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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 km^2 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 nemerteans, 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 Fijordland	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

assessment tools tend to be over-parameterized (e.g., Gordon et al., 2008; Koop et al., 2012), including CMIST (Drolet et al., 2017), there was no basis in the application of CMIST to JTMD organisms that would allow a meaningful evaluation of individual question contributions or weighting (i.e., since these species have not invaded there is no independent basis for comparing model performance). Thus, all 17 questions were retained and scored. One minor modification was made to the original scoring rubric: Question 17 (*Is the species known or generally considered to be invasive anywhere in the world*?) originally stated "No, but has traits related to invasion" for scoring level 2, but was revised to state "No, but it has been noted outside of its native range" in order to account for species with limited information available that have moved beyond their native range and do not have recorded impacts.

Risk scores for NIS invertebrate species known to have been associated with JTMD were calculated by two assessors independently using CMIST in conjunction with the life history database, with a random subsample scored by a third assessor to check for consistency. These scores were then averaged to obtain the final risk score for each species-ecoregion combination. All assessors were knowledgeable about marine invasions (but not practicing risk assessors). Each assessor used the species literature database and their own knowledge of invasions and marine species to score each JTMD species for each of the five ecoregions in the eastern Pacific that were known to have received JTMD (Fig. 1) i) Gulf of Alaska; ii) North American Pacific Fijordland; iii) Oregon, Washington, Vancouver Coast and Shelf; iv) Northern California; and v) Hawaii (based on the Spalding et al., 2007 Marine Ecoregions of the World (MEOW) classification system). Each species was assessed for each ecoregion, though not all species were sampled from each ecoregion, due to the potential that species may have arrived in any of the ecoregions but were not detected during the opportunistic sampling events. The Strait of Georgia/Puget Sound ecoregion was not included because we did not receive any confirmed reports of JTMD and oceanographic models suggest that this region would not be expected to receive JTMD directly (Maximenko et al., 2012; Lebreton and Borreo, 2013). However, this region is connected by a myriad of vectors to other ecoregions along the Pacific coast of North America such that JTMD-associated species could indirectly arrive to the Strait of Georgia/Puget Sound ecoregion. To facilitate risk assessment, background information including ecosystems and habitat types present, sea surface temperature range, extent of species transport vectors operating in the region, and presence of species-at-risk, was compiled for each of the ecoregions for which assessments were to be undertaken and life history/invasion impact data were gathered for species associated with JTMD. Guidelines created by the CMIST developers provided further context for the screening tool questions (Drolet et al., 2016). Consistent with the intended application of CMIST, justification and sources of information used to answer each question were noted for each entry. The lower and upper 95% confidence intervals around the medians, of the combined invertebrate species per ecoregion were reported. The effects of ecoregion and inter-assessor variability were assessed using Repeated Measures General Linear Model for all taxa.

3. Results

There was no significant difference between assessors ($F = 3.106$, $p = 0.07$) and therefore Monte Carlo adjusted risk scores were averaged across assessors. For the 131 species associated with JTMD assessed here, CMIST scores ranged from approximately 1.99 (lower risk) to 6.86 (higher risk) depending on the species and the ecoregion (Fig. 2; Appendix A). Although specific risk thresholds have not been identified for CMIST, the tool was able to provide a relative risk ranking for each JTMD species assessed. The higher-risk species (relative to other species scored from JTMD) among all ecoregions were well-known global invaders including the mussel *Mytilus galloprovincialis* (e.g., Branch and Steffani, 2004), the ascidian *Didemnum vexillum* (e.g., Coutts and Forrest, 2007), the crab *Hemigrapsus sanguineus* (e.g., Klassen, 2012), and the sea star *Asterias amurensis* (e.g., Hayes et al., 2005) (Fig. 2). In addition, plotting CMIST adjusted Likelihood of Invasion and adjusted Impact of Invasion scores (Fig. 3) allows the identification of those

