

1. PROJECT INFORMATION

Title	Analysis of distributional, environmental, and life history attributes of Japanese Tsunami Marine Debris (JTMD) biota
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2. YEAR 3 PROGRESS SUMMARY

a. Describe progress.

We have made substantial progress on our scope of work. We have completed our modification of the PICES Risk Analysis Database. We have completed most of the proposed analyses although the work would benefit from some continued refinement and interpretation. As detailed below, the revision/modification of the database to convert attributes to binary or categorical data and address data gaps required a bit more effort than anticipated. The situation, if anything, improved the integrity of the analysis but took more time than expected. However, we are pleased with the current state of the database and think that the analyses are interesting and contribute to our understanding of JTMD biota. The work contributes to the overall ADRIFT project priorities by providing qualitative and quantitative synthesis and evaluation of JTMD species attributes, while also identifying attributes that distinguish JTMD species with known invasion histories from those with no prior invasion history.

3. ABSTRACT

Over 275 species have been transported 1000s of km on Japanese Tsunami Marine Debris (JTMD). While it is now evident that drifting debris can successfully transport marine species 1000s of km, there is a lack of information on the life history, environmental, and distributional characteristics of the JTMD species. Project ADRIFT supported the development of a database of distributional, environmental, and life history information for many of the JTMD species. We modified that database to 1) quantify variability in attributes of JTMD species along statistically independent gradients using non-metric multidimensional scaling analysis and 2) compare traits of JTMD species with known invasion histories to remaining JTMD species. The 135 species included in this analysis represent 12 phyla, with Mollusca, Crustacea, and Bryozoa each contributing slightly over 20% of the total. The reported native realm for this group of species covers the globe, ranging from the Southern Ocean to the Arctic. However, the majority are native to the NW Pacific, followed by NE Pacific, and the Central Indo-Pacific. Additionally, most species have no prior invasion history (>50%) while the remainder have a known invasion history (23%), are cryptogenic (an unknown origin) (14%), or have an unclear establishment (4%). Our quantitative analysis indicated that the geographic distribution of cryptogenic species was statistically distinct from species with and without any invasion history, but there was no distributional difference between species with and without invasion history. Cryptogenic species had greater representation in the Arctic, Temperate and Tropical North Atlantic, and Southern Australia and New Zealand. We documented significant differences between species with and without invasion histories based on environmental and life history attributes. Species with known invasion histories were distinguished by a greater occurrence on temperate reef habitat and artificial and hardpan substrates; they were more common in subtropical and tropical waters and more protected habitats; and they exhibited greater salinity tolerance. We then identified species with no prior invasion history whose attributes were most similar to those with known invasion history. This group included 45 species, and 20 of those are already reported to occur in the NE Pacific. The remaining 25 species, which are most similar to JTMD species with invasion histories but not yet established in the NE Pacific, are within the Phyla Annelida (1 species), Bryozoa (12), Cnidaria (2), Echinodermata (1), and Mollusca (8). When considering warmer regions, such as the Hawai`ian Islands, there are also 25 species not yet reported from the Central Indo-Pacific, 10 of which are distinct from the 25 species not yet present in the NE Pacific. However, only one of those species has a documented native range that extends into tropical waters, the Cnidarian *Halecium tenellum*. Overall, this effort contributes to the synthesis goals of the ADRIFT project by providing a qualitative and quantitative evaluation of JTMD species attributes and identifying attributes that distinguish species with known invasion histories from those with no prior invasion history.

4. PROJECT DESCRIPTION

In the nearly five years since the devastating 2011 Tohoku earthquake and tsunami, it has become evident that, in addition to a myriad of social, economic, and environmental concerns associated with the tragedy, hundreds of coastal species from Japan have crossed the Pacific Ocean in association with tsunami debris, including species that have become invasive and caused ecosystem and economic damage elsewhere. As of January 2017, we have documented the arrival of >650 debris items, referred to as Japanese Tsunami Marine Debris Biofouling Items (JTMD-BF) 1-651. Debris items include docks, buoys, boats, pallets, and wooden structures. All of these items were identified as JTMD based on evidence as reviewed in Carlton et al., 2017. Briefly, we considered a debris items as JTMD if it 1) had clear identification such as a serial or registration number that was linked to an object lost during the tsunami of 2011; 2) had clear biological evidence of originating primarily from the Tohoku coast of Japan; or 3) a combination of these factors.

A monumental effort by many researchers and taxonomists has generated a comprehensive list of species associated with JTMD. Although identification and genetic verification is ongoing, there are nearly 300 taxa that have been collected on JTMD collected along North American and the Hawai`ian Archipelago since 2012. While the movement of marine species around the globe through anthropogenic activities, such as ballast water and hull fouling, has been a concern for some time (Carlton and Geller 1993, Carlton 1996, Ruiz et al. 1997, Callaway et al. 2006), the transport of such large numbers of marine species across ocean basins via massive amounts of marine and terrestrial debris appears to be a new phenomenon that has not yet been well documented.

JTMD has certain unique attributes in comparison with other known marine vectors, such as ship hull fouling and ballast water (Sylvester et al. 2011; Lo et al. 2012; Murray et al. 2012). Ships arrive in known locations and at measurable frequencies whereas JTMD, which is propelled by winds and currents and thus travels at much slower speeds than ships, can arrive almost anywhere at any time – arguably the most stochastic transport vector yet described. Due to the slow rates of transport by currents rather than propulsion, the effects of drag and dislodgement will be substantially reduced on JTMD in comparison with ship hull fouling (Clarke Murray et al. 2012). Furthermore, JTMD transports large numbers of adults, rather than larval stages that are more common in ballast water.

As of January 2017, only one JTMD species, the striped beakfish *Oplegnathus fasciatus*, has been observed free-living in along the west coast of North America (in Oregon and Washington). At this time, we do not know if any of these JTMD species will become established outside of their current distributional range as a result of the earthquake and tsunami. As part of an international effort to evaluate the risks associated with JTMD and associated species, a database of life history, distributional, and environmental attributes of many JTMD species was developed for reference and analysis.

a) Research Purpose

In addition to evaluating potential risks associated with JTMD species, we have a unique opportunity to examine those species that arrived on JTMD in greater detail in order to (1) increase our understanding of transoceanic dispersal of coastal species; and (2) advance one of the least understood aspects of invasion ecology – why some species are successfully transported to novel habitats outside of their current biogeographic range when others are not? The work contributes to the synthesis goals of the ADRIFT project, provides a qualitative and quantitative evaluation of JTMD species attributes, and identifies attributes that distinguish JTMD species with known invasion histories from those with no prior invasion history.

b) Objectives

We modified the JTMD database to focus on attributes with broad coverage across species in order to 1) quantify variability in attributes along statistically independent gradients; and 2) compare traits of JTMD species with known invasion histories to remaining JTMD species.

c) Methods

We began our efforts using the version of PICES' Risk Analysis JTMD database available in spring 2016. We added additional species until approximately May 2016, at which time we needed to finalize the species list for analysis. In January 2017, we removed a small number of species and updated nomenclature based on the most current JTMD species list from Dr. James Carlton. Therefore, our final database includes 135 species (Table A1).

Given that any robust statistical comparison among the JTMD species requires complete, or nearly complete, coverage across attributes, we took the following steps to modify the database. First, we incorporated cited and verified information presented by Dr. Michio Otani. Second, we added Phylum, Class, Order, and Family to the database. Third, we addressed inconsistencies among researchers in temperature regimes, (e.g. some entered data into the native temperature regime tab, but information was not included under the survival temperature regime tab). This information was added based on the reasoning that if a species can live in a certain temperature in its native range, then it can survive under that temperature regime as well. Fourth, we filled in some missing dropdown or multi-select fields based on information available in the "See Details" field, when deemed appropriate. Select information on congeners was used to fill in some fields. Fifth, we generated four categories for invasion history. These categories are:

- 1. Yes = clear invasion history outside of native range**, with clearly documented establishment in non-native areas
- 2. No = not found outside of native range**
- 3. Cryptogenic = species with unknown origin**, meaning their native range is unclear (even if they were introduced via human-mediated transport, there is no way to know if the region of introduction was non-native or a reintroduction to their native region)

4. Unclear = species with 'unclear establishment', meaning the species was introduced to a region outside their native range (via human-mediated transport) but has not established or was not documented since that first introduction event.

To validate these invasion history categories, we consulted the database, western and Japanese literature sources, and completed some further literature review to ensure we incorporated the most current information. Additionally, in late April - early May 2016, the categorization was compared with the global invasion status of JTMD species compiled by Paul Fofonoff, Smithsonian. A final consultation with Drs. Jim Carlton and Greg Ruiz resulted in the categorization presented in the modified database.

