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

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

Abstract: This data 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,-158.00) using a 1-meter square Multiple Opening and Closing Nets and Environmental Sampling System (MOCNESS, 200um mesh). 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). These data include sample information and accession links to raw sequence data at The National Center for Biotechnology Information (NCBI). 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/700961

Description: NCBI Sequence Read Archive (SRA) accession numbers for fastq sequence files for each zooplankton community sample

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

Acquisition Description:

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

Processing Description:

BCO-DMO processing notes:

* commas in the data were replaced with semicolons to support export as csv format.

Deployment Information

Deployment description for R/V Falkor FK140613

Student Cruise #3 More about this cruise from the Schmidt Ocean Institute page:https://schmidtocean.org/cruise/net-gains-at-station-aloha/

Instrument Information

Instrument	Illumina MiSeq

Description	Illumina MiSeq using V3 chemistry (300-bp, paired-end)
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.

Instrument	quantitative PCR by the Evolutionary Genetics Core Facility (Hawaii Institute of Marine Biology)
Description	*local description not specified*
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 raises 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	Agilent 2100 Bioanalyzer
Description	*local description not specified*
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.