

Japanese Tsunami Marine Debris: biofouling debris log along the Hawaii, Washington and Oregon coasts from 2012-2014 (JTMD-BF project)

Website: <https://www.bco-dmo.org/dataset/491211>

Version: 21 October 2013

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Project

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

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Dataset Description

Sample log of debris collected from available JTMD items to assess species diversity, total abundance, density, and biomass. Information in this log includes sample identification numbers, date collected and date the sample arrived for analysis, the method of sampling (e.g., scraped or individuals were sampled), the source of the sample (e.g. boat, bumper, seawall), a description of the organisms removed from the debris, preservation method, current location of the sample, whether photographs were taken and their location, and various notes and comments.

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

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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
sample	Unique number of bulk sample. Any individual items removed would be given a secondary number. e.g. 1 barnacle removed from Sample_1 would be labelled Sample_1.1 and entered in this database with Sample ID = 1.1	unitless
register_num	Debris item number if catalogued in JTMD database (e.g. JTMD-BF-01); assigned by Carlton. See dataset 'debris register'.	unitless
date_samp	Date debris item sampled	unitless
date_arr	Estimated date that debris arrived for study	unitless
source	Where sample came from such as boat, float, bumper.	unitless
method	How sample was collected	unitless
sample_descrip	Contents of the sample such as organisms or size fraction of	unitless
preservation	Preservation history of the sample	unitless
location	Laboratory location of the sample	unitless
images	Presence of images and where they stored currently	unitless
note	Note on whether information was logged in "JTMD_MasterNotes" file	unitless
comment	Any notes of interest	unitless

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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) and through quantitative replicate samples to determine numerical abundance, density, frequency, and biomass. In addition, species accumulation and rarefaction curves will be determined 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 ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$).
- 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-1266417

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