biological sources of error in the methodology, determine the accuracy of the method across a range of environmental conditions, and complete one paired field experiment that compares the grazing impact of naupliar and protozoan micro-grazers in a model subtropical coastal ecosystem.

Note: This project is funded by an NSF EAGER award.

Related publications:
Jungbluth, M.J., Goetze, E., and Lenz, P.H. 2013. Measuring copepod naupliar abundance in a subtropical bay using quantitative PCR. Marine Biology, 160: 3125-3141. doi: 10.1007/s00227-013-2300-y

Jungbluth, M.J., and Lenz, P.H. 2013. Copepod diversity in a subtropical bay based on a fragment of the mitochondrial COI gene. Journal of Plankton Research, 35(3): 630-643. doi: 10.1093/plankt/fbt015

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1255697

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