Finally, variables that were included in the statistical analyses, hereafter referred to as “attributes”, were transformed in binary or numerical data. For example, a species could be present in 8 of the 20 geographic regions. Therefore, there could be too many potential combinations for clear interpretation. Therefore, we included all “Realms” and “Regions” in the database with a binary entry system for each species. For each species, there would be a “0” if the species was not present in a particular “Realm” and “1” if it was present. For attributes with less than 10 possible combinations, such as “Reproductive Mode”, we developed a numerical classification (1 = gonochoristic/dioecious, 2 = hermaphrodite/monoecious). Therefore, the final database had 100 fields, which often included multiple fields per attribute. For example, there are 12 Realms so we refer to “Realm” as the attribute and the actual Realms 1 through 12 as the database fields.

Specific changes that may be of particular interest are presented in further detail below. Many of the fields were developed based on Lee & Reusser (2012).

1) Within the attribute “Vector,” the categories Infrastructure Development, Research and Education, Aquarium and Plant trade, and Habitat Restoration and Mitigation were never used so were removed. Only two species fell under the vector category Live Seafood (namely *Asterias amurensis* and *Didemnum vexillum*) so this category was also removed. The categories Hull fouling (recreational), Hull fouling (commercial), and Hull fouling (not specified) were combined into one broad hull fouling category, as we didn’t need the distinction between commercial and recreational hull fouling for the purposes of this analysis.

2) Within the attribute “Temperature”, the category Mild temperate was removed. Without guidelines for the temperature regimes, most species were filled out as “See Details.” In order to translate the temperature information contained within the details tab to temperature categories, we used temperature intervals shown to be critical for marine biota, based on Payne et al. 2012. Cold temperate should never rise above 20°C, and warm temperate should never fall below 12°C (Payne et al. 2012). We found the mild temperate category arbitrary, as it could be either cool temperate or warm temperate as well, and found it hard to decipher between the two, so it was removed.

3) Within the attribute “Depth Regime”, the category Coastal Fringe was used only once to describe *Telmatogeton japonicus*, so it was removed. The categories Upper Intertidal, Middle Intertidal, and Lower Intertidal were combined to form one category Intertidal. Bathyal, Hadal, and Abyssal were combined into one category Bathyal, which now encompasses all depths >200m. The categories Surface Epipelagic, Shallow Epipelagic, Deep Epipelagic, Mesopelagic, Bathypelagic, Abyssopelagic, and Hadopelagic were never used and were removed.

4) Within the attribute “Ecosystem”, Rocky Intertidal and Rocky Subtidal were combined into one category Rocky, as the distinction between the environment above and below the low tide mark is already covered by Depth Regime. The categories Oyster/mussel Reef, Worm Reef, and Coralline Algae Reef were combined into one category Temperate Reef because all are found in temperate, cooler environments. Coral Reef was kept distinct as it is correlated with warmer, tropical environments.

5) For the attribute “Habitat”, the categories Epibenthic, Epiphytic, and Epizoic were combined into one category Epibenthic”. The categories Semi-Infaunal and Infaunal were combined to simply Infaunal.

6) For the attribute “Substrate”, the categories Gravel, Cobble, and Rock were combined to simply Rock.

7) At this point, there were still a high number of “Not Found” entries. Therefore, we relied on qualitative data from Dr. Michio Otani, appropriate related species information contained within the details tab, additional review of select literature, and a logical rationale. Certain changes were made for species without further information or related species information. For example, few higher-level eukaryote coastal invertebrate species are asexually reproducing, so the default for a species without that information available is that it does not reproduce asexually.

8) The database at this stage had 135 species, 20 attributes, and 135 fields. Any attributes or species that still had poor coverage were removed for quantitative analysis. The following data-poor attributes were removed: salinity regime reproductive, temperature regime reproductive, second vector, maturity size, maturity age, broodsper year, fecundity, egg size, longevity, and forage mode. The following data poor species, all with < 65% data coverage, were also removed: *Tectura emydia*, *Hippothoa imperforata*, *Placiphorella stimpsoni*, *Bankia bipennata*, *Havelockia versicolor*, *Arabella semimaculata*, *Hydrodendron gracile*, *Gromia oviformis*. *Cibicides lobatulus* was also depleted on account of taxonomic dissimilarity (the reproductive categories in this JTMD invertebrate database didn’t make sense for the type of reproduction performed by *C. lobatulus*). The final database for quantitative analysis included 126 species (Table A1) with 16 attributes and 100 fields (Table A2). There were four additional attributes for species with known invasion history (Non-native Realm, Non-native Region, Non-native Temperature, and Non-native Salinity) and 132 fields (Table A2).

Qualitative Synthesis

We compiled summaries of JTMD species across various categories of interest, such as Phyla or invasion history, to provide some synthesis of the attributes of all 135 species in the database. The number of species examined depended on the coverage across attributes. We had good coverage on 135 species and include a qualitative synthesis of those species. We had >95% coverage for 126 species, which were used in the quantitative analysis described below.

Quantitative Analysis

Nonmetric Multidimensional Scaling (NMS) was used to ordinate species in multi-dimensional space. NMS is an iterative process to rank and place n entities on k dimensions (axes) that minimize the stress of the k -dimensional configuration (McCune and Mefford 1999). JTMD species with adequate information ($n = 126$) and 16 attributes were included in the initial analysis. A measure of 'stress', which indicates the departure from monotonicity in the relationship between the dissimilarity (distance) in the original p -dimensional space and distance in the reduced k -dimensional ordination space, was determined. Pearson correlation analysis was used to examine the relationships between NMS axis scores and variables (distributional, environmental, and life history attributes) included in the analysis, which provides information on which attributes account for separation along axes. Significance levels for the correlation analyses were corrected for multiple comparisons using the Bonferroni correction. PC-ORD Version 7 was used for NMS analyses (McCune and Mefford 1999).

Initially we compared all species with adequate coverage across variables ($n = 126$), which included all four invasion history categories (cryptogenic, unclear, invasion history, no invasion history). We chose to analyze the species matrix in two ways. First, we used only the geographic distribution information (Realm and Region). Second, we used only the environmental and life history attributes. We adopted this approach because it is expected that species with invasion histories may have disjointed geographic distributions that could influence the separation of groups in what could be considered a biased manner. Given we were also interested in the similarities in environmental and life history attributes independent of geographic distribution, we decided to complete both analyses for comparison.

We also wanted to determine if there were significant differences in attributes among species groups with different invasion histories. Therefore, we completed a Multi-Response Permutation Procedure, which estimates a weighted mean within-group distance (δ) to determine the probability of the observed δ compared with δ generated with random clusters. We completed two analyses, one including species categorized as cryptogenic, known invasion history, and no known invasion history ($n = 126$) and the other with only those species with and without invasion history ($n = 103$). The six species with unclear establishment were removed from both analyses due to their low number and ambiguous status.

We completed Indicator "Species" Analysis (ISA) on the species x attribute matrices to determine which attributes were statistically significant indicators of each group (cryptogenic,

invasion history, and no invasion history). An ISA combines information on relative abundance and frequency of occurrence to identify attributes that are most characteristic of each group. In this analysis, certain attributes, such as “Developmental Mode” could be indicators of group separation, which means that there are statistically different frequencies of occurrence of planktonic developers in one group compared to another. Statistical significance was determined based on Monte Carlo tests with 5000 permutations for comparison with observed Indicator Values. Analyses were completed using PC-ORD 7.0.

Finally, to further explore attributes only of JTMD species with known invasion histories, we completed two additional ordinations, one with only geographic distribution information (Realm, Nonnative Realm, Region, and Nonnative Region) and the other with only environmental and life history attributes. Our aim was to evaluate patterns and highlight differences among this group of species (n = 31), which are of particular interest in terms of risk evaluation.

d) Results

Qualitative Synthesis

The 135 JTMD species included in the database represent 12 phyla, with Mollusca, Crustacea, and Bryozoa each contributing slightly over 20% of the total (Fig. 1). Four phyla (Foraminifera, Chordata, Cercozoa, and Sipuncula) were each represented by one species. As noted, a species had to have broad coverage across attributes for inclusion in the final database. This was the only criterion as there was no systematic selection of species for analysis. However, it should be noted that taxa had to be identified to species (or rarely a species complex, such as *Jassa marmorata* complex) with a high level of confidence for inclusion. Therefore, there is likely some biased representation based on ease of identification, prior knowledge of taxa, and somewhat uneven taxonomic effort across phyla. However, we consider the 135 species to be a representative subset of the biota (~300 taxa) that have been documented on JTMD.

