Metadata associated with genomic and genetic data collected from organisms obtained on BOWLs landers, R/V Oceanus June 22-27, 2014 (BOWLS project)

Website: https://www.bco-dmo.org/dataset/662996
Data Type: Cruise Results
Version: 1
Version Date: 2016-10-26

Project
» Biodiversity, connectivity and ecosystem function in organic-rich whale-bone and wood-fall habitats in the deep sea (BOWLS)

Contributors	Affiliation	Role
Smith, Craig R.	University of Hawaii at Manoa (SOEST)	Principal Investigator
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Abstract
Metadata associated with genomic and genetic data collected from organisms obtained on BOWLs landers, R/V Oceanus June 22-27, 2014.

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Coverage

Spatial Extent: **N**:65.09983 **E**:-63.16567 **S**:43.9087 **W**:-127.59288
Temporal Extent: 2014-06-22

Methods & Sampling

The investigators deployed four free-vehicle Bone-Wood Landers (BOWLs) as moorings that (1) sink autonomously to the deep-sea floor, (2) expose 9 controlled experimental substrates of whale bone, wood, or inert materials at the seafloor for months to years, and (3) upon acoustic command, enclose each experimental substrate in a sealed 500-micrometer mesh bag and returns to the ocean surface. This new BOWL technology allows controlled quantitative study of biotic colonization, biodiversity, ecosystem function and connectivity for bone, wood and other experimental substrates in the deep sea at relatively low fabrication and ship-time costs.

Genomic methods:
RAD_seq = This is 2b-RAD Single Nucleotide Polymorphism (SNP) data collected with the Wang et al. 2012 protocol. The raw reads will be deposited in NCBI Small Read Archive. The data is Illumina SE 50bp data.

mt_genome = This is Illumina PE 150bp data derive from total genomic DNA extracted from the organisms

listed in the spreadsheet. The raw reads will be deposited in NCBI Small Read Archive and the assembled mitochondrial genome will be submitted to NCBI GenBank.

Endosymbiont_genome = This is Illumina PE 150bp data derive from total genomic DNA extracted from the organisms listed in the spreadsheet. The raw reads will be deposited in NCBI Small Read Archive and the assembled endosymbiont genome will be submitted to NCBI GenBank.

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- column names reformatted to comply with BCO-DMO standards
- removed 'm' from depth column entries
- converted lat and lon from degrees and decimal minutes to decimal degrees"
- replaced spaces with underscores

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Data Files

File
BOWLS_sample_log.csv (Comma Separated Values (.csv), 2.11 KB) MD5:486a926a5d242cb00bbe628d5257e7c3 Primary data file for dataset ID 662996

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Related Publications

Wang, S., Meyer, E., McKay, J. K., & Matz, M. V. (2012). 2b-RAD: a simple and flexible method for genome-wide genotyping. Nature Methods, 9(8), 808–810. doi:10.1038/nmeth.2023
Methods

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Parameters

Parameter	Description	Units
genomic_method	The genomic method used to analyze specimen: RAD_seq = restriction site-associated DNA sequencing (RADSeq); mt_genome = mitochondrial genome sequencing; Endosymbiont_genome = Endosymbiont genome was sequenced	unitless
taxon	broad taxonomic group	unitless
species	genus and species name	unitless
lander	BOWLS lander identifier	unitless
lab_identifier	specimen identifier	unitless
block_bone	substrate identifier; NA=not applicable	unitless
individuals	number of individuals found in colonized substrate; NA=not applicable	individuals
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
depth	sample depth	meteres

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Instruments

Dataset-specific Instrument Name	Illumina SE
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Used for the RADSeq 50 bp data
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	Illumina PE
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Used for the mitochondrial and endosymbiont genome 150bp data
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.

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Deployments

OC1406B

Website	https://www.bco-dmo.org/deployment/568626
Platform	R/V Oceanus
Start Date	2014-06-22
End Date	2014-07-05

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Project Information

Biodiversity, connectivity and ecosystem function in organic-rich whale-bone and wood-fall habitats in the deep sea (BOWLS)

Website: http://craigrsmithlab.com/bowls-project/

Coverage: Off the Oregon and Washington State coast; roughly 43.833N, 127.5W to 47.3N, 127.4W

Description from NSF award abstract:
Organic-rich habitat islands support specialized communities throughout natural ecosystems and often play fundamental roles in maintaining alpha and beta diversity, thus facilitating adaptive radiation and evolutionary novelty. Whale-bone and wood falls occur widely in the deep-sea and contribute fundamentally to biodiversity and evolutionary novelty; nonetheless, large-scale patterns of biodiversity, connectivity, and ecosystem function in these organic-rich metacommunity systems remain essentially unexplored.

The PIs propose a novel comparative experimental approach to evaluate bathymetric, regional, and inter-basin variations in biodiversity and connectivity, as well as interactions between biodiversity and ecosystem function, in whale-bone and wood-fall habitats at the deep-sea floor. Their experiments will use bottom landers to carry and hold samples of bone and wood and a control substrate (basalt) at two depths (1500 and 3000 m), 250-500 km apart, in the NE Pacific and SW Atlantic basins, with quantitative recovery of the colonizing assemblages 15 month later. Each depth will have three replicates. Their experiments will test fundamental hypotheses concerning biodiversity (genetic and taxonomic) and biogeography of macrofaunal and microbial

organisms exploiting these resource-rich habitats in energy limited deep-sea environments, and will explore the utility of whale-bone and wood falls as model experimental systems to address patterns of connectivity and decomposer function in the deep sea.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1155188

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