Data from: Iacchei, M., E. Butcher, E. Portner, Goetze, E. (in press) It's about time: Insights into temporal genetic patterns in oceanic zooplankton from biodiversity indices.

Website: https://www.bco-dmo.org/dataset/681997
Data Type: Cruise Results
Version: 10 February 2017
Version Date: 2017-02-10

Project
» Basin-scale genetics of marine zooplankton (Plankton Population Genetics)
» Does habitat specialization drive population genetic structure of oceanic zooplankton? (Plankton_PopStructure)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **Lat**:22.75 **Lon**:-158
Temporal Extent: 2012-09-01 - 2013-10-31

Dataset Description

This dataset consists of mitochondrial sequence data and specimen information for two species of copepods, *Haloptilus longicornis* and *Pleuromamma xiphias*, collected at an open ocean time series site in the North Pacific Subtropical Gyre (station ALOHA, 22.45N, 158W) during 11 of the routine Hawai'i Ocean Time-series (HOT) research cruises from September of 2012 to October of 2013 (HOT-246 to HOT-256). Data for *Haloptilus longicornis* include a 546 base-pair fragment of mitochondrial cytochrome *c* oxidase subunit II for each of 483 individuals (mean of 44 animals per cruise). Data for *Pleuromamma xiphias* include a 551 base-pair fragment of mitochondrial cytochrome *c* oxidase subunit I for each of 510 individuals (mean of 46 animals per cruise). Information is also provided on the HOT cruise number, date, and specific tow from which each individual was collected. Life stage and sex of each animal are also noted when identifiable

These data are associated with the forthcoming publication:
Iacchei, M., E. Butcher, E. Portner, Goetze, E. (in press) It's about time: Insights into temporal genetic patterns in oceanic zooplankton from biodiversity indices. *Limnology and Oceanography*

The unique haplotypes in these data are also available under NCBI accession numbers KY560470 - KY560514 [*Haloptilus longicornis*], KY560515 - KY560565 [*Pleuromamma xiphias*].

The following files have been included in this dataset (note that the sequence IDs in these files differ from the

NCBI sequence IDs):
HOT-HALO.fasta: A fasta-formatted text file containing sequences for a portion of the mitochondrial cytochrome *c* oxidase subunit II gene (COII; 546 bp) for 483 *Haloptilus longicornis* individuals collected at Station ALOHA.

HOT-PLXI.fasta: A fasta-formatted text file containing sequences for a portion of the mitochondrial cytochrome *c* oxidase subunit I gene (COI; 551 bp) for 510 *Pleuromamma xiphias* individuals collected at Station ALOHA.

HALO.csv and PLXI.csv: Converted to csv from an Excel file consisting of one worksheet for *Haloptilus longicornis* and one worksheet for *Pleuromamma xiphias.* In each worksheet, column headings designate:
sample_id: the sample ID number associated with the original organism collected, DNA extraction, and PCR amplification.
sequence_id: the sample ID number associated with sequences analysed for the project.
genus: Genus of the collected organism.
species: Species of the collected organism.
cruise: The cruise number for the Hawai'i Ocean Time Series (HOT) cruise on which the specimen was collected.
tow: The net tow number on which the specimen was collected.
collection_date: The date on which the specimen was collected, formatted as yyyy-mm-dd.
stage_sex: The life stage (Copepodite or Adult) of the individual, and the sex (Copepodite, Female, Male).
stage: The life stage (Copepodite or Adult) of the individual. Column added by BCO-DMO from the original stage_sex column for ease of use.
sex: The sex (Copepodite, Female, or Male) of the individual. Column added by BCO-DMO from the original stage_sex column for ease of use.
mtCO*_sequence: The mtDNA sequence (COII for *Haloptilus longicornis;* COI for *Pleuromamma xiphias*) associated with that individual. This sequence matches the sequence associated with the Sequence ID number in the respective fasta file.