The reported native realm for these 135 JTMD species covers the globe (Fig. 2) with species ranging from the Southern Ocean (hydrozoan *Obelia longissima*) to the Arctic (amphipod *Ampithoe lacertosa*). However, the majority are native to the NW Pacific, followed by NE Pacific, and the Central Indo-Pacific (Fig. 3). Given that our aim was to summarize key attributes of JTMD species and then compare those attributes across groups with different prior invasion histories, an initial step was to categorize each species by invasion history. The majority of species had no invasion history (>50% of the total), and the remainder had a known invasion history (23%), an introduction but unclear establishment (4%), or were cryptogenic (unknown origin) (14%) (Table 1). Hence, most of the JTMD species have no invasion history. However, many of the species have documented transport vectors and, as JTMD is arguably a newly documented species transport vector, we wanted to determine the prior transport history for each species (Fig. 3). Eight transport categories were documented, and the greatest number of species (40) were reported as hull fouling, followed by transported through aquaculture and fisheries activities and ballast water (Fig. 4).

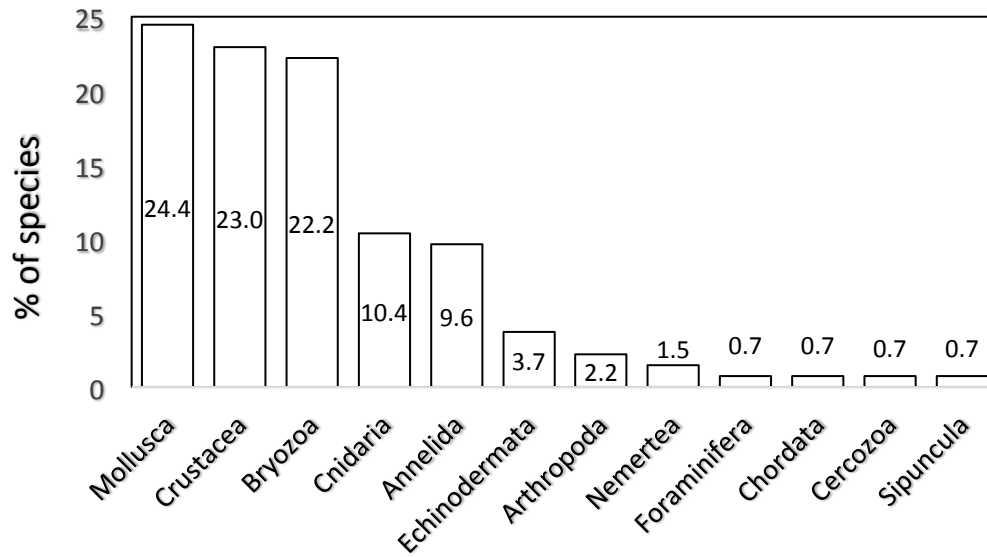


Figure 1. Percent of species (n = 135) per phyla. The number of species per phyla is given within each bar. Twelve phyla are represented in the database.

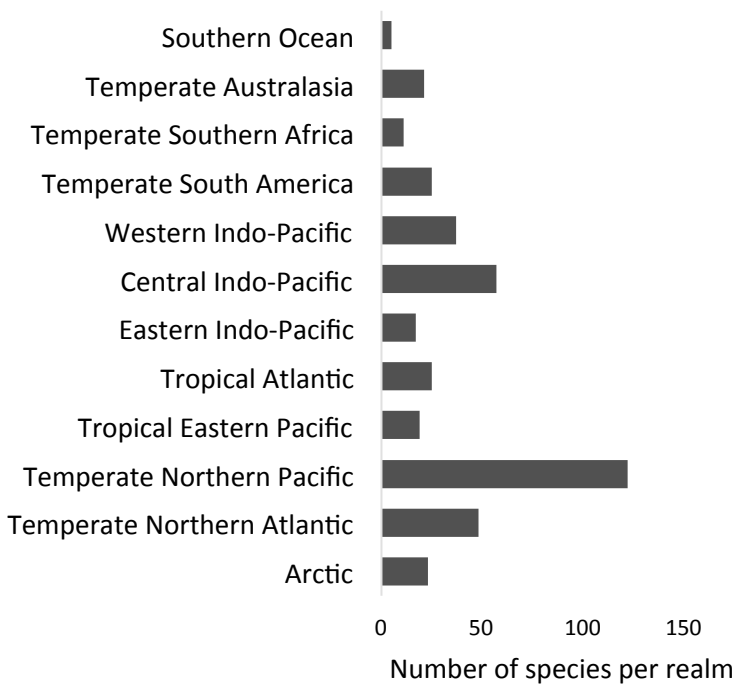


Figure 2. The reported native realm of origin for all 135 JTMD species. Number of species found per realm is reported and species can fall under multiple realms. The realms are ordered geographically from the south to north.

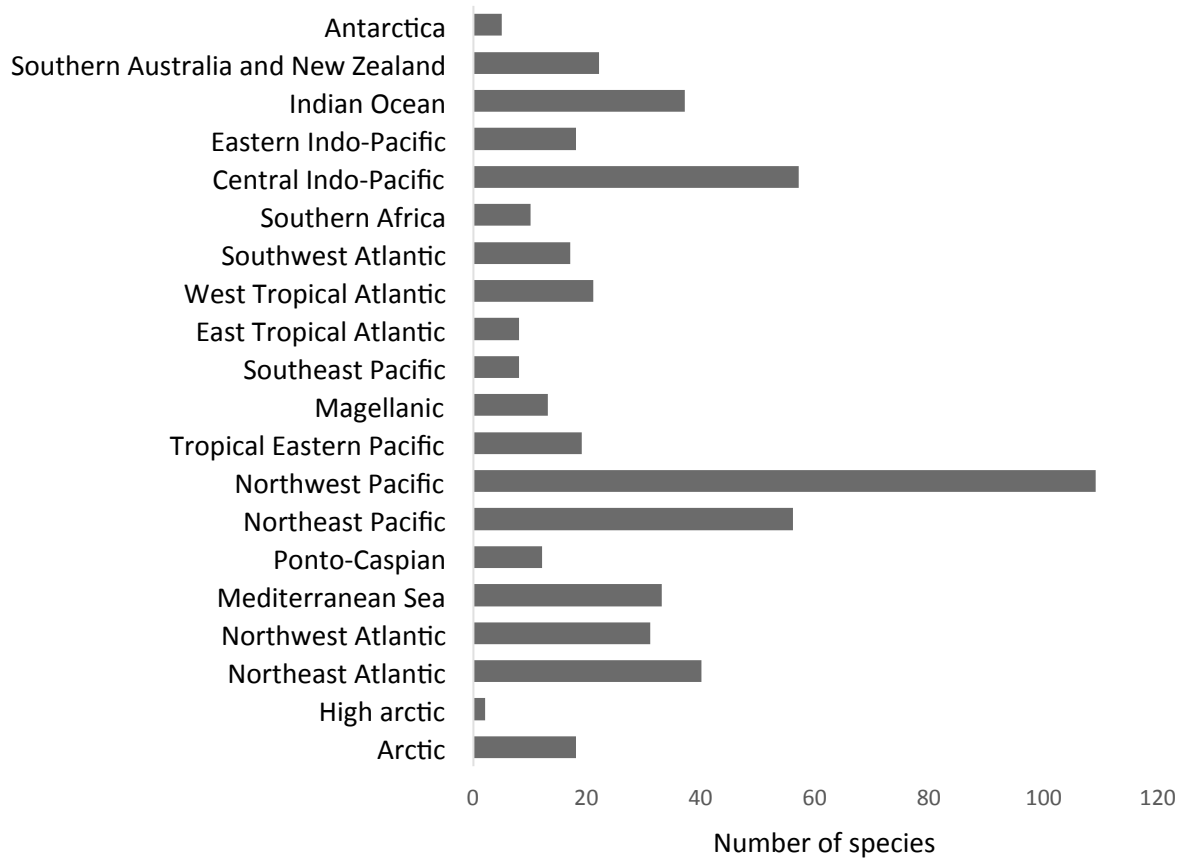


Figure 3. The native regions for 135 JTMD species, based on the Marine Ecoregions of the World. Number of species found per region is shown, and species can fall under multiple regions if applicable. Regions are ordered from south to north.