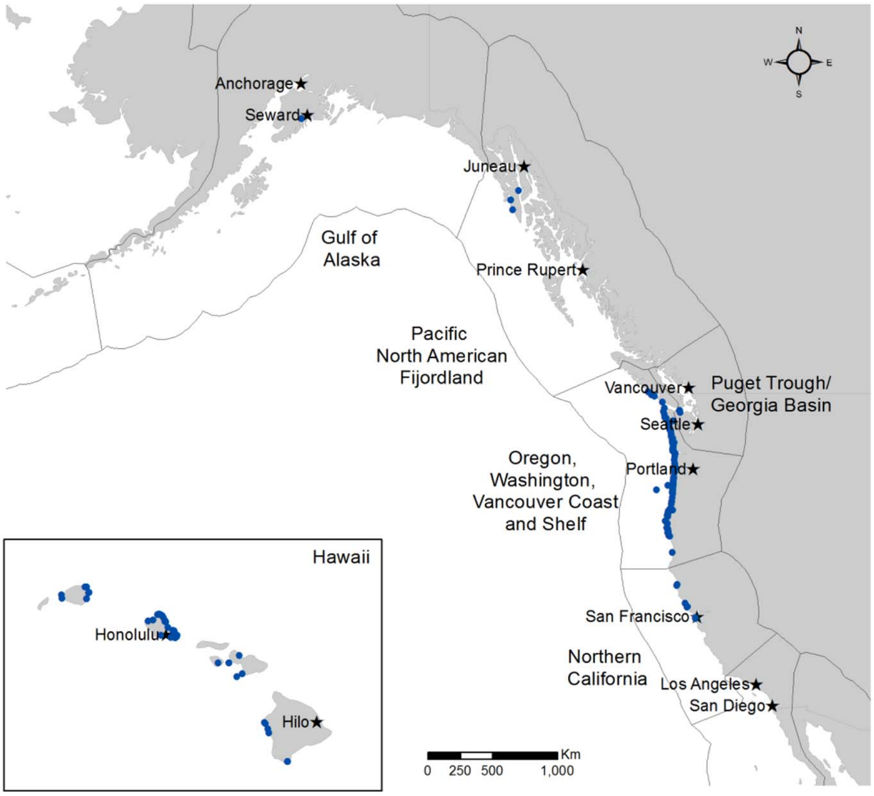

Fig. 1. MEOW ecoregions of Pacific North America and Hawaii showing JTMD landings (blue dots) used in this study. Major cities (stars) are shown for reference. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

