Dataset: 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.

Project(s): Hawaii Ocean Time-series (HOT): Sustaining ocean ecosystem and climate observations in the North Pacific Subtropical Gyre (HOT)
Basin-scale genetics of marine zooplankton (Plankton Population Genetics)
Does habitat specialization drive population genetic structure of oceanic zooplankton? (Plankton_PopStructure)

Abstract: This submission 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, 22.45°N, 158°W) 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 includes a 546 base-pair fragment of mitochondrial cytochrome c oxidase subunit II for each of 483 individuals (mean of 44 animals per cruise), along with information 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. Data for Pleuromamma xiphias includes a 551 base-pair fragment of mitochondrial cytochrome c oxidase subunit I for each of 510 individuals (mean of 46 animals per cruise), along with information 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 were used to investigate the temporal variation in the genetic composition of populations of these two planktonic copepod species at station ALOHA through an annual cycle. For a complete list of measurements, refer to the supplemental document 'Field_names.pdf', and a full dataset description is included in the supplemental file 'Dataset_description.pdf'. The most current version of this dataset is available at: http://www.bco-dmo.org/dataset/681997

Description: Temporal genetic patterns in P. xiphias and H. longicornis - Mitochondrial data, station ALOHA

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.

Acquisition Description:

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 m^2, 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*

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.

Deployment Information

Deployment description for Unknown Platform HOT_cruises

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.

Instrument Information

Instrument	mesh ring net
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 Name	Ring Net
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).

Instrument	

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 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 rises and lowers the temperature of the block in discrete, pre-programmed steps. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

Instrument	Folsom Plankton Splitter
Description	Following net retrieval, bulk plankton were quantitatively split using a Folsom plankton splitter.
Generic Instrument Name	Folsom Plankton Splitter
Generic Instrument Description	A Folsom Plankton Splitter is used for sub-sampling of plankton and ichthyoplankton samples.