Invasion History	Number of species	Percentage of species
No invasion history	79	58.5
Known invasion history	31	23.0
Cryptogenic - unknown origin	19	14.1
Introduced, but unclear establishment	6	4.4

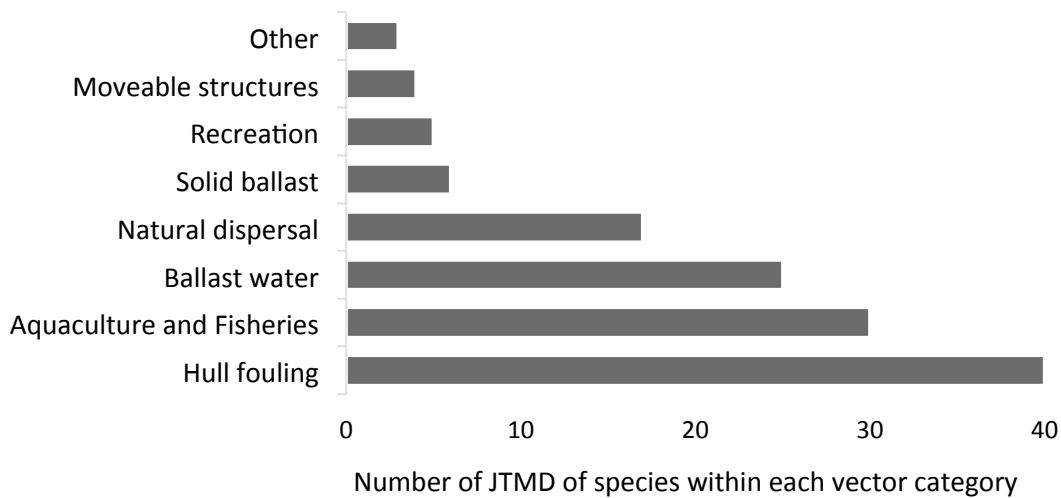


Figure 4. The number of JTMD species reported to have been transported for each vector included in the database. Each species can be documented under multiple vectors. A total of 58 species out of 135 total have been documented on a vector, including all 6 of the species with unclear establishment, all 31 of the species with a known invasion history, 13 of the 19 cryptogenic species, and 8 that were documented on a vector but have no invasion history. The “Other” category is used for *Dendostrea folium* and *Sphaerozium nitidus*, which were both cited as spreading through the Suez canal with no further vector information, and for *Amblyosyllis speciosa*, which was classified as “Other” by the EPA Atlas of Non-Indigenous Species without additional information.

Estimates of the number of propagules (or individuals) entering a new area are needed to generate a meaningful estimate of propagule pressure, which in at least some instances has been correlated with likelihood of successful establishment (Lockwood et al. 2005, Lo et al. 2012, Capinha et al. 2013). The literature review included an estimate of abundance in native, and when applicable, non-native, habitats. However, the vast majority of species (>90) had at least one citation that reported the species to be “common”. Additionally, a relatively large number of species (n = 40) were reported to be abundant or common as well as few or rare, likely highlighting the spatial and temporal variation in abundance. Thus, given the difficulty in assigning a valid estimate of natural abundance and the potential mismatch between native abundance and actual abundance on JTMD, we did not include the attribute “Abundance” in the quantitative analysis.

QUANTITATIVE ANALYSIS

We present the results of analyses based on the 121 species that comprised three of the invasion categories: cryptogenic, known invasion history, and no invasion history. Given that there were only 5 species with unclear invasion history and the results were similar with or without these species, we removed them to facilitate comparison among the remaining species.

Geographic Distribution across Invasion Histories

The variability among the 121 species was well-described with a two-dimensional ordination that accounted for 79% of the variation among the species' geographic distributions (stress = 12.2, 55 iterations). Axis 1 accounted for 55% of the variation among species and Axis 2 for 33% of the variation. The greatest separation was between species from the Western Indo-Pacific and those from the Temperate North Pacific. While the geographic distribution of cryptogenic species was statistically distinct from species with and without any invasion history (MRPP pairwise comparisons $P < 0.001$), there was no difference between species with and without invasion history ($P = 0.36$). Cryptogenic species had greater representation in the Arctic, Temperate and Tropical North Atlantic, and Southern Australia and New Zealand.

Environmental and Life History Attributes across Invasion Histories

The ordination of the 121 species based only on environmental and life history attributes also accounted for a high level of variation (79%) (stress = 16.7, 94 iterations). Axis 1 accounted for 42% of the variation and separated species primarily on feeding, reproduction, and developmental mode along with native temperature regimes and habitats (Fig. 5). Axis 2 accounted for 21% of the variation in the data set and separated species primarily on salinity tolerance, substrate, and developmental mode. Axis 3 accounted for 17% of the total variation and separated species primarily on differences in native temperature (Table 2).

There was distinction between species with and without invasion histories and between cryptogenic species and those with no invasion history (MRPP $P < 0.001$). However, as a group, cryptogenic species were similar to those with invasion history ($P = 0.08$). The indicator analysis demonstrated that cryptogenic species were characterized by a greater representation in cold and cool waters as well as either deeper, water column habitats or coastal shores associated with vegetation. Species with known invasion history were distinguished by a greater representation on temperate reefs, more fouling species, and more species found on hardpan and artificial substrates.

Given the ambiguity associated with cryptogenic species and their statistical distinction, we also completed an ordination using only species with and without invasion histories. The ordination of the 103 species with and without known invasion history based on environmental and life history attributes accounted for a similarly high level of variation (72%) (stress = 17, 69 iterations). Similar to the analysis with 126 species, Axis 1 accounted for 39% of the variation and separated species based on feeding, reproduction, and developmental mode and native temperature regime (Fig. 6). Axis 2 accounted for 18% of the variation in the data set and separated species primarily on salinity tolerance, habitat, and developmental mode. Axis 3 accounted for 15% of the total variation and separated largely based on temperature.

There was also a significant statistical separation between species with and without invasion histories (MRPP, $P < 0.001$). Based on the indicator analysis, species with known invasion

history were distinguished by a greater occurrence on temperate reef habitat and artificial and hardpan substrates as well as a greater representation of fouling organisms. Species with known invasion history were also more commonly present in subtropical and tropical waters and more protected habitats and they exhibited greater salinity tolerance. Asexual reproduction was moderately, but significantly, less common in species with known invasion history.

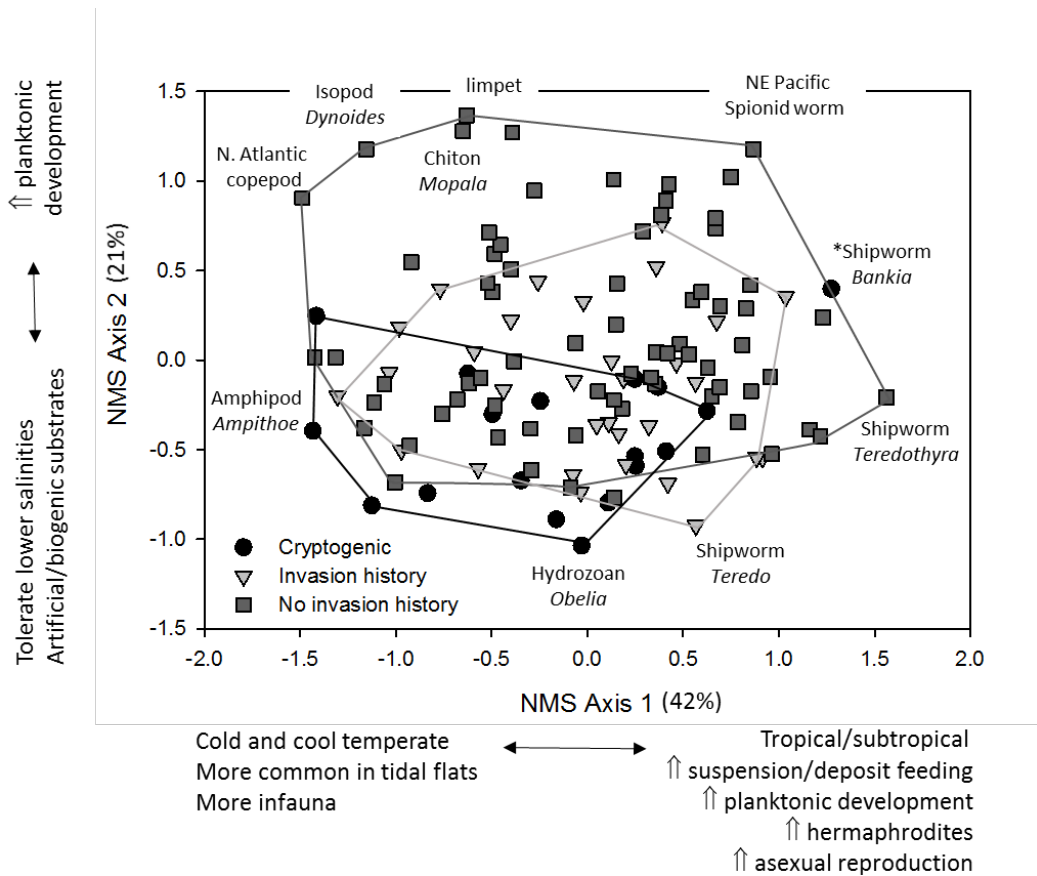


Figure 5. Ordination of 121 JTMD species with invasion history categorization. Attributes significantly correlated with axis scores are included. See Table 2 for additional details on the correlation analysis. Note that the *shipworm *Bankia*, although cryptogenic, is well separated from the other cryptogenic species.

