Population genomics study on the planktonic copepod Haloptilus longicornis: RADSeq data and metadata (Plankton Population Genetics project)

Website: https://www.bco-dmo.org/dataset/699954
Data Type: Cruise Results
Version: 0
Version Date: 2017-05-15

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

Contributors	Affiliation	Role
Goetze, Erica	University of Hawaii at Manoa (SOEST)	Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Population genomics study on the planktonic copepod Haloptilus longicornis: RADSeq data and metadata

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Dataset Description

This data submission consists of specimen collection information and next-generation sequencing data (Illumina MiSeq v3 - 300bp PE reads) from pooled DNA libraries of three putative Haloptilus longicornis clades that have sympatric distributions in the North Atlantic Ocean. Specimens were collected during the 2010 Atlantic Meridional Transect cruise (AMT20). 113 total H. longicornis were pooled into three clades as defined by reciprocal monophly and fixed differences in mtDNA cytochrome oxidase c subunit II. The aim of this project is to utilize reduced representation genomic data to assess whether there is concordance between the three putative H. longicornis clades demarcated with mtCOII and clades determined using other regions of the genome. Earlier work indicates only two clades are detected using microsatellite loci, and this project will broaden the genomic scope of that investigation.

The sequences are archived at NCBI,
BioProject PRJNA369182 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA369182]

The publisher requires that this item is embargoed until **2018-01-01**. Please check back after **2018-01-01**.

Methods & Sampling

If you have further questions, please contact the corresponding author (Dr. Erica Goetze): egoetze[at]hawaii[dot]edu.

From the cruise report: not yet available

Sample collection. A total of 113 H. longicornis individuals from three putative clades were collected from five different locations in the North Atlantic Basin during the Atlantic Meridional Transect cruise in 2010 (AMT20) for

this analysis. 81 individuals from putative clade 1 were collected from two sites, 20 individuals from putative clade 2 were collected from four sites (one of which was the same as one of the clade one locations), and 12 individuals from putative clade 3 were collected from the same four sites as the clade 2 individuals.

Data Processing Description

Contact: Erica Goetze for any questions, or for subsequent use of these data.

BCO-DMO Processing Notes:
added conventional header with dataset name, PI name, version date
modified parameter names to conform with BCO-DMO naming conventions
combined SRA metadata with collection information
converted latitude and longitude to decimal degrees

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Parameters

Parameter	Description	Units
bioproject_accession	NCBI BioProject accession number	unitless
biosample_accession	NCBI BioSample accession number	unitless
library_ID	NCBI Library identifier	unitless
title	NCBI sample title	unitless
sample_name	short sample identifier	unitless
design_description	NCBI Free-form description of the methods used to create the sequencing library; a brief 'materials and methods' section.	unitless
filename	NCBI file name	unitless
cruise_id	cruise identifier	unitless
station	station number	unitless
lat_collection	latitude; north is positive	decimal degrees
lon_collection	longitude; east is positive	decimal degrees
date_collection	collection date formatted as yyyy-mm-dd	unitless

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 2500
Generic Instrument Name	Automated DNA Sequencer
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	WP2
Generic Instrument Name	Bongo Net
Dataset-specific Description	200µm mesh size; 0-300 meters vertical haul to collect copepods.
Generic Instrument Description	A Bongo Net consists of paired plankton nets, typically with a 60 cm diameter mouth opening and varying mesh sizes, 10 to 1000 micron. The Bongo Frame was designed by the National Marine Fisheries Service for use in the MARMAP program. It consists of two cylindrical collars connected with a yoke so that replicate samples are collected at the same time. Variations in models are designed for either vertical hauls (OI-2500 = NMFS Pairovet-Style, MARMAP Bongo, CalVET) or both oblique and vertical hauls (Aquatic Research). The OI-1200 has an opening and closing mechanism that allows discrete "known-depth" sampling. This model is large enough to filter water at the rate of 47.5 m3/minute when towing at a speed of two knots. More information: Ocean Instruments, Aquatic Research, Sea-Gear

Dataset-specific Instrument Name	
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

JC079

Website	https://www.bco-dmo.org/deployment/540458
Platform	RRS James Cook
Report	http://dmoserv3.whoi.edu/data_docs/Goetze/AMT22_cruise/jc079.pdf
Start Date	2012-10-10
End Date	2012-11-24
Description	The AMT22 cruise set sail from Southampton in the UK on 10 October 2012 and arrived in Punta Arenas, Chile on 24 November 2012. The final cruise report and other cruise information, including all science components, can be found online at the Atlantic Meridional Transect webpage (http://www.amt-uk.org/Cruises), or through the British Oceanographic Data Centre (BODC) (http://www.bodc.ac.uk/projects/uk/amt/). Zooplankton ecology data from the project "Does habitat specialization drive population genetic structure of oceanic zooplankton?" (NSF OCE-1029478) were collected on this cruise.

JC053

Website	https://www.bco-dmo.org/deployment/737883
Platform	RRS James Cook
Start Date	2010-10-12
End Date	2010-11-25
Description	From: https://www.bodc.ac.uk/resources/inventories/cruise_inventory/report/9969/ AMT20 (JC053) is the third cruise of the third phase of the Atlantic Meridional Transect (AMT) programme. The programme is hosted by Plymouth Marine Laboratory in collaboration with the National Oceanography Centre, Southampton, provides an exceptional opportunity for nationally and internationally driven collaborative research, and provides a platform for excellent multi-disciplinary oceanographic research. As an in situ observation system, AMT informs on changes in biodiversity and function of the Atlantic ecosystem during this period of rapid change to our climate and biosphere. The aims of the AMT programme [www.amt-uk.org] are to quantify the nature and causes of ecological and biogeochemical variability in the planktonic ecosystems of the Atlantic Ocean, and to assess the effects of this variability on biological carbon cycling and air-sea exchange of radiatively active gases and aerosols. Between 1995 and 2005 marine and atmospheric data were collected twice a year along a 13,500 km transect in the Atlantic Ocean. The cruise track enabled biogeochemical measurements to be made within the poorly studied North and South Atlantic oligotrophic gyres as well as within equatorial and coastal upwelling regions. The range of ecosystems sampled has facilitated the calibration and validation of newly developed techniques, provided a testbed for comparative ecology and enabled the development of atmospheric and oceanographic models. The unique AMT dataset continues to be deposited and made available to the wider community through the British Oceanographic Data Centre.

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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

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1338959

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