Flow cytometry results for naupliar grazing laboratory experiments conducted from 2012-2013 (EAGER: Copepod nauplii project)

Website: https://www.bco-dmo.org/dataset/637720
Data Type: experimental
Version: 1
Version Date: 2016-02-04

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

Contributors	Affiliation	Role
Goetze, Erica	University of Hawaii at Manoa (SOEST)	Principal Investigator
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Abstract
These data report initial and final measurements of prey abundances in bottle incubation experiments to measure naupliar grazing, 2012-2013.

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Coverage

Spatial Extent: **Lat**:21.4322 **Lon**:-157.7797
Temporal Extent: 2013-05-29 - 2013-06-05

Dataset Description

These data report initial and final measurements of prey abundances in bottle incubation experiments to measure naupliar grazing.

Acquisition Description

All samples were collected from surface water in Southern Kaneohe Bay, Oahu, Hawaii (21°25’56.7”N,

157°46’47.1”W).

Pro, Syn, Peuk, PE+Peuk, HBact data: These data were collected and analyzed by flow cytometry as described in Selph et al. (2011). Briefly, samples were preserved (0.05% paraformaldehyde, final concentration), and frozen to -80°C within 1 h. Batches of samples were thawed, stained with Hoechst 34442 (1 µg/mL final concentration) and analyzed on a flow cytometer (Beckman Coulter Altra) with dual laser excitation (UV range and 488 nm, 200 mW and 1 W, respectively), mated to a Harvard Apparatus syringe pump for quantitative delivery (100 µl at 50 µl min-1). Resulting listmode files were analyzed off-line using FlowJo software (Treestar). Populations determined, based on red fluorescence (chlorophyll, 680±20 nm), orange fluorescence (phycoerythrin, 575±20 nm), blue fluorescence (DNA, 450±40 nm), and light scatter signals (forward and 90°). Distinguishable populations were *Prochlorococcus*, *Synechococcus*, Photosynthetic Eukaryotes (PEUK), High phycoerythrin-containing PEUK (PE+Peuk), and non-pigmented prokaryotes (a.k.a. heterotrophic bacteria, HBACT).

Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- reformatted date from m/d/yyyy to yyyy-mm-dd
- replaced spaces with underscores
- replaced '<' with 'lt_'

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Related Publications

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
General

Selph, K. E., Landry, M. R., Taylor, A. G., Yang, E.-J., Measures, C. I., Yang, J., … Bidigare, R. R. (2011). Spatially-resolved taxon-specific phytoplankton production and grazing dynamics in relation to iron distributions in the Equatorial Pacific between 110 and 140°W. Deep Sea Research Part II: Topical Studies in Oceanography, 58(3-4), 358–377. doi:10.1016/j.dsr2.2010.08.014
Methods

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Related Datasets

IsRelatedTo

Goetze, E., Lenz, P., Selph, K. E. (2021) **Metadata for field dilution experiments to measure community microzooplankton grazing rates in Kaneohe Bay, HI from 2012-2013 (EAGER: Copepod nauplii project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-02-04 doi:10.26008/1912/bco-dmo.637670.1 [view at BCO-DMO]

IsSupplementedBy

Goetze, E., Selph, K. E., Lenz, P. (2016) **Field conditions during grazing experiments in Kaneohe**

Bay, HI during 2012-2013 (EAGER: Copepod nauplii project). Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2016-02-02) Version Date 2016-02-02 http://lod.bco-dmo.org/id/dataset/637695 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
experiment	experiment id	unitless
date_local	local date	yyyy-mm-dd
sample	sample id	unitless
abund_Syn	Synechococcus	cells/mL
abund_Peuk	Photosynthetic Eukaryotes	cells/mL
abund_PE_Peuk	high PhycoErythrin-containing Photosynthetic eukaryotes	cells/mL
abund_Hbact	non-pigmented prokaryotes (Heterotrophic bacteria)	cells/mL

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Flow Cytometer
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

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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

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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