Table 2.

Correlations between axis scores from the Nonmetric Multidimensional Scaling ordinations and the Japanese Tsunami Marine Debris species attributes included in the analysis. Ordination included 121 species that could be identified as cryptogenic, known invasion history, or no invasion history. Only correlations that are significant after correction for multiple comparisons ($r > 0.350$) are included. See Table A2 for attribute details.

Attributes	Axis 1	Attributes	Axis 2	Attributes	Axis 3
Trophic (↑ suspension & deposit feeding)	0.807	Development (direct ⇒ planktonic)	0.369	Subtropical	0.768
Reproduction (gonochoristic ⇒ hermaphroditic)	0.529	Submerged aquatic veg.	-0.354	Tropical	0.540
Development (direct ⇒ planktonic)	0.484	Reproduction (sexual ⇒ asexual)	-0.375	Coral reef	0.383
Asexual Reproduction (sexual ⇒ asexual)	0.398	Cool temperate	-0.386	Cool temperate	-0.363
Tropical	0.390	Oligohaline	-0.411		
Subtropical	0.377	Flotsam	-0.423		
Macroalgae beds	-0.358	Fouling	-0.465		
Kelp forests	-0.355	Temperate reef	-0.466		
Rocky ecosystems	-0.332	Artificial substrate	-0.515		
Mud substrate	-0.392	Biogenic	-0.542		
Cold water	-0.337	Polyhaline (18 to >30)	-0.552		
Infaunal	-0.451	Mesohaline (5 to <18)	-0.581		
Tidal flat ecosystems	-0.470				
Cool temperate	-0.808				

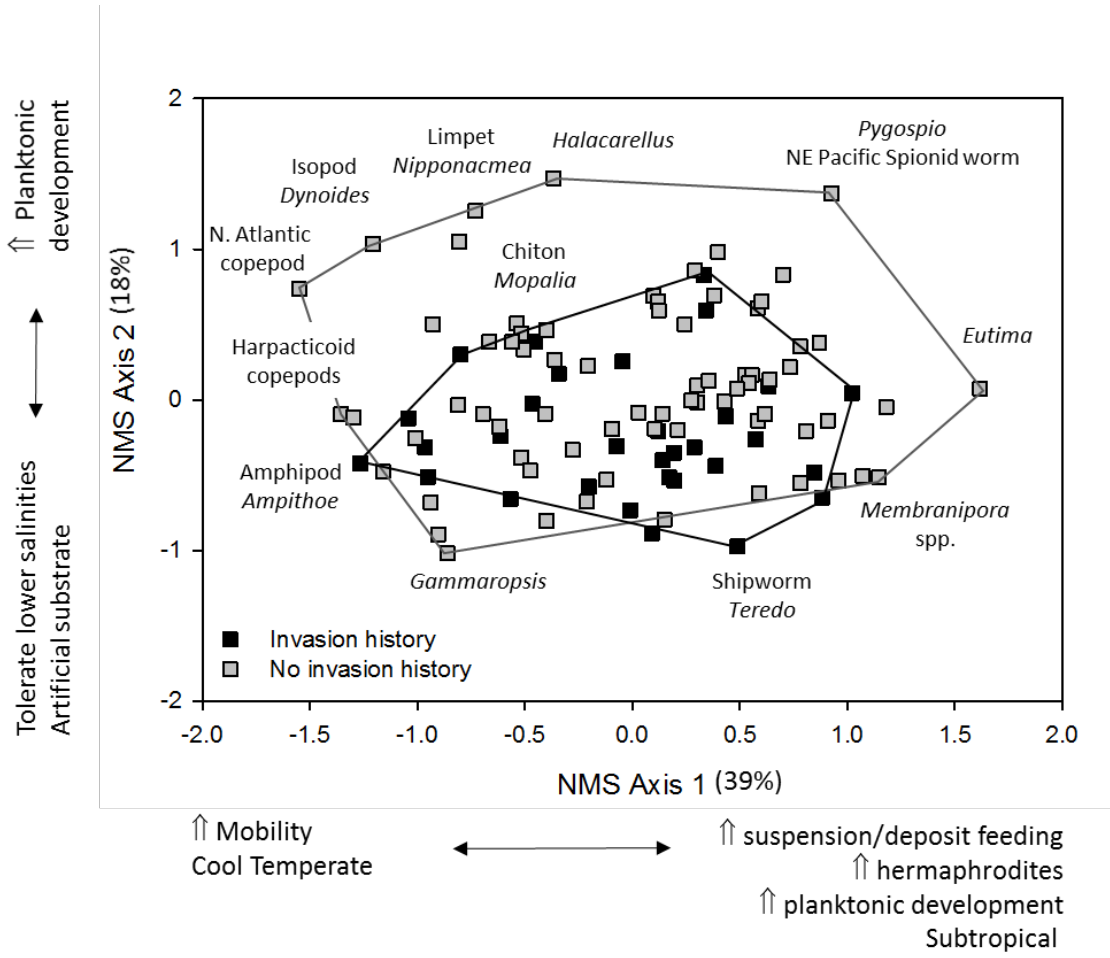


Figure 6. Ordination of 103 JTMD species with known invasion history. Attributes significantly correlated with axis scores are included. See Table 3 for additional details on the correlation analysis.

Table 3

Correlations between axis scores from the Nonmetric Multidimensional Scaling ordinations and the Japanese Tsunami Marine Debris species attributes included in the analysis. Ordination included 103 species that could be identified as known invasion history or no invasion history. Only correlations that are significant after correction for multiple comparisons ($r > 0.350$) are included. The attribute “Development” is included for Axis 2 as it was the only marginally significant positive correlate. See Table A3 for attribute details.

Attributes	Axis 1	Attributes	Axis 2	Attributes	Axis 3
Trophic (↑ suspension & deposit feeding)	0.806	Development (direct ⇒ planktonic)	0.300*	Subtropical	0.634
Reproduction (gonochoristic ⇒ hermaphroditic)	0.497	Fouling	-0.437	Tropical	0.475
Development (direct ⇒ planktonic)	0.440	Artificial substrate	-0.446	Cool temperate	-0.411
Asexual Reproduction (sexual ⇒ asexual)	0.403	Biogenic	-0.503		
Tropical	0.383	Mesohaline (5 to <18)	-0.648		
Subtropical	0.360	Polyhaline (18 to >30)	-0.691		
Tide flat ecosystems	-0.440				
Macroalgae beds	-0.420				
Cold water	-0.407				
Rocky ecosystems	-0.405				
Cool temperate	-0.512				
Mobility	-0.808				

e) Discussion

The Tohoku earthquake and tsunami resulted in catastrophic loss and suffering. Despite the monumental challenges associated with recovery and rebuilding efforts, the Japanese government generously committed substantial resources to improving our understanding of the JTMD debris field, its associated biota, and potential risks associated with both of these. As a result of these efforts, there is now a comprehensive list of JTMD species supplemented with a detailed database that summarizes key information on the distributional, environmental, and life history characteristics of JTMD biota. This information is useful to researchers focused on understanding marine transport and dispersal as well as invasion ecology. The database, as well as derived products, will also be of use to managers and of interest to the public.

The ability to predict biological invasions remains notoriously challenging (Kolar & Lodge 2002; Romanuk et al. 2009). Although various predictors appear promising in a particular taxonomic group or scenario, there is often minimal success when more broadly applied. Related efforts have sought to identify life history traits associated with successful invaders. Such an approach can be used to evaluate relevant hypotheses, such as whether or not successful invaders have higher reproductive rates (Sol et al. 2012). Our focus was to synthesize key attributes within the JTMD species pool, identify those attributes that account for the variation within the JTMD species pool, and highlight those attributes that vary between JTMD species with and without known invasion histories. Theoretically, the outcome of such efforts can help focus management and monitoring activities

Based on geographic distribution alone, there was substantial structuring of the JTMD species and cryptogenic species were distinct from those with and without invasion history. Not surprisingly, cryptogenic species had a broader geographic representation. However, when analyzed with the environmental and life history attributes, we also documented a substantial amount of group separation within the JTMD species pool. It is interesting that life history attributes accounted for much of the separation across species, including trophic status, reproductive mode, and development mode.

