NCBI Sequence Read Archive (SRA) accession numbers for fastq sequence files for each zooplankton community sample (Plankton Population Genetics project)

Website: https://www.bco-dmo.org/dataset/700961
Data Type: Other Field Results
Version:
Version Date: 2017-05-25

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

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Table of Contents

- Coverage
- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

Coverage

Spatial Extent: **Lat**:22.75 **Lon**:-158
Temporal Extent: 2014-06-13 - 2014-06-19

Dataset Description

These data include sample information and accession links to sequence data at The National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA).

This data submission consists of metabarcoding data for the zooplankton community in the epipelagic, mesopelagic and upper bathypelagic zones (0-1500m) of the North Pacific Subtropical Gyre. The goal of this study was to assess the hidden diversity present in zooplankton assemblages in midwaters, and detect vertical gradients in species richness, depth distributions, and community composition of the full zooplankton assemblage. Samples were collected in June 2014 from Station ALOHA (22.75, -158) using a 1 meter square Multiple Opening and Closing Nets and Environmental Sampling System (MOCNESS, 200um mesh), on R/V Falkor cruise FK140613. Next generation sequence data (Illumina MiSeq, V3 chemistry, 300-bp paired-end) of the zooplankton assemblage derive from amplicons of the V1-V2 region of 18S rRNA (primers described in Fonseca et al. 2010). The data includes sequences and read count abundance information for molecular OTUs from both holoplanktonic and meroplanktonic taxa

Related dataset containing OTU tables and fasta sequences (representative / most abundance read for each OTU):
Metabarcoding zooplankton at station ALOHA: OTU tables and fasta files

Methods & Sampling

SAMPLE INFORMATION

Sample identifiers include the following codes.

MOCNESS tow
FA3: Night sampling
FA4: Day sampling

Depth range:
N1: 1500-1000m
N2: 1000-700m
N3: 700-500m
N4: 500-300m
N5: 300-200m
N6: 200-150m
N7: 150-100m
N8: 100-50m
N9: 50m-0m

Wet-sieved zooplankton size fractions
SF1: 0.2-0.5 mm
SF2: 0.5-1.0 mm
SF3: 1.0-2.0 mm

Data Processing Description

BCO-DMO processing notes:
* commas in the data were replaced with semicolons to support export as csv format.

[table of contents | back to top]

Data Files

File
SRA.csv (Comma Separated Values (.csv), 20.94 KB) MD5:22200d6c11cd04c32cf3a29e3d687956 Primary data file for dataset ID 700961

[table of contents | back to top]

Parameters

Parameter	Description	Units
analysis_name	Descriptive name of analysis including percent clustering and subsampling or no subsampling	unitless
lat	Latitude of sample site (Station ALOHA)	decimal degrees
lon	Longitude of sample site (Station ALOHA)	decimal degrees
library_ID	Short unique identifier for the sequencing library.	unitless
bioproject_accession	NCBI BioProject identifier	unitless
biosample_accession	NCBI BioSample identifier	unitless
title	Short description that will identify the dataset on public pages.	unitless
library_strategy	Amplicon = Sequencing of overlapping or distinct PCR or RT-PCR products	unitless
library_source	Metagenomic = Mixed material from metagenome	unitless
library_selection	PCR = Source material was selected by designed primers	unitless
library_layout	Paired-end or Single	unitless
platform	Sequencing platforms [Illumina]	unitless
instrument_model	Illumina instrument and model used for sequencing	unitless
design_description	Free-form description of the methods used to create the sequencing library; a brief materials and methods section.	unitless
bioproject_link	bioproject_link	unitless
biosample_link	biosample_link	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina MiSeq using V3 chemistry (300-bp, paired-end)
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	Agilent 2100 Bioanalyzer
Generic Instrument Name	Bioanalyzer
Generic Instrument Description	A Bioanalyzer is a laboratory instrument that provides the sizing and quantification of DNA, RNA, and proteins. One example is the Agilent Bioanalyzer 2100.

Dataset-specific Instrument Name	quantitative PCR by the Evolutionary Genetics Core Facility (Hawaii Institute of Marine Biology)
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)

[table of contents | back to top]

Deployments

FK140613

Website	https://www.bco-dmo.org/deployment/700613
Platform	R/V Falkor
Start Date	2014-06-13
End Date	2014-06-19
Description	Student Cruise #3 More about this cruise from the Schmidt Ocean Institute page:https://schmidtocean.org/cruise/net-gains-at-station-aloha/

[table of contents | back to top]

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

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1255697
NSF Division of Ocean Sciences (NSF OCE)	OCE-1338959
NSF Division of Ocean Sciences (NSF OCE)	OCE-1029478

[table of contents | back to top]