Population analysis and metagenomics of Japanese tsunami marine debris mussels along the Hawaii, Washington and Oregon coasts in 2012 (JTMD-BF project)

Website: https://www.bco-dmo.org/dataset/552349
Version: 2015-02-27

Project
» Testing the Invasion Process: Survival, Dispersal, Genetic Characterization and Attenuation of Marine Biota on the 2011 Japanese Tsunami Marine Debris Field. (JTMD-BF)

Contributors	Affiliation	Role
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Dataset Description

A major objective of the JTMD project was to characterize the biodiversity of the arriving and landed JTMD fauna and flora. One constituent of the landed biota were mussels in the genus *Mytilus*, known to be member of a species complex (including species native to western North America). We therefore undertook genetic analysis of *Mytilus* contained on JTMD for purposes of species identification. To augment morphological assessment of diversity of JTMD fouling organisms, we performed metabarcoding, in which bulk samples were extracted for DNA and DNA barcoding markers sequenced in parallel.

Access to this dataset is temporarily RESTRICTED until publication. Please contact the PI for further information

Methods & Sampling

Mytilus specimens were collected from Japanese tsunami marine debris (JTMD) from 2012-2014 at coastal sites in Washington, Oregon and Hawaii.

Population level analysis of focal JTMD species. Mytilus spp. were one of the most common organisms on JTMD. Cytochrome c oxidase subunit III was chosen for species identification of mussels because available female-specific primers allowed a simpler approach to species discrimination than the standard COI primers, which amplify both male and female sequences and complicate analyses. The proposed method of pooling tissues for bulk DNA extraction and post-sequencing analysis of haplotype variation was set aside due to presumed sequence error observed when sequencing individual mussel amplicons. Instead, 695 mussels were extracted for DNA and sequenced individually on the Ion Torrent platform. Addition of index nucleotides to PCR products allowed post-sequencing separation of sequences by source mussel. Bins of reads from individual mussels were mapped to reference sequences of female M. galloprovincialis, M. trossulus, and M. coruscus. Known distribution of Mytilus suggested that mussels in Japan would be M. galloprovincialis. A sample of mussels for which Ion Torrent sequencing resulted in identification as M. trossulus or M. coruscus were reanalyzed by preparation of new PCR product and Sanger sequencing.

Metagenomic analysis of JTMD assemblages. Four 15 cm2 samples were scraped from the sides and top of the floating dock "Misawa 1" that beached near Newport Oregon in June 2012. Samples were preserved in ethanol and shipped to Moss Landing Marine Laboratories. Entire samples were decanted of ethanol and homogenized in an IKE Basic Mill. Ten grams of each sample were extracted with the Mo Bio Powersoil Mega DNA extraction kit (Mo Bio, Carlsbad, CA). Cytochrome c oxidase subunit I was PCR amplified, and prepared for sequencing on the Ion Torrent PGM. Resulting reads were pooled, quality and size filtered, and assembled into operational taxonomic units (OTUs) using the Velvet assembler. Gene OTUs were compared to eukaryotic COI sequences culled from Genbank by using variants of the search term for COI (COI, COX1, Cytochrome oxidase subunit I, Cytochrome c oxidase subunit I, etc...) and excluding prokaryota. We also specifically searched for COI sequences associated with of morphologically identified JTMD specie and congeners, as well as con-familials when morphological identification was limited to the family level.

Data Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- renamed parameters to BCO-DMO standard
- replaced blanks with underscores

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Related Publications

Carlton, J. T., Chapman, J. W., Geller, J. B., Miller, J. A., Carlton, D. A., McCuller, M. I., ... & Ruiz, G. M. (2017). Tsunami-driven rafting: Transoceanic species dispersal and implications for marine biogeography. Science, 357(6358), 1402-1406. https://doi.org/10.1126/science.aao1498
Results

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Parameters

Parameter	Description	Units
taxon	phylum and more specific taxonomic group	unitless
species	genus and species name	unitless
accession_number	Genbank record that matched the recovered seqeunce	unitless
pairwise_id	Pairwise Identity is the percent similarity between recovered sequence and the Genbank record	unitless

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Instruments

Dataset-specific Instrument Name	DNA sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Ion Torrent platform
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	Homogenizer
Generic Instrument Name	Homogenizer
Dataset-specific Description	IKA Basic Mill
Generic Instrument Description	A homogenizer is a piece of laboratory equipment used for the homogenization of various types of material, such as tissue, plant, food, soil, and many others.

Dataset-specific Instrument Name	Thermal Cycler
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

JTMD_2012

Website	https://www.bco-dmo.org/deployment/552342
Platform	Carlton_shore
Start Date	2012-12-01
End Date	2014-11-30
Description	Japanese tsunami marine debris collection

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Project Information

Testing the Invasion Process: Survival, Dispersal, Genetic Characterization and Attenuation of Marine Biota on the 2011 Japanese Tsunami Marine Debris Field. (JTMD-BF)

Coverage: North Pacific Ocean (W and E)

I. Biodiversity; Population and Food Web Analysis; Viability and Reproductive Condition; Dispersal Track and Growth History; Shellfish Pathogens/Parasites

This project seeks to document the biodiversity of Japanese species on arriving tsunami-generated debris, through morphological and genetic identification (including massively parallel DNA sequencing of whole community samples) andthrough quantitative replicate samples to determine numerical abundance, density, frequency, and biomass. In addition, species accumulation and rarefaction curves will be determinded to estimate total inbound diversity.

Focuses include:

- Population structure of selected taxa, based on size/age class distributions.
- Viability and reproductive condition of selected taxa, based on fecundity, gonadal indices, and/or spore production, upon arrival.
- Food web analyses based upon tissue stable isotope ratios *(*δ13C and δ15N*).*
- Dispersal track and growth history of selected taxa based on oxygen isotopic and elemental composition of shell calcite.
- Identity and prevalence of parasites and pathogens in oysters (*Crassostrea gigas*) and mussels (*Mytilus galloprovincialis*).

II. Biotic Attrition Over Time

Comparison of dead species assemblages on JTMD to live assemblages to assess the fate and alteration of debris communities over time.

III. Genetic Matching of Novel Invasions With JTMD Biota

Genetically characterize populations of target species so that if and when new invasions are detected, or when previously established invasions appear to be newly expanding or appearing in new locations, genetic studies can be undertaken to determine if these events are related to the JTMD phenomenon.

This is a Rapid Response Grant.

2020-09-30: Final data was not submitted for this project. The data for this research are available at the Dryad data depository (http://dx.doi.org/10.5061/dryad.rh01m). Contact Dr. Carlton for more information.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1266234

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