Given the focus on risk assessment and the need to evaluate the likelihood of a negative outcome associated with any of the JTMD species becoming established outside their native regions, the direct comparison of JTMD species with and without invasion histories is the most relevant. We documented statistically significant differences between species with and without known invasion histories. Species with known invasion history were more commonly present in (but not necessarily limited to) sub-tropical and tropical areas, more protected habitats, and exhibited greater salinity tolerance. Given the statistical distinction between JTMD species with and without invasion history, we can compare the species with no known invasion history that are most closely located in three-dimensional space to the statistically distinct group of species with known invasion histories. Such an approach allows us to ask the question “which species have similar attributes?” For example, the multivariate analysis decomposes the species x attribute database into three axes of variation and each species is essentially assigned a

position in three-dimensional species (i.e., an x-, y-, and z-value). We can then identify the JTMD species with no known invasion history that are most similar to those with prior invasions. This approach identified 45 JTMD species with no known invasion history from the Phyla Annelida, Bryozoa, Crustacea, Cnidaria, Echinodermata, Mollusca, and Nemertea that were within the same coordinate space as JTMD species with known invasion history. However, 20 of those species are already reported to occur in the NE Pacific, leaving 25 species from the Phyla Annelida (1), Bryozoa (12), Cnidaria (2), Echinodermata (1), and Mollusca (8) that are most similar to JTMD species with invasion histories but not yet established in the NE Pacific. When considering warmer regions that received large amounts of JTMD, such as the Hawai`ian Islands, there are also 25 species not yet reported from the Central Indo-Pacific, 10 of which are distinct from the 25 species not yet present in the NE Pacific. However, only one of those species has a documented native range that extends into tropical waters, the Cnidarian *Halecium tenellum*.

Overall, the database development and related analyses provide a qualitative and quantitative synthesis of the JTMD biota that contributes to both basic understanding of species' ocean transport and invasion ecology. While JTMD species known to have established outside their native ranges are clearly of concern, particularly in geographic areas where they have not yet established, the analyses presented here may be able to highlight species with similar attributes that may be of concern. Our efforts can complement other approaches to identifying species of concern.

f) Challenges

As noted above, the time required to finalize the database for analysis was longer than anticipated. Additionally, given the need to have information across all attributes for most species to complete a robust analysis, some attributes, primarily life history traits, could not be included due to poor coverage. While unfortunate, we moved ahead to develop a system for reviewing the species and their attributes to address or eliminate data deficiencies. Given that the majority of the attributes were distributional and environmental, there is potentially less concern with the challenges of analyzing related species as many of the attributes should not be as constrained as related traits, such as growth rate, fecundity, and life span. Given the broad phylogenetic representation, it is quite interesting that there is some clear delineation among species with different invasion histories. Overall, we have completed the proposed analyses but, as noted above, we can envision other, related analyses and summaries that would contribute to the overall ADRIFT effort.

g) Achievements

The compilation of such detailed geographic, environmental, and life history information for >100 species was a monumental achievement alone! The thorough and comprehensive effort of many researchers and taxonomists to collect and identify this unique suite of species is a valuable contribution to both the scientific and management community. The synthesis of the distributional, environmental, and life history attributes of at least a subset of the species will

be an important resource for improving basic understanding of species transport, attributes related to successful invasions, and potentially contribute to overall risk assessment

h) Literature Cited

- Callaway, R. M., S. L. Miao, and Q. F. Guo. 2006. Are trans-Pacific invasions the new wave? *Biological Invasions* 8:1435-1437.
- Capinha, C., L. Brotons, and P. Anastacio. 2013. Geographical variability in propagule pressure and climatic suitability explain the European distribution of two highly invasive crayfish. *Journal of Biogeography* 40:548-558.
- Carlton, J. T. 1996. Pattern, process, and prediction in marine invasion ecology. *Biological Conservation* 78:97-106.
- Carlton, J. T., and J. B. Geller. 1993. Ecological Roulette - the global transport of nonindigenous marine organisms *Science* 261:78-82.
- Hayes, K. R., and S. C. Barry. 2008. Are there any consistent predictors of invasion success? *Biological Invasions* 10:483-506.
- Kolar, C. S., and D. M. Lodge. 2002. Ecological predictions and risk assessment for alien fishes in North America. *Science* 298:1233-1236.
- Kulhanek, S. A., A. Ricciardi, and B. Leung. 2011. Is invasion history a useful tool for predicting the impacts of the world's worst aquatic invasive species? *Ecological Applications* 21:189-202.
- Lee II H and Reusser DA (2012) Atlas of Nonindigenous Marine and Estuarine Species in the North Pacific. Office of Research and Development, National Health and Environmental Effects Research Laboratory, EPA/600/R/12/631.
- McCune, B., and M. J. Mefford. 1999. PC-ORD: multivariate analysis of ecological data. MjM Software Design.
- Payne MC, Brown CA, Reusser DA, Lee II H (2012) Ecoregional analysis of nearshore sea-surface temperature in the North Pacific. *PLoS One* 7(1):e30105.
- Lo, V. B., C. D. Levings, and K. M. A. Chan. 2012. Quantifying potential propagule pressure of aquatic invasive species from the commercial shipping industry in Canada. *Marine Pollution Bulletin* 64:295-302.
- Lockwood, J. L., P. Cassey, and T. Blackburn. 2005. The role of propagule pressure in explaining species invasions. *Trends in Ecology & Evolution* 20:223-228.
- Murray, C. C., T. W. Theriault, and P. T. Martone. 2012. Adapted for invasion? Comparing attachment, drag and dislodgment of native and nonindigenous hull fouling species. *Biological Invasions* 14:1651-1663.
- Romanuk, T. N., Y. Zhou, U. Brose, E. L. Berlow, R. J. Williams, and N. D. Martinez. 2009. Predicting invasion success in complex ecological networks. *Philosophical Transactions of the Royal Society B-Biological Sciences* 364:1743-1754.
- Ruiz, G. M., J. T. Carlton, E. D. Grosholz, and A. H. Hines. 1997. Global invasions of marine and estuarine habitats by non-indigenous species: Mechanisms, extent, and consequences. *American Zoologist* 37:621-632.

Sol, D., J. Maspons, M. Vall-Llosera, I. Bartomeus, G. E. Garcia-Pena, J. Pinol, and R. P. Freckleton. 2012. Unraveling the Life History of Successful Invaders. *Science* 337:580-583.

Sylvester, F., O. Kalaci, B. Leung, A. Lacoursiere-Roussel, C. C. Murray, F. M. Choi, M. A. Bravo, T. W. Therriault, and H. J. MacIsaac. 2011. Hull fouling as an invasion vector: can simple models explain a complex problem? *Journal of Applied Ecology* 48:415-423.

5. OUTPUTS

a. Completed and planned publications

We plan to publish the work presented here although we are uncertain what journal will be selected. While we would like to contribute this work to the currently planned Special Issue in *Marine Pollution Bulletin*, the level of effort required to finalize the database for statistical analysis put us behind schedule for the February 1 deadline. It would also be worthwhile to consider whether a comparison between this analysis and the expert risk assessment would be an interesting and valuable addition.

We also plan to publish a manuscript detailing aspects of work completed during Year 1 entitled “The mussel *Mytilus galloprovincialis* on Japanese tsunami marine debris: A potential model species to characterize a novel transport vector,” written by Jessica A. Miller, James T. Carlton, John W. Chapman, Jonathan B. Geller and Greg Ruiz. We are aiming for the Special Issue of *Marine Pollution Bulletin* but our submission will not be ready by February 1. If late submissions are not accepted, we will likely aim for the Special Issue of *Invasion Biology*, edited by Jim Carlton.

b. Poster and oral presentations at scientific conferences or seminars

Carlton, J.T., Chapman, J.W., Geller, J.B., Miller, J.A., Ruiz, G., Carlton, D., and McCuller, M. 2016. The invasion process model and the transoceanic dispersal of coastal marine organisms by Japanese tsunami marine debris. 9th International Conference on Marine Bioinvasions, Sydney, Australia.

Gillman RA, Miller JA, Clarke Murray C, Carlton JT, Ruiz GM, Otani M, Nelson J, Wong J. 2016. Japanese Tsunami Marine Debris (JTMD): A closer look at its passengers. Poster presented at: State of the Coast - Oregon's Coastal Conference. Gleneden Beach, OR

Gillman RA, Miller JM, Clarke Murray C, Carlton JT, Ruiz G, Otani M, Nelson J, Wong J. 2016. Distributional, environmental, and life history variation of Japanese Tsunami Marine Debris (JTMD) biota. North Pacific Marine Science Organization 2016 Annual Meeting. San Diego, CA

Miller, Jessica, A. 2014. Tracking marine biota on Japanese tsunami marine debris. Seventh International Symposium on Aquatic Animal Health, Portland, Oregon.