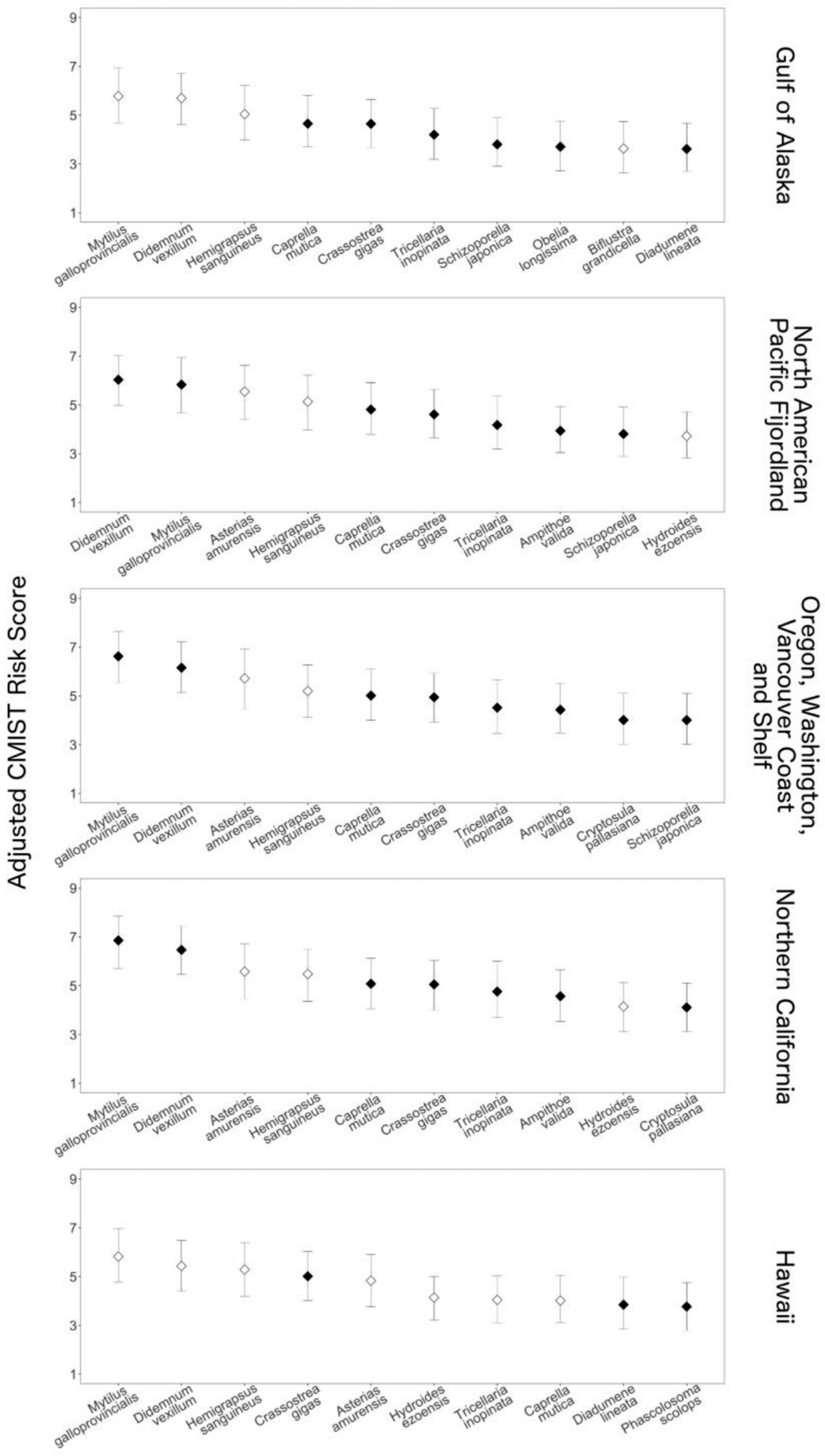

Fig. 2. The ten highest risk invertebrate species by ecoregion: Gulf of Alaska, North American Pacific Fijordland, Oregon, Washington, Vancouver Coast and Shelf, Northern California, and Hawaii. Error bars are 95% confidence intervals derived from the Monte Carlo simulation that includes assessor uncertainty. Filled diamonds denote non-native species already present in the ecoregion prior to JTMD arrival while open diamonds denote non-native species not already present in the ecoregion.

higher risk species that have both high likelihood of invasion and impacts (i.e., the upper right quadrant of these figures).

Overall, Northern California had the highest median, per capita, and individual maximum and minimum risk scores (Table 1). Adjusted CMIST risk scores were significantly different by region (Fig. 2; repeated measures GLM: $F = 30.240$, $p < 0.001$). Hawaii had the highest cumulative risk (species risk summed across all species) due to the highest number of species associated with JTMD that were not native to that region (127), and therefore the highest number of potential invasions rather than higher risk species on average. In contrast, Oregon, Washington, Vancouver Coast and Shelf had the lowest cumulative risk due to fewer novel JTMD-associated species for that region. Although we do not know the total number of JTMD arrivals per ecoregion, it appears the Oregon, Washington, Vancouver Coast and Shelf area received substantially more objects (based on reports/collections recognizing potential bias; Fig. 1) than the other ecoregions

