Stable isotope ratios collected from Japanese tsunami marine debris along the Hawaii, Washington and Oregon coasts during 2012 (JTMD-BF project)

Website: https://www.bco-dmo.org/dataset/553088
Version: waiting for revised data sumission

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
Miller, Jessica	Oregon State University (OSU-HMSC)	Principal Investigator
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Dataset Description

This dataset includes tissue stable isotope ratios (δ13C and δ15N) from specimens collected from the 2012 Japanese tsunami marine debris.

We compared $d^{13}C$ and $d^{15}N$ isotope ratios among *Mytilus galloprovincialis* from JTMD and from the docks Misawa Fishing Port, Japan (the origin of the Agate beach dock populations) and with the North American mussels, *Mytilus californianus* and *Mytilus trossulus* to partially assess trophic histories of JTMD species.

Access to this data is temporarily RESTRICTED. Please contact the PI's for further information.

Data Processing Description

Estuarine and marine δ15N isotope ratios of M. trossulus were combined.

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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

Parameters for this dataset have not yet been identified

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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-1266397

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