Population genomics study on the planktonic pteropod Cuvierina spp.: RADSeq data and metadata (Plankton Population Genetics project)

Website: https://www.bco-dmo.org/dataset/699933
Data Type: Cruise Results
Version: 1
Version Date: 2017-05-15

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

Contributors	Affiliation	Role
Goetze, Erica	University of Hawai'i at Mānoa (SOEST)	Principal Investigator
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Coverage

Spatial Extent: **N**:41.48 **E**:-25 **S**:-30.17 **W**:-39
Temporal Extent: 2004-07-01 - 2012-11-12

Dataset Description

This dataset includes RADSeq data as well as NCBI Short Read Archive (SRA) BioProject and BioSample accessions and collection metadata from animals collected on Atlantic Meridional Transect 22 (AMT22) in Oct. - Nov. 2012. Field work was conducted on the RRS James Cook cruise JC079. See NCBI GenBank Bioproject PRJNA369277 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA369277]

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

Methods & Sampling

Please refer to the paper for methodological details. If you have further questions, please contact the corresponding author (Dr. Erica Goetze): egoetze[at]hawaii[dot]edu.

From the cruise report:

Sample collection. Plankton samples were collected with 0.71m diameter bongo nets (200, 333 µm), and with an RMT1 midwater trawl (333 µm) that has a nominal mouth area of 1m2. A total of 50 plankton tows were conducted along the cruise leg (Table 1), with 35 tows conducted using the bongo and 14 samples collected with the RMT net. The bongo tows were oblique tows that sampled from between 211 to 488 m depth and the surface (324m average maximum depth of tow). The bongo samples will be used for quantitative estimates of animal abundance along the cruise leg (target species only, tows conducted with timedepth-

recorder and flowmeter). The RMT tows were also oblique tows that sampled between 62 to 216 m depth and the surface (153 m average maximum depth of tow). All tows except one (station 42) were conducted at night, in order to efficiently sample the migratory community.

Sample handling and preservation. All plankton from the 200 µm mesh bongo net was preserved immediately in 100% ethyl alcohol for use in molecular studies, including DNA sequencing and microsatellite genotyping (and possibly RAD tag sequencing), in addition to estimates of abundance of target species. Plankton material from the 333 µm mesh bongo net and the RMT net was sorted live immediately following collection, and animals were individually identified, and preserved in acetone, RNALater, cryopreserved, and in some cases used for live imaging prior to preservation. These animals will be used for molecular, genomic and transcriptomic analyses. Both RNA/DNA ratios and prosome length - dry weight relationships will be used as measures of animal condition in copepods. In total, over 17,000 animals from 40 target species were individually sorted and preserved for this panel of measurements. Following live sorting and imaging of the 333 µm samples, the remaining plankton was preserved either in 4% buffered formalin or 100% ethyl alcohol for morphological studies.

Illumina sequence files:

This submission consists of reduced representation genomic data for 26 individual pteropod specimens in the genus Cuvierina. Specimens were collected during the Atlantic Meridional Transect cruise in 2012 (AMT22) as well as a Mar-Eco cruise. Our research goals were to examine genomic divergence and species boundaries in these morphologically and ecologically distinct pteropod populations in adjacent ocean regions of the subtropical and equatorial Atlantic. We are interested in local adaptation of these populations to distinct oceanographic habitats.

Genetic data consists of 300 bp paired-end sequence reads generated using an Illumina MiSeq sequencer. Two MiSeq lanes were run; approximately 400mB to 1GB of data were generated for each library, with a mean of 700mB per individual. Libraries for individuals #1, 2, 3, 4, 9, 10, 11, 12, 16, 17, 18, 19, and 25 were run together on a single MiSeq lane, and libraries for individuals #5, 6, 7, 8, 13, 14, 15, 20, 21, 22, 23, 24, and 26 were run together on a second lane.

The raw data was cleaned of adapters, trimmed of poor sequence, and filtered for non-specific sequencing. Cutadapt v. 1.9.1 was used to remove the Truseq Illumina Adapters (LT), using a 90% mismatch parameter (-e 0.10) and a minimum adapter match overlap of 12 bp (-O 12). Reads that did not contain an adapter (potentially non-specific sequencing) were removed from the dataset (--discard-trimmed). Read 1 and read 2 were paired using the custom python script, "fastqCombinePairedEnd.py", and read pairs were verified using the custom Perl script, "FastqPairedEndValidator.pl". Trimmed, cleaned, and paired reads were checked for sequence quality using FastQC.

This post-sequence processing resulted in three files included for each individual library: *.R1.fq (All read 1s that paired with a read 2), *.R2.fq (All read 2s that paired with a read 1), and *.R1.clean.fq_singles.fastq (unpaired reads), with the * representing each respective putative Cuvierina sp. individual.

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
biosample_accession	NCBI BioSample accession number	unitless
library_ID	NCBI Library identifier	unitless
filename	NCBI filename	unitless
sample_title	NCBI sample title	unitless
cruise_id	cruise identifier	unitless
station	station number	unitless
date_collection	collection date formatted as yyyy-mm-dd	unitless
lat_collection	latitude; north is positive	decimal degrees
lon_collection	longitude; east is positive	decimal degrees
sample_id	sample identifier	unitless
sample_name	short sample identifier	unitless

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 2500
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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.

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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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