Methods & Sampling

Collection: Bulk zooplankton were collected at an open ocean time series site in the North Pacific Subtropical Gyre (station ALOHA, 22.45N, 158W) during 11 of the routine Hawai'i Ocean Time-series (HOT) research cruises at approximately monthly intervals from September of 2012 to October of 2013 (HOT-246 to HOT-256). Mesozooplankton were collected using a 1 m2, 200 um-mesh ring net towed obliquely from a mean maximum depth of 155 m (SD = 31 m) to the sea surface. Zooplankton for this study were collected from three nighttime tows completed between the hours of 2200-0200 on consecutive nights for each sampling period so that all collections for a single cruise were collected within three days of one another. Following net retrieval, bulk plankton were quantitatively split using a Folsom plankton splitter, and 1/4 of the material was preserved in 95% non-denatured ethyl alcohol (EtOH) and stored at -20C. From these bulk collections, 50 *Haloptilus longicornis* and 50 *Pleuromamma xiphias* individuals were sorted from each net tow for use in this study.

mtDNA Sequence Generation: For both *H. longicornis* and *P. xiphias,* DNA was extracted using the Qiagen DNeasy Blood and Tissue Kit (Qiagen, Inc., Valencia, CA). For *H. longicornis*, a 546 base-pair fragment of the mitochondrial cytochrome *c* oxidase subunit II (mtCOII) gene was amplified by polymerase chain reaction (PCR) with species-specific primers COII_F6 and COII_R9. For *P. xiphias,* a 551 base-pair fragment of the mitochondrial cytochrome *c* oxidase subunit I (mtCOI) was amplified by PCR using species-specific primers PLXI_VH and PLXI_VL. Specific information on primer sequences, PCR reaction mixes, thermal cycler conditions, and PCR purification is provided in the manuscript associated with this submission. Purified PCR products were sequenced on an ABI 3730XL capillary sequencer (Applied Biosystems, Foster City, CA). Sequences were aligned, edited and trimmed using Geneious 7.0.6 (Biomatters, Ltd., Auckland, New Zealand). Unique haplotypes were identified using the Haplotype Collapser and Converter in FaBox 1.35 (http://users-birc.au.dk/biopv/php/fabox/), and deposited with their respective protein translations in GenBank under accession numbers: KY560470 - KY560565. An mtDNA sequence for each individual specimen is deposited in this BCO-DMO submission as part of one of two fasta files. Each fasta file contains the mtDNA sequence fragments from all individuals from a single species aligned together.

Methodology is further described in the paper itself:
Iacchei, M., E. Butcher, E. Portner, Goetze, E. (in press) It's about time: Insights into temporal genetic patterns in oceanic zooplankton from biodiversity indices. *Limnology and Oceanography*

Data Processing Description

BCO-DMO Processing:
- re-formatted the date column to yyyy-mm-dd;
- created separate columns for stage and sex;
- generated csv files from the Excel file submitted.

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Data Files

File
lacchei_files.csv (Comma Separated Values (.csv), 1.21 KB) MD5:fcd82646a576b7bca53cd77ad333855a Primary data file for dataset ID 681997

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Parameters

Parameter	Description	Units
file_link	Link to data file containing sequence information.	unitless
description	Description of data in file.	unitless

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Instruments

Dataset-specific Instrument Name	Folsom Plankton Splitter
Generic Instrument Name	Folsom Plankton Splitter
Dataset-specific Description	Following net retrieval, bulk plankton were quantitatively split using a Folsom plankton splitter.
Generic Instrument Description	A device for sub-sampling of plankton and ichthyoplankton samples by splitting, developed by Dr. Folsom of the Scripps Institute of Oceanography. Ideally suited for splitting plankton samples with minimal debris. A measured volume of plankton sample is placed in the undivided section of the drum. This is rotated 120 degrees to divide the stirred sample with a separating blade. Standard Methods suggests splitting until a subsample of 200-500 individuals is obtained.