Miller, J.A., Carlton, J.T., Chapman, J.W., Geller, J.B., Ruiz, G. 2016. The mussel *Mytilus galloprovincialis* on Japanese Tsunami Marine Debris: a potential model species to characterize a novel transport vector. 9th International Conference on Marine Bioinvasions, Sydney, Australia.

c. Education and outreach

April 13-14, 2016. Marine Debris Action Plan Workshop, in Newport, OR. Reva Gillman attended the Marine Debris Action Plan Workshop, put on by the NOAA Marine Debris Program. While there, she showcased samples of JTMD species, as well as presented an informational poster on JTMD species to participants of the Marine Debris Workshop. She also sent out additional materials (informative JTMD species booklet) later on for those who were interested.

September 16, 2016. Reva Gillman presented a talk for students from the Educational Opportunities at OSU. She gave a tour of the Miller lab and the rest of Hatfield Marine Science Center for soon-to-be OSU undergraduate freshman. The students were from underrepresented groups. They were shown samples of JTMD species and discussed the research. They were also shown the display that included a piece of the Japanese dock that washed up in Newport, OR, (the Agate Beach Dock) as well as the exhibit at Hatfield Marine Science Center showcasing JTMD species.

6. RESEARCH STATUS AND FUTURE STEPS/PLANS

Overall, we feel that we have accomplished our proposed objectives. While we have not yet finalized a manuscript for peer-review, as we have some additional synthesis, interpretation and writing, the information and graphics provided should be a valuable contribution to the overall ADRIFT project. As noted above, a more direct comparison between this analysis and the qualitative assessment generated through the risk analysis could be a valuable addition. We will be working on these aspects over the next two months.

Table A1. List of 135 species included in distributional, environmental, and life history database of Japanese Tsunami Marine Species. Species in bold were included in the qualitative synthesis but not the quantitative analysis due to missing information.

Species	Invasion Category
<i>Aetea anguina</i>	Cryptogenic
<i>Aetea truncate</i>	Cryptogenic
<i>Amblyosyllis speciosa</i>	Known invasion history
<i>Amphisbetia furcate</i>	No known invasion history
<i>Ampithoe lacertosa</i>	Cryptogenic
<i>Ampithoe valida</i>	Known invasion history
<i>Anomia cytaeum</i>	No known invasion history
<i>Aphelasterias japonica</i>	No known invasion history
<i>Arabella semimaculata</i>	No known invasion history
<i>Arbocuspis bellula</i>	No known invasion history
<i>Arbopercula angulate</i>	Cryptogenic
<i>Arca boucardi</i>	No known invasion history
<i>Arca navicularis</i>	No known invasion history
<i>Asterias amurensis</i>	Known invasion history
<i>Balanus crenatus</i>	No known invasion history
<i>Balanus glandula</i>	Known invasion history
<i>Balanus trigonus</i>	Known invasion history
<i>Bankia carinata</i>	Cryptogenic
<i>Bankia bipennata</i>	Unclear
<i>Biflustra grandicella</i>	Known invasion history
<i>Biflustra irregulata</i>	No known invasion history
<i>Bougainvillia muscus</i>	Cryptogenic
<i>Callopora craticula</i>	No known invasion history
<i>Caprella mutica</i>	Known invasion history
<i>Caprella penantis</i>	Cryptogenic
<i>Celleporella hyalina</i>	No known invasion history
<i>Celleporina nordenskjoldi</i>	No known invasion history
<i>Celleporina porosissima</i>	No known invasion history
<i>Celleporina umbonata</i>	No known invasion history
<i>Chthamalus challenger</i>	Known invasion history
<i>Cibicides lobatulus</i>	No known invasion history
<i>Crassostrea gigas</i>	Known invasion history
<i>Crepidula onyx</i>	Known invasion history

<i>Cryptosula pallasiana</i>	Known invasion history
<i>Dactylopodamphiascopsis latifolius</i>	No known invasion history
<i>Dendostrea folium</i>	Known invasion history
<i>Dendronotus frondosus</i>	No known invasion history
<i>Diadumene lineata</i>	Known invasion history
<i>Didemnum vexillum</i>	Known invasion history
<i>Dolabella auricularia</i>	No known invasion history
<i>Dynoides spinipodus</i>	No known invasion history
<i>Endeis nodosa</i>	Known invasion history
<i>Entodesma navicula</i>	No known invasion history
<i>Escharella hozawai</i>	No known invasion history
<i>Eulalia quadrioculata</i>	No known invasion history
<i>Eutima japonica</i>	No known invasion history
<i>Exochella tricuspis</i>	No known invasion history
<i>Gammaropsis japonicas</i>	No known invasion history
<i>Gromia oviformis</i>	Cryptogenic
<i>Halacarellus schefferi</i>	No known invasion history
<i>Halecium tenellum</i>	No known invasion history
<i>Halosydna brevisetosa</i>	No known invasion history
<i>Harmothoe imbricata</i>	Cryptogenic
<i>Harpacticus nicacensis</i>	No known invasion history
<i>Harpacticus pacificus</i>	No known invasion history
<i>Harpacticus septentrionalis</i>	No known invasion history
<i>Havelockia versicolor</i>	No known invasion history
<i>Hemigrapsus sanguineus</i>	Known invasion history
<i>Hermisenda crassicornis</i>	No known invasion history
<i>Heterolaophonte discophora</i>	No known invasion history
<i>Hiatella orientalis</i>	Known invasion history
<i>Hippothoa imperforata</i>	No known invasion history
<i>Hydrodendron gracile</i>	No known invasion history
<i>Hydroides ezoensis</i>	Known invasion history
<i>Hytissa numisma</i>	Unclear
<i>Ianiropsis serricaudis</i>	Known invasion history
<i>Jassa marmorata</i> complex	Known invasion history
<i>Laevichlamys irregularis</i>	No known invasion history
<i>Limaria hakodatensis</i>	No known invasion history
<i>Lyrodus takanoshimensis</i>	Known invasion history
<i>Megabalanus rosa</i>	Known invasion history

<i>Megabalanus zebra</i>	Known invasion history
<i>Membranipora conjunctiva</i>	No known invasion history
<i>Membranipora raymondi</i>	No known invasion history
<i>Membranipora serrilamella</i>	No known invasion history
<i>Membraniporopsis serrilamelloides</i>	No known invasion history
<i>Metridium dianthus</i>	Cryptogenic
<i>Microporella borealis</i>	No known invasion history
<i>Microporella pulchra</i>	No known invasion history
<i>Mitrella moleculina</i>	No known invasion history
<i>Modiolus nipponicus</i>	No known invasion history
<i>Mopalia seta</i>	No known invasion history
<i>Musculus cupreus</i>	No known invasion history
<i>Mytilisepta yessoensis</i>	Unclear
<i>Mytilus coruscus</i>	No known invasion history
<i>Mytilus galloprovincialis</i>	Known invasion history
<i>Mytilus trossulus</i>	No known invasion history
<i>Nereis pelagica</i>	Cryptogenic
<i>Nipponacmea habei</i>	No known invasion history
<i>Obelia griffin</i>	Cryptogenic
<i>Obelia longissima</i>	Cryptogenic
<i>Oedignathus inermis</i>	No known invasion history
<i>Oerstedia dorsalis</i>	No known invasion history
<i>Orthopyxis caliculata</i>	Cryptogenic
<i>Orthopyxis platycarpa</i>	No known invasion history
<i>Pacificincola perforata</i>	Unclear
<i>Paralaophonte congenera</i>	No known invasion history
<i>Paramphiascella fulvofasciata</i>	Cryptogenic
<i>Parastenhelia spinosa</i>	No known invasion history
<i>Parathalestris intermedia</i>	No known invasion history
<i>Paschinnites coruscans</i>	No known invasion history
<i>Patiria pectinifera</i>	No known invasion history
<i>Perinereis nigropunctata</i>	No known invasion history
<i>Phascolosoma scolops</i>	Known invasion history
<i>Placiphorella stimpsoni</i>	No known invasion history
<i>Plumularia setacea</i>	Cryptogenic
<i>Pocillopora damicornis</i>	No known invasion history
<i>Pseudoctomeris sulcata</i>	No known invasion history
<i>Pygospio californica</i>	No known invasion history

<i>Sarsamphiascus minutus</i>	No known invasion history
<i>Scaechlamys squamata</i>	No known invasion history
<i>Schizoporella japonica</i>	Known invasion history
<i>Semibalanus cariosus</i>	No known invasion history
<i>Septifer virgatus</i>	No known invasion history
<i>Sertularella mutsuensis</i>	No known invasion history
<i>Smittoidea spinigera</i>	No known invasion history
<i>Sphaerozius nitidus</i>	Unclear
<i>Spirobranchus polytrema</i>	Unclear
<i>Stenothoe crenulata</i>	Known invasion history
<i>Syllis elongate</i>	No known invasion history
<i>Syllis hyaline</i>	Cryptogenic
<i>Tectura emydia</i>	No known invasion history
<i>Telmatogeton japonicus</i>	Known invasion history
<i>Temnotrema sculptum</i>	No known invasion history
<i>Teredo navalis</i>	Known invasion history
<i>Teredothyra smithi</i>	No known invasion history
<i>Tetrastemma nigrifrons</i>	No known invasion history
<i>Tricellaria inopinata</i>	Known invasion history
<i>Trypanosyllis zebra</i>	No known invasion history
<i>Tubulipora masakiensis</i>	No known invasion history
<i>Tubulipora pulchra</i>	No known invasion history
<i>Walkeria uva</i>	Cryptogenic
<i>Watersipora mawatarii</i>	No known invasion history
<i>Watersipora subatra</i>	Known invasion history
<i>Zeuxo normani</i>	Cryptogenic

Table A2. Attribute name and associated field values for all Japan Tsunami Marine Species (JTMD) included in the database.