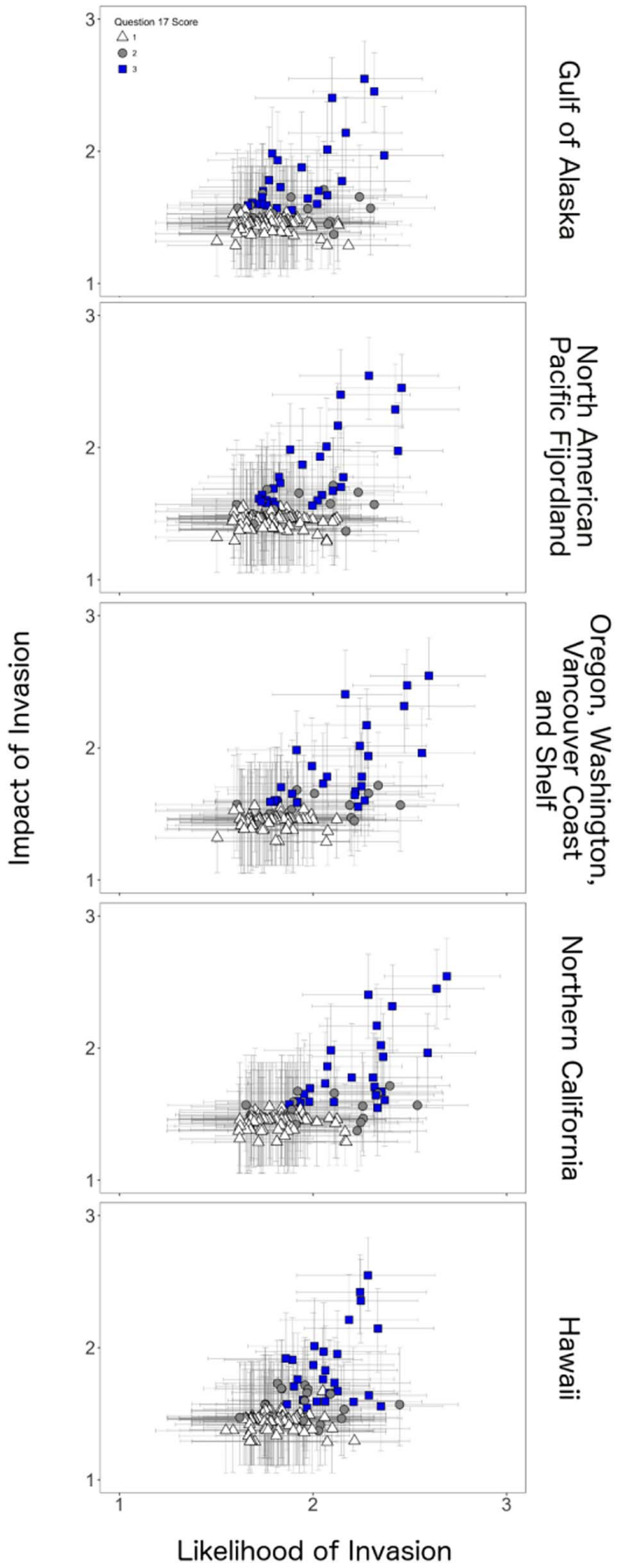

Fig. 3. CMIST scores decomposed into the two component scores, Impact of Invasion (y-axis) and Likelihood of Invasion (x-axis) for the 131 invertebrate species assessed for each of the five ecoregions (Gulf of Alaska, North American Pacific Fijordland, Oregon, Washington, Vancouver Coast and Shelf, Northern California, and Hawaii). Error bars represent the uncertainty intervals derived from the Monte Carlo procedure that includes assessor uncertainty. Species include those that are known to be invasive elsewhere (blue square), not known to be invasive elsewhere (open triangle), and those observed outside their native range (grey circle) as scored in CMIST Question 17. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