Dataset-specific Instrument Name	mesh ring net
Generic Instrument Name	Ring Net
Dataset-specific Description	Mesozooplankton were collected using a 1 m2, 200 um-mesh ring net towed obliquely from a mean maximum depth of 155 m (SD = 31 m) to the sea surface.
Generic Instrument Description	A Ring Net is a generic plankton net, made by attaching a net of any mesh size to a metal ring of any diameter. There are 1 meter, .75 meter, .25 meter and .5 meter nets that are used regularly. The most common zooplankton ring net is 1 meter in diameter and of mesh size .333mm, also known as a 'meter net' (see Meter Net).

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Specific information on primer sequences, PCR reaction mixes, thermal cycler conditions, and PCR purification is provided in the manuscript associated with this submission.
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

HOT_cruises

Website	https://www.bco-dmo.org/deployment/58879
Platform	Multiple Vessels
Report	http://hahana.soest.hawaii.edu/hot/
Start Date	1988-10-31
Description	Since October 1988, the Hawaii Ocean Time-series (HOT) program has investigated temporal dynamics in biology, physics, and chemistry at Stn. ALOHA (22°45' N, 158°W), a deep ocean field site in the oligotrophic North Pacific Subtropical Gyre (NPSG). HOT conducts near monthly ship-based sampling and makes continuous observations from moored instruments to document and study NPSG climate and ecosystem variability over semi-diurnal to decadal time scales.

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Project Information

Basin-scale genetics of marine zooplankton (Plankton Population Genetics)

Coverage: Atlantic Ocean, 46 N - 46 S

Description from NSF award abstract:
Marine zooplankton show strong ecological responses to climate change, but little is known about their capacity for evolutionary response. Many authors have assumed that the evolutionary potential of zooplankton is limited. However, recent studies provide circumstantial evidence for the idea that selection is a dominant evolutionary force acting on these species, and that genetic isolation can be achieved at regional spatial scales in pelagic habitats. This RAPID project will take advantage of a unique opportunity for basin-scale transect sampling through participation in the Atlantic Meridional Transect (AMT) cruise in 2014. The cruise will traverse more than 90 degrees of latitude in the Atlantic Ocean and include boreal-temperate, subtropical and tropical waters. Zooplankton samples will be collected along the transect, and mitochondrial and microsatellite markers will be used to identify the geographic location of strong genetic breaks within three copepod species. Bayesian and coalescent analytical techniques will test if these regions act as dispersal barriers. The physiological condition of animals collected in distinct ocean habitats will be assessed by measurements of egg production (at sea) as well as body size (condition index), dry weight, and carbon and nitrogen content. The PI will test the prediction that ocean regions that serve as dispersal barriers for marine holoplankton are areas of poor-quality habitat for the target species, and that this is a dominant mechanism driving population genetic structure in oceanic zooplankton.

Note: This project is funded by an NSF RAPID award. This RAPID grant supported the shiptime costs, and all the sampling reported in the AMT24 zooplankton ecology cruise report (PDF).

Online science outreach blog at: https://atlanticplankton.wordpress.com

Does habitat specialization drive population genetic structure of oceanic zooplankton? (Plankton_PopStructure)

Coverage: Global Ocean

Description from NSF award abstract:
This research will test whether habitat depth specialization is a primary trait driving large-scale population genetic structure in open ocean zooplankton species. Very little is known about population connectivity in marine zooplankton. Although zooplankton were long thought to be high-gene-flow systems with little genetic differentiation among populations, recent observations have challenged this view. In fact, zooplankton species may be genetically subdivided at macrogeographic, regional, or even smaller spatial scales. Recent studies also indicate that subtle, species-specific ecological factors play an important role in controlling gene flow among plankton populations. The investigator hypothesizes that depth-related habitat, including diel vertical migration (DVM) behavior, plays a critical role in controlling dispersal of plankton among ocean regions, through interactions with ocean circulation and bathymetry. This study will compare the population genetic structures of eight planktonic copepods that utilize different depth-related habitats, in order to test key predictions of genetic structure based on the interaction of organismal depth with the oceanographic environment. The objectives of the research are to:
1) Develop novel nuclear markers that can be used to resolve genetic structure and estimate gene flow among copepod populations,
2) Characterize the spatial patterns of gene flow among populations in distinct ocean regions of the Atlantic, Pacific, and Indian Oceans for eight target species using a multilocus approach, and
3) Test the central hypothesis that depth-related habitat will significantly impact the extent of genetic structure both across and within ocean basins, the magnitude and direction of gene flow among populations, and in the timing of major slitting events within species.

