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The invasion risk of species associated with Japanese Tsunami Marine Debris in Pacific North America and Hawaii[☆]

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ABSTRACT

Marine debris from the Great Tsunami of 2011 represents a unique transport vector for Japanese species to reach Pacific North America and Hawaii. Here we characterize the invasion risk of invertebrate species associated with tsunami debris using a screening-level risk assessment tool – the Canadian Marine Invasive Screening Tool (CMIST). Higher-risk invertebrate invaders were identified for each of five different ecoregions. Some of these are well-known global invaders, such as the mussel *Mytilus galloprovincialis* and the ascidian *Didemnum vexillum* which already have invasion histories in some of the assessed ecoregions, while others like the sea star *Asterias amurensis* and the shore crab *Hemigrapsus sanguineus* have yet to invade large portions of the assessed ecoregions but also are recognized global invaders. In general, the probability of invasion was lower for the Gulf of Alaska and Hawaii, in part due to lower climate matches and the availability of other invasion vectors.

1. Introduction

On March 11, 2011, a 9.0 magnitude earthquake struck off the coast of Honshu, Japan, creating a devastating tsunami that reached heights of up to 40 m and inundated 562 km² in northern Japan (Mori et al., 2011). This tsunami sent millions of tons of Japanese Tsunami Marine Debris (JTMD) from terrestrial and coastal environments into the ocean (Ministry of the Environment, Japan, 2012). Although the specific types (wood, plastic, vessels, etc.) and origins of the resulting debris field were not quantified, it is clear that many objects were colonized by Japanese coastal species (Carlton et al., 2017). While the rafting of organisms on marine debris is not a new phenomenon and likely has been occurring for eons, especially on terrestrial and marine vegetation (Lewis et al., 2005; Thiel and Gutow, 2005), human-mediated activities have drastically increased the amount of debris in our oceans (Barnes, 2002; Gregory, 2009; Rech et al., 2016), dominated by plastic which does not readily biodegrade like plant material. A number of recent studies have identified a wide variety of taxa that are able to colonize

marine debris. For example, Goldstein et al. (2014) documented 95 taxa from 11 phyla on plastic debris in the North Pacific Ocean. Although marine debris can remain at sea for considerable periods of time, especially if entrained into the North Pacific gyre (i.e., “garbage patch”) (e.g., Moore et al., 2001) a portion will eventually come ashore in coastal ecosystems and these landings have the potential to deliver non-indigenous species (NIS) to novel locations.

Debris landings in Pacific North America and Hawaii associated with the Great Tsunami of 2011 that include rafting of potential NIS from Japan could result in new invasions, some of which may result in ecological and economic impacts (i.e. high risk invaders). This would be consistent with marine invasions globally where a subset of established NIS becomes truly invasive (e.g., Williamson, 1996). Invasive species cost countries billions of dollars each year and often are identified as the second greatest threat to native biodiversity after habitat loss (Williamson, 1996; Sala et al., 2000; Colautti et al., 2006). Further, the direct negative impacts of biological invasions on fisheries and aquaculture operations are well documented, and there is growing evidence

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invasive species have the ability to alter ecosystem function, negatively affecting native species/communities, and reducing the ecological integrity of these native systems (e.g., Bax et al., 2003; Colautti et al., 2006). Thus, given this unique event, it is important to identify potential NIS associated with JTMD that could pose a higher risk to coastal ecosystems in Pacific North America (California to Alaska) and Hawaii.

A variety of tools have been developed to evaluate the risk a species poses to a given area, using different combinations of factors thought to influence invasion success (reviewed in Kumschick and Richardson, 2013). Risk scoring schemes can provide a relatively quick way to screen and rank species without conducting time- and data-intensive quantitative risk analyses (e.g., Therriault and Herborg, 2007; Leung et al., 2012). Thus, they can be used to inform NIS management by rapidly screening a large number of species, allowing limited resources to be directed towards those NIS posing the greatest risk. Screening-level tools for NIS are generally based on the answers to a series of questions to determine if a species is a threat (high risk) or not. The most common screening-level tool types are either decision trees (Reichard and Hamilton, 1997; Kolar and Lodge, 2002; Caley and Kuhnert, 2006) or scoring systems (Pheloung et al., 1999; Daehler et al., 2004; Copp et al., 2009; Drolet et al., 2016). Although decision trees work well in situations related to import (i.e., allow or not allow), scoring systems allow ranking of species based on perceived risk thereby providing a prioritized list of NIS for potential management intervention or policy development. All of these assessment tools rely on some understanding of the species (biology, tolerances, etc.) and previous invasion history (if available) in order to identify those NIS most likely to become invasive in the risk assessment area. Thus, data-poor NIS can be more challenging to assess independent of the tool applied, especially those lacking any prior invasion history since most high risk invasive species were not predicted to be high-impact invaders until they resulted in substantial impacts elsewhere.