(Murray et al., 2018). Also, each ecoregion had different levels of invasion history, with some of the JTMD species already having been introduced by other vectors (Fig. 2). In fact, of the higher risk invertebrate species assessed using CMIST, the number of existing invaders in the five assessed ecoregions ranged from 15 in Northern California to 8 in Hawaii (see open diamonds in Fig. 2), recognizing that not all of these species are necessarily distributed throughout the entire ecoregion they are present in. For each ecoregion, *Mytilus galloprovincialis*, *Didemnum vexillum*, and *Hemigrapsus sanguineus* consistently were identified as the highest risk invaders independent of these species being either previously present or absent from these ecoregions (Fig. 2).

4. Discussion

A large diversity of non-indigenous species reached Pacific North American and Hawaiian coasts via rafting on JTMD, including species with well-documented global invasion histories and documented impacts (e.g., *Mytilus galloprovincialis*, *Didemnum vexillum*, *Asterias amurensis*, and *Hemigrapsus sanguineus*). Of the species assessed, molluscs and crustaceans were common on JTMD – a finding consistent with other studies that have found these taxonomic groups entrained in other NIS vectors (e.g., Ruiz et al., 2015). Many of these species also have been introduced to other ecoregions around the world by a variety of human-mediated invasion vectors including commercial and recreational vessels and via aquaculture-mediated movements. Although some NIS have already established in our focal ecoregions prior to JTMD arrival via other invasion vectors, newly arriving individuals of the same species on JTMD may pose additional risks (see Hanyuda et al., 2017 for JTMD algae). For example, Roman and Darling (2007) showed that additional genetic diversity acquired via multiple introduction events can result in increased invasion success by avoiding potential genetic bottlenecks. Also, Roman (2006) reported how a cryptic invasion by the European green crab *Carcinus maenas* in Atlantic Canada resulted in an increase in invaded range owing to different environmental tolerances between the initial invasion event and one about 100 years later. In general, the addition of new alleles to a population could result in increased environmental tolerances, fitness and ultimately invasion success (Roman, 2006; Geller et al., 2010).

Two advantages of the CMIST tool as applied here included: 1) the explicit incorporation of uncertainty in the risk score; and 2) the reliance on fewer questions to be answered compared to other screening-level risk assessment tools (Drolet et al., 2016) recognizing that even with only 17 questions CMIST may be over-parameterized (Drolet et al., 2017) – an issue faced by other risk assessment tools (e.g., Gordon et al., 2008; Koop et al., 2012). As with all risk assessments, readily available information is critical. The application of CMIST to JTMD species that were either well-known or recognized high impact invaders (e.g., *Mytilus* or *Didemnum*) worked well as we were able to screen a high volume of species in a relatively short period of time with readily available information as intended for a screening-level risk assessment process. However, perhaps not surprisingly, for this assessment overall there was considerable variation in available literature among JTMD species assessed. Despite our efforts to include the Japanese literature for JTMD species assessed, we recognize additional literature might be available for some species that could reduce uncertainty in future assessments. As CMIST was applied here, species that had not been previously reported outside their native range or lacked documented impacts in the literature scored lower overall (see below) and thus risk may have been underestimated. By design the CMIST scoring rubric relies on the best available information (Drolet et al., 2016) and despite the potential over-parameterization (i.e., some questions not informative with respect to invasion risk; Drolet et al., 2017) additional sensitivity analyses would be required to determine thresholds for tool application. In addition, taxonomic resolution was required to apply CMIST so only those species with fully ascribed binomials were assessed with the tool such that organisms only resolved to higher taxonomic levels (i.e., genus or family) were not screened, including some that could be higher risk to North American ecosystems. Another taxonomic issue is not recognizing a NIS when present such that impacts are attributed to native "pests" simply due to poor taxonomy. Thus, although molecular approaches might help to identify these NIS when co-occurring with native congeners it likely will remain a challenge attributing impacts to them such that they appear more benign than they really are.