Drawing on genomic resources (cDNA libraries) recently developed by the PI, five (or more) polymorphic nuclear markers will be developed for each species. These new markers will be used, in combination with the mitochondrial gene cytochrome oxidase I, to characterize the population genetic structure of each species throughout its global distribution using graph theoretic and coalescent analytical techniques. Gene flow among populations and the timing of major splitting events will be estimated under a coalescent model (IMa), and

empirical support for the hypothesis of depth-related trends in population structure will be assessed using graph theoretic congruence tests. Because the depth specialization and diel vertical migration behaviors of the target species are representative of distinct zooplankton species groups, the results of this study will have broad implications for understanding and predicting the genetic structure of these important grazers in pelagic ecosystems.

Publications produced with support from this award include:
Burridge, A., Goetze, E., Raes, N., Huisman, J., Peijnenburg, K. T. C. A. (in revision) Global biogeography and evolution of *Cuvierina* pteropods. *BMC Evolutionary Biology*.

Andrews, K. R., Norton, E. L., Fernandez-Silva, I., Portner†, E. Goetze, E. (in press) Multilocus evidence for globally-distributed cryptic species and distinct populations across ocean gyres in a mesopelagic copepod. *Molecular Ecology.*

Halbert , K. M. K., Goetze, E., Carlon, D. B. (2013) High cryptic diversity across the global range of the migratory planktonic copepods *Pleuromamma piseki* and *P. gracilis*. *PLOS One* 8(10): e77011. doi:10.1371/journal.pone.0077011

Norton , E. L., Goetze, E. (2013) Equatorial dispersal barriers and limited connectivity among oceans in a planktonic copepod. *Limnology and Oceanography* 58: 1581-1596.

Peijnenburg, K. T. C. A., Goetze, E. (2013) High evolutionary potential of marine zooplankton. *Ecology & Evolution* 3(8): 2765-2781. doi: 10.1002/ece3.644 (both authors contributed equally).

Fernandez-Silva, I., Whitney, J., Wainwright, B., Andrews, K. R., Ylitalo-Ward, H., Bowen, B. W., Toonen, R. J., Goetze, E., Karl, S. A. (2013) Microsatellites for Next-Generation Ecologists: A Post-Sequencing Bioinformatics Pipeline. *PLOS One* 8(2): e55990. doi:10.1371/journal.pone.0055990

Bron, J. E., Frisch, D., Goetze, E., Johnson, S. C., Lee, C. E., Wyngaard, G. A. (2011) Observing Copepods through a Genomic Lens. *Frontiers in Zoology* 8: 22.

Goetze, E. (2011) Population differentiation in the open sea: Insights from the pelagic copepod *Pleuromamma xiphias*. *Integrative and Comparative Biology* 51: 580-597.

Master's theses supported under this award include:

Emily L. Norton. *Empirical and biophysical modeling studies of dispersal barriers for marine plankton*. (2013). University of Hawaii at Manoa.

K. M. K. Halbert. *Genetic isolation in the open sea: Cryptic diversity in the Pleuromamma piseki - P. gracilis species complex*. (2013). University of Hawaii at Manoa.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1260164
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NSF Division of Ocean Sciences (NSF OCE)	OCE-1522572

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