To inform potential monitoring, management or policy development around Japanese species arriving on JTMD, a risk assessment method that allows prioritization is desired. A recently developed marine screening-level risk assessment tool for NIS, the Canadian Marine Invasive Screening Tool (CMIST), follows the sequence of events in the invasion process: arrival, survival, establishment, spread, and impact. CMIST uses 17 generalized and non-taxon specific questions (Drolet et al., 2016) related to both the invasion process and a species' potential impacts. Further, CMIST uses Monte Carlo simulation to allow uncertainty to be captured explicitly in the risk assessment score. This tool recently was applied to characterize the invasion risk of *Didemnum vexillum* in Atlantic Canada (Moore et al., 2018) and here we applied CMIST to species associated with JTMD to characterize the relative risk posed to Pacific North American and Hawaiian ecosystems. Specifically, we focused on invertebrates, of which > 300 taxa have been identified in association with JTMD items thus far (Carlton et al., 2017).

2. Methods

2.1. Species associated with JTMD

Over 600 confirmed JTMD objects (based on multiple lines of

evidence (presented in Carlton et al., 2017) arriving on the shores of Pacific North America and Hawaii were opportunistically sampled for invertebrate, algae, and fish species since June 2012 (when JTMD began arriving *en masse*). Of the invertebrates associated with JTMD, five groups (mollusks, annelids, cnidarians, bryozoans, and crustaceans) composed 85% of the species diversity (Carlton et al., 2017). Although interception and sampling of JTMD items continues, our assessment of JTMD species risk is limited to those identified as of May 2016 given ongoing taxonomic revisions for many groups of organisms. Biological samples were processed morphologically with genetic verification for some organisms and identified to the lowest taxonomic level possible. All invertebrates identified to the species level were retained for screening for potential invasion risk ($N = 131$; 36 molluscs, 35 crustaceans, 18 bryozoans, 15 annelids, 13 cnidarians, 5 echinoderms, 2 nemertean, 1 tunicate, and 6 others) while others were not assessed here because higher level taxonomic information confounds the environmental tolerances, life history characteristics, and potential impacts of an organism rendering risk scores less informative. A literature search and review was conducted for each species generating a database that included information on invasion history, native range, introduced range, environmental tolerances and life history characteristics. Initial search terms included species/taxonomic names and then targeted data gaps more specifically (e.g. reproduction, temperature, distribution, etc.). This information came from a variety of sources (e.g. primary publications, reports, databases, internet searches, etc.) in both the international (English) and Japanese literature. Approximately 1600 papers, 6 reference books, and up to 17 websites formed the basis for this literature search that resulted in a database (<https://invasions.si.edu/nemesis/jtmd/searchTaxa.jsp>) that was used in the risk assessment.

2.2. CMIST risk assessment

The potential risk of JTMD species arriving to Pacific North America and Hawaii was determined using CMIST. CMIST was developed based on the different steps in the invasion process (Drolet et al., 2016) and explicitly distinguishes the two risk components: 'Likelihood of Invasion' and 'Impact of Invasion' (Kumschick and Richardson, 2013). There are 17 CMIST questions and each of them is scored on a scale between 1 and 3 ('Low' = 1 to 'High' = 3) (Drolet et al., 2016, Table 1). A mean score is calculated for the Likelihood of Invasion (i.e., questions 1–8) and Impacts of Invasion (i.e. questions 9–17) and these scores are then multiplied to obtain an overall relative risk score ranging from 1 to 9. In addition to answering each risk question, assessors also assign a qualitative uncertainty score ('Low certainty' = 1 to 'High certainty' = 3) for each question. This uncertainty largely reflects the quality of information available and its interpretation when answering the CMIST questions. Potential uncertainty imposed via the CMIST tool itself (i.e. linguistic uncertainty sensu Regan et al., 2002) is generally addressed in the guidance document for CMIST application and discussions among assessors prior to species screening reduced inter-assessor variability (<http://www.bio.gc.ca/science/monitoring-monitorage/cmist/usage-en.php>). The question answers and associated uncertainty ranking are used in a Monte Carlo randomization procedure to generate an adjusted risk score that includes uncertainty (Drolet et al., 2016). Although risk

Table 1

Summary statistics of the entire suite of non-indigenous species (NIS) scored. Native species scores were excluded for each ecoregion. Cumulative risk refers to the sum of all risk scores for the ecoregion and Per Capita risk is the Cumulative Risk divided by N, the number of species included for each ecoregion.

Region	Median	Lower 95% CI	Upper 95% CI	Cumulative risk	Per capita risk	Min score	Max score	N
Gulf of Alaska	2.69	2.58	2.76	326.30	2.84	1.99	5.78	115
North American Pacific Fjordland	2.71	2.60	2.77	343.86	2.89	1.99	6.03	119
Oregon, Washington, Vancouver Coast & Shelf	2.72	2.61	2.84	315.37	3.00	2.00	6.62	105
Northern California	2.76	2.66	2.86	349.60	3.04	2.15	6.86	115
Hawaii	2.73	2.66	2.81	371.60	2.93	2.14	5.82	127

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