Attribute	Definition
Realm (Native and Non-native)	
Realm_1	Arctic
Realm_2	Temperate Northern Atlantic
Realm_3	Temperate Northern Pacific
Realm_4	Tropical Eastern Pacific
Realm_5	Tropical Atlantic
Realm_6	Eastern Indo-Pacific
Realm_7	Central Indo-Pacific
Realm_8	Western Indo-Pacific
Realm_9	Temperate South America
Realm_10	Temperate Southern Africa
Realm_11	Temperate Australasia
Realm_12	Southern Ocean
Region (Native and Non-native)	
Reg_1	Arctic
Reg_2	High arctic
Reg_3	Northeast Atlantic
Reg_4	Northwest Atlantic
Reg_5	Mediterranean Sea
Reg_6	Ponto-Caspian
Reg_7	Northeast Pacific
Reg_8	Northwest Pacific
Reg_9	Tropical Eastern Pacific
Reg_10	Magellanic
Reg_11	Southeast Pacific
Reg_12	East Tropical Atlantic
Reg_13	West Tropical Atlantic
Reg_14	Southwest Atlantic
Reg_15	Southern Africa
Reg_16	Central Indo-Pacific
Reg_17	Eastern Indo-Pacific
Reg_18	Indian Ocean
Reg_19	Southern Australia and New Zealand
Reg_20	Antarctica
Temperature regime (Native and Non-native)	
Temp_1	Cold water
Temp_2	Cool temperate
Temp_3	Warm temperate
Temp_4	Subtropical
Temp_5	Tropical
Salinity regime (Native and Non-native)	
Sal_1	Freshwater = <0.5
Sal_2	Oligohaline = 0.5 - <5
Sal_3	Mesohaline = 5 - <18
Sal_4	Polyhaline = 18 - <30
Sal_5	Euhaline = 30 - <40
Sal_6	Hypersaline = ≥ 40

Fertilization mode	
1	Internal fertilization
2	External fertilization
Reproductive mode	
1	Gonochoristic/dioecious
2	Hermaphrodite/monoecious
Spawning type	
1	Broadcast
2	Spermcast
3	Not applicable
Development mode	
1	Direct Development
2	Benthic larva
3	Lecithotrophic larva
4	Planktotrophic larva
5	Planktonic larva type unspecified
6	Lecithotrophic, and planktotrophic (<i>Dendronotus fronfusus</i> only)
Asexual reproduction	
1	Does not reproduce asexually
2	Binary fission Splitting into two approximately equal parts
3	Budding/fragmentation: splitting into unequal parts. Buds may form on the body of the "parent"
4	Parthenogenesis: the development of an unfertilized egg in animals.
Adult mobility	
1	Sessile
2	Facultatively mobile: species with limited mobility, in particular to repositioning themselves in response to environmental disturbances e.g., sea anemones
3	Actively mobile: mobility is a normal part of at least part of the adult life cycle - at least in spurts. Not dependent upon distance traveled
Depth regime	
Depth_1	Supralittoral
Depth_2	Intertidal
Depth_3	Shallow subtidal = >0 - 30m
Depth_4	Deep subtidal = >30 - 200m
Depth_5	Bathyal = >200
Ecosystem	
Eco_1	Coastal shore = Sediment environments along the coast that are affected by the tides and water activity shore waves, i.e. sandy beaches
Eco_2	Tide flats = Relatively flat, sediment areas that are submerged or exposed by the changing tides. Includes mud flats
Eco_3	Sediment subtidal = Sediment that is covered by a body of water at all times, without exposure to air due to tides
Eco_4	Submerged aquatic vegetation SAV= Sediment environments that include and are dominated by aquatic plants that are covered by water, i.e. seagrass
Eco_5	Marsh = Intertidal sediment environments dominated by vegetation that is rooted in the soil. i.e. marsh grasses and salt tolerant succulents
Eco_6	Rocky = Rocky intertidal rocky environments on coastal shore that are periodically exposed to both air and water. The zone between the high and low tide mark and rocky subtidal rocky environments below low tide mark that are always submerged by water

Eco_7	Coral reef = Areas where the rocky substrate is dominated by reef forming coral animals
Eco_8	Temperate reef = Oyster/mussel reef hard substrate that is covered or formed by bivalve shells; Worm Reef hard substrate that is predominantly composed of worm tubes; Coralline Algae Hard substrate that is predominantly composed of calcified algae, either the encrusting or unattached rhodolith form
Eco_9	Mangrove = Intertidal sediment environments dominated by salt-tolerant trees and shrubs. Found in tropical and subtropical areas
Eco_10	Macroalgal beds = Sediment environments where macroalgae are dominant and shape the habitat characteristics e.g., algal mats of Ulva, Porphyra
Eco_11	Kelp forest = Hard substrate that supports the growth of very large brown algae Laminariales and/or Fucales. These habitats tend to be subtidal and occur in mid and high latitudes
Eco_12	Fouling = Hard substrate such as a boat hull that supports a community of organisms
Eco_13	Water column = Open water habitat where organisms are completely surrounded by water no surfaces, sides, or floors; within the pelagic zone
Eco_14	Floating plants or macroalgae = Large mats/rafts of plants or algae that float unattached on the water's surface in the open ocean
Eco_15	Flotsam = Aggregated floating debris in the open ocean
Habitat	
Hab_1	Pelagic = Organisms inhabiting the water column exclusive of the layer immediately above the bottom
Hab_2	Demersal = Mobile animals living on or near the bottom and that swim as a normal part of their routine and not just in response to disturbance
Hab_3	Epibenthic = Sessile e.g., barnacles, algae and vagile e.g., snails organisms living on the surface of inorganic hard substrates including man-made structures, Epiphytic = Living on surface of living or dead plant, or Epizoic = living on surface of a living or dead animal
Hab_4	Under rock = Species that live beneath rock or other hard substrates e.g., shell rubble, debris
Hab_5	Borer = Organisms that bore into living or dead hard substrate
Hab_6	Infaunal = Animals living within sediment; Semi-infaunal = Animals partially buried in sediment and partially exposed in the water column
Substrate	
Subst_1	Mud = $\geq 75\%$ by weight of particles < 0.063 mm in size
Subst_2	Sand = $\geq 75\%$ by weight of particles in the size range of 0.063 - 2 mm
Subst_3	Mixed fine sediment = Combination of mud and sand, where the two classes constitute $> 95\%$ of the weight
Subst_4	Rock: Gravel $\geq 75\%$ by weight of particles in the range of 2 - 64 mm; Cobble $\geq 75\%$ by weight of particles in the size range of 64–256 mm; Rock Boulder particles > 256 mm or bedrock unbroken rock
Subst_5	Mixed sediments = Sand and mud with gravel or cobble, where gravel and cobble each constitute $> 5\%$ but $< 75\%$ of the sediment weight.
Subst_6	Organic sediment = Sediment with high proportion of vegetative detritus. $> 30\%$ organic matter $> 17\%$ organic carbon
Subst_7	Hardpan = Sand, silt, or clay particles that are slightly cemented to well cemented together to form a hard, and often flat, consolidated surface
Subst_8	Biogenic = Substrate composed of the surface of living or dead organisms
Subst_9	Artificial substrate = Hard substrates placed into estuarine or oceanic environments

Exposure

Exp	Exposed
Semi_exp	Semi-exposed
Protect	Protected
V_protect	Very protected

Trophic status

1	Herbivore
2	Omnivore
3	Predator
4	Detritivore
5	Suspension feeder
6	Deposit feeder
7	Herbivore, Suspension feeder
8	Suspension feeder, deposit feeder