There were many species on JTMD that were data limited either due to a lack of study (e.g., biology, environmental tolerances) or lack of previous invasion history (invasion vectors, impacts) which often resulted in these species receiving lower scores in our application of CMIST. By design CMIST questions must be scored (i.e., can't be left blank or "0") using higher level taxonomic or more general information/data if required, but this is partially offset by the higher uncertainty scores for these species that gets incorporated into the adjusted risk score. The invasion probability questions in CMIST are related to the potential for species to arrive, survive, reproduce, and spread, based on the known history of the species. With the exceptions of Hawaii (too warm for some species) and Gulf of Alaska (too cold for some species), most of the species assessed here had relatively good climate match between the source location in Japan and the receiving environments along the west coast of North America from North American Pacific Fijordland to Northern California. Of the five ecoregions assessed here, Northern California arguably has the highest climate/habitat match to the Tohoku region of Japan where most JTMD species are believed to have originated. However, since many of these species are not known from other invasion vectors (Carlton et al., 2017) despite general taxonomic association with other invasion vectors (i.e., Ruiz et al., 2015 as > 50% of assessed JTMD species were molluscs or crustaceans), they would have scored lower in our application of CMIST for arrival and spread questions, which include all invasion vectors despite potentially scoring higher for survival and reproduction potential. Each question is weighted equally in the overall score, which means these survival and reproduction questions only counted for a small fraction of the score (3 out of 17 questions). Also, since many of the species that originated from Japan have no previous reports outside their native range, their potential impacts were scored lower in our assessment.

Assessing the potential impacts of species with no prior invasion history also remains a challenge despite efforts to predict impacts (e.g., Blackburn et al., 2014: Ojaveer et al., 2015). Further, even where invasions are well documented, the impacts for the majority of known marine species have not been evaluated, leading to an absence of data for risk assessments (Ruiz et al., 1999; Ruiz et al., 2011a). In our application of CMIST, the lack of demonstrated impacts were scored as "1" or "Low" assuming there were no closely related species with documented impacts. Thus, these species are being treated as "innocent until proven guilty" (sensu Azmi et al., 2015). However, recognizing this is not the most precautionary approach, assuming a higher level of impact such as "Intermediate" (or "2" in CMIST) as suggested by Azmi et al. (2015) (and adjusting the impact scores for the species with information accordingly) would then result in universally inflated CMIST scores in this context where many species encountered on JTMD lack any prior invasion history ultimately resulting in a longer list of potentially risky species to watch for. Thus, the highest risk species identified here were well-known invaders with previously documented, significant impacts in other parts of the world, like *Mytilus galloprovincialis* and *Didemnum vexillum*. While past invasion history is often the best available predictor of future impacts (e.g., Reichard and Hamilton, 1997; Boudouresque and Verlaque, 2002), there exists many examples where a species introduction has had unexpected/unpredicted impacts based on its earlier invasion history or lack thereof. Unfortunately only time will tell if such a species reaches Pacific North America or Hawaii on JTMD. More importantly, the lack of scientific evidence of impacts does not equal no impact – something that needs to be clearly communicated to managers and policy makers.

Overall, risk varied by region, with Northern California having the highest median and per capita risk scores among ecoregions and the Gulf of Alaska having the lowest. Northern California also had the highest minimum and maximum CMIST scores for individual species further highlighting the risk JTMD species could pose. This is perhaps not surprising given the Northern California ecoregion includes San Francisco Bay which has a well-documented invasion history (e.g., Cohen and Carlton, 1998; Cox, 1999; Ruiz et al., 2011b). Hawaii also has a substantial number of invasive species (e.g. Carlton and Eldredge, 2009, 2015) and our analyses showed that Hawaii had the largest number of novel JTMD species, hence cumulative risk (summed over these species) was highest but the per capita risk was lower possibly due to the less favourable climate match between Japan and this ecoregion. Further, in Oregon, Washington, Vancouver Coast and Shelf and North American Pacific Fijordland, 7 of the 10 highest risk species have already been introduced by other vectors. In contrast, Hawaii is relatively less invaded by these species with only 3 of the 10 highest risk species already present.

