Identification of copepod gut contents analyzed at San Francisco State University in 2013 (Food Limitation in Copepod nauplii project)

Website: https://www.bco-dmo.org/dataset/546723
Data Type: Other Field Results
Version: 2
Version Date: 2021-06-10

Project
» Feeding and food limitation in copepod nauplii, the neglected life stage (food limitation in copepod nauplii)

Contributors	Affiliation	Role
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Dataset Description

Field collected copepod gut content sequences were identified either by comparison to our sequence library of local copepod species or using a sequence similarity approach. Sequences were Blasted using NCBI's web_blast.pl script (http://ncbi.nlm.nih.gov/blast/docs/web_blast.pl). The Blast output was manipulated with perl scripts we wrote to isolate the accession numbers for the BLAST hits, use the accession numbers to get the full records using NCBI's Batch Entrez (http://www.ncbi.nlm.nih.gov/sites/batchentrez), and get the taxonomic information from the full records. See nauplii_gutcontent_sequence.pdf for the output of these programs. We then compared the taxonomic information among the top 10% BLAST scores to assign the sequence to the lowest, taxonomic level shared by the top scoring hits.

Related Reference:

* Craig, Carrie, Wim J. Kimmerer, and C. Sarah Cohen. 2014. A DNA-based method for investigating feeding by copepod nauplii. Journal of Plankton Research 36 (1): 271-275

Methods & Sampling

See Methodology (pdf).

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- replaced blanks with underscores

- Oithona davisae + other -->' changed to 'Oithona_davisae_and_other
- reformated date from mmm/dd/yyyy to yyyy-mm-dd
- removed commas and apostrophes

BCO-DMO data manager processing notes

* Version 2 (2021-06-10) replaces version 1 (2015-01-15). There was an unsupported character in the source file in comment "Rust_pulls_it_out_of_Fungi...". Converted to utf-8.

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Data Files

File
molec_gut_content.csv (Comma Separated Values (.csv), 208.78 KB) MD5:adbd5544ae2246052d5afcf80a784753 Primary data file for dataset ID 546723

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Parameters

Parameter	Description	Units
station	tow location	unitless
date	tow date	yyyy-mm-dd
contig_name	??	unitless
sequence_id	squence identification: sample name followed by sequence number. TDF=adult; TDN = nauplii	unitless
stage	copepod life stage: N=nauplius	unitless
copepod_sp	copepod species - id from SF barcode library	unitless
taxon_Perl	taxonomic id of prey item in gut using Perl program with 10% cut-off	unitless
taxon_level_Perl	taxonomic level of tax id'd from Perl	unitless
taxon_Claident	taxonomic id of prey items in gut using Claident with default settings against SSU_genus database	unitless
taxon_level_Claident	taxonomic level of taxon id'd with Claident	unitless
taxon_notes_Claident	comments on identity matching success	unitless
min_identity_SAP	minimum identity probability of prey items in gut using SAP (Statistical Assignment Program) http://ib.berkeley.edu/labs/slatkin/munch/StatisticalAssignmentPackage.html	proportion
posterior_prob_100_SAP	taxonomic name of SAP results for exact match	unitless
taxon_level_100_SAP	taxonomic level of taxon id'd with SAP and 100% probability	unitless
posterior_prob_95_100_SAP	taxonomic name of SAP results for identity probability at 95-100%	unitless
taxon_level_95_100_SAP	taxonomic level of taxon id'd with SAP and identity probability at 95-100%	unitless
probability	SAP probability	percent
warning_comment	warnings and comments from SAP run	unitless

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Instruments

Dataset-specific Instrument Name	Automated Sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	ABI 3130 Genetic Analyzer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	HPLC
Generic Instrument Name	High-Performance Liquid Chromatograph
Generic Instrument Description	A High-performance liquid chromatograph (HPLC) is a type of liquid chromatography used to separate compounds that are dissolved in solution. HPLC instruments consist of a reservoir of the mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by high pressure pumping of the sample mixture onto a column packed with microspheres coated with the stationary phase. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase.

Dataset-specific Instrument Name	Plankton Net
Generic Instrument Name	Plankton Net
Dataset-specific Description	Mesh size 100 microns or 150 microns
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	Thermal Cycler
Generic Instrument Name	Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. 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. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

Kimmerer_2013

Website	https://www.bco-dmo.org/deployment/546436
Platform	SFSU RTC
Start Date	2009-09-01
End Date	2014-08-31
Description	Copepod feeding studies

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Project Information

Feeding and food limitation in copepod nauplii, the neglected life stage (food limitation in copepod nauplii)

Coverage: San Francisco Estuary

This project will investigate feeding by copepod nauplius larvae, the most abundant metazoans in the sea. It will answer three questions: 1) How does food selection by adults and nauplii differ when they are fed multiple prey species in the laboratory? 2) How does food selection by adults and nauplii differ when they are feeding on natural prey assemblages? and, 3) How do growth, development, and survival differ between copepodites and nauplii when their growth is food limited? Comparative experiments and field-based measurements will contrast the food consumed, and the effects of food limitation, between nauplii and later life stages. This contrast will include attributes of food such as size, taxon, and motility, and will include experiments with cultured prey offered singly or in a mixture, and natural prey, and apply genetic techniques to determine prey consumption by a predatory copepod. Copepods will be collected from the San Francisco Estuary, with four species selected for experiments to span taxonomic groups, sizes, salinity ranges, and general feeding behavior. A variety of techniques will be applied to account for the inevitable biases and limitations of each; all but one have previously been applied in our laboratories. These will include laboratory feeding experiments using cultured prey individually and in mixtures, and experiments using natural prey. Consumption of prey in experimental bottles will be measured as chlorophyll concentration and through particle counts by microscopy and flow cytometry. Radioactively labeled prey will be used in short incubations to determine feeding on particular prey types. Samples from the field will be examined for gut fluorescence. Separate experiments will determine how nauplii and copepodites survive and grow at different concentrations of food. Investigations of feeding by a predatory copepod (Tortanus dextrilobatus) will use molecular techniques to identify mitochondrial and nuclear DNA from diverse suspected prey species. Specific primers will be developed for common zooplankton species consumed by T. dextrilobatus in the laboratory. General primers and screening protocols developed here will be useful for identifying food web interactions in other estuarine communities.

Copepod nauplii are important both in their diverse trophic roles in ocean foodwebs and in the population dynamics of copepods. Nauplii have a completely different feeding apparatus from later stages, and the first feeding stage can be very sensitive to starvation, making these life stages critical to population dynamics. Yet extant copepod population models treat nauplii as miniature adults. This work will provide valuable input to the growing efforts at modeling ocean ecosystems.

Further details from final report (pdf)

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0929075

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