The differing risk reflects the different invasion vectors, habitat types, and climate matches to donor ecoregions and invasion hotspots like San Francisco Bay (Ruiz et al., 2011b). For example, the survival and establishment of a species in a new ecoregion is an important and limiting step in the invasion process (e.g., Gollasch, 2002; Blackburn et al., 2011). Here, as in other risk assessments, we used empirically-derived temperature and salinity thresholds where known, and native range environmental proxies otherwise. These environmental thresholds are not strict limits and do not account for plasticity and adaptation that are commonly seen in invasive species (e.g., Sakai et al., 2001). In addition to the role the physical and chemical receiving environment plays, the native biological community also plays a role in determining invasion success. In CMIST, two of the 17 questions refer to temperature and salinity tolerances pertaining to survival and reproduction, while a third question refers to availability of suitable habitat. In contrast to some other risk assessment tools where climate match can lead to zero probability of introduction (e.g. Gollasch and Leppäkoski, 2007), there are no zero rankings with CMIST and the species are ranked on a qualitative scale. Therefore, overestimation may occur where tropical species could be ranked higher risk in arctic areas even though the probability of survival might be very low. This represents a trade-off applying screening-level risk assessment tools compared to more specific detailed-level risk assessment tools.

In addition to the documented free-living invertebrate NIS on JTMD thus far, parasite and disease organisms entrained with JTMD or its associated species that would otherwise lack a potential invasion vector could pose additional risks to Pacific North American ecosystems. The high risk species *Mytilus galloprovincialis* and its hydroid parasite *Eutima* were both detected on JTMD objects (Calder et al., 2014; G. Ruiz, unpublished data) and assessed here. While the risk of known parasites and associated species are addressed in one question of CMIST, the data on parasite diversity for many invertebrate group remains limited and, where present, there is often considerable uncertainty about the potential consequences of parasites and diseases. Also, a number of parasites have complex life history strategies requiring multiple hosts to complete their life cycle. It is possible that newly arriving JTMD species could serve as intermediate and/or final hosts for parasites or diseases that might be arriving to the same area by other vectors (e.g., ballast water), allowing previously unsuccessful invasions to succeed. A similar unexpected consequence occurred with the historical transport of Pacific oyster (*Crassostrea gigas*) and Atlantic oyster (*Crassostrea virginica*), where entire oyster communities were imported to Pacific North American coastal ecosystems for aquaculture production, thereby allowing a number of hitchhiking organisms to be moved as well. These movements have been implicated in the establishment of many species along the Pacific coast. For example, several NIS were introduced with oysters to California (Carlton, 1979; Ruiz et al., 2011a) and to British Columbia (Levings et al., 2002; Gillespie, 2007; Daniel and Therriault, 2007), including a number of high impact species such as the oyster drills *Urosalpinx cinerea* and *Ocinebrellus inornata*.

The application of CMIST to JTMD species confirmed the presence of high risk NIS on JTMD objects: two JTMD species (*Asterias amurensis* and *Mytilus galloprovincialis*) are among the International Union for the Conservation of Nature's (IUCN) world's worst invasive species (Lowe et al., 2000). It is important to note that some of this risk could be reduced through mitigation actions. For example, intervention that removes fouled JTMD items immediately following detection from beaches or adjacent coastal waters can reduce the risk of invasion by reducing the propagule load to native ecosystems, which can lower establishment success of many NIS (sensu Simberloff, 2009). Given the time lag in invasion population dynamics (Crooks and Soulé, 1999) and detection thresholds (Regan et al., 2006; Fagan et al., 2002; Neubert and Parker, 2004; Rout et al., 2009), monitoring in the coming decades is warranted, especially for those higher risk species identified here.

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