Non-native Bacterial and Viral Pathogens in Ballast Water: Potential for Impacts to ESA-listed Species under NOAA's Jurisdiction

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Introduction

NOAA is investigating the potential impacts of ballast water discharges on listed species protected under the federal Endangered Species Act (ESA), in order to understand what regulatory measures are needed to protect listed species. To assist those investigations, this report reviews the current level of understanding of the potential for non-native bacteria or viruses that are pathogenic to ESA-listed species (including proposed and candidate species) that fall under NOAA's jurisdiction to be carried in ballast water and released into waters where the listed species occur, and to infect and impact those species. To prepare this report I reviewed the scientific literature, interviewed experts, and consulted other relevant information sources.

The review discusses the presence of relevant non-native bacterial or viral pathogens in source regions, the potential for such pathogens to be taken up in and transported in ballast water, the volumes of ballast water transferred between source regions and relevant U.S. waters, the capacity of pathogens to survive ballast transport and release, the potential for listed species to be exposed to these pathogens, and the potential impacts to listed species if exposed, insofar as these quantities, capacities or probabilities are known or can be reasonably estimated.

In this report, "non-native" refers to species or distinct strains that are not native to the waters that they are released into, and includes the release of non-U.S. pathogens, strains or genotypes of pathogens into U.S. waters as well as the transfer of such pathogens from one part of the U.S. into another part where they are not native. The review thus considers ballast water's potential role both in transferring pathogens into U.S. waters from outside the U.S., and in transferring pathogens into new regions of the U.S. from regions of the U.S. where they are present as either native or non-native pathogens.

ESA-listed species that fall under NOAA's jurisdiction

As of May 13, 2010, there were 136 species or subspecies listed as endangered, threatened, proposed or candidate species under the ESA that fall under NOAA's jurisdiction.¹ Nine of these—5 cetacean, 3 pinniped and one fish species—are not found in U.S. waters (Appendix 1) and are not considered further in this report.² The 127 taxa

¹ The listed species and population groups considered in this report are based on the endangered and threatened marine species listed on the NOAA Fisheries/Office of Protected Resources web page at http://www.nmfs.noaa.gov/pr/species/esa, accessed on 5/13/2010. Changes to NOAA's posted list that were made since that date have not been included.

² Species, subspecies or population groups that do not occur in U.S. waters cannot be directly affected by the transport of pathogens into U.S. waters in ballast water. However, indirect impacts may be possible. For example, a bacterium or virus introduced into southern California waters might then spread into Mexican waters in the Gulf of California where the endangered Vaquita porpoise (*Phocoena sinus*) and

that occur in U.S. waters consist of 11 cetacean, 5 pinniped, 6 sea turtle, 18 fish, 2 mollusk, 84 coral and 1 plant species or subspecies (Appendix 2).

Some of these are further subdivided into various types of population groups, designated as Distinct Population Segments (DPS), Evolutionary Significant Units (ESU), runs, populations or portions of ranges, with one or several such groups listed rather than the whole species or subspecies. In the remainder of this report I refer to entities listed as any of these various types of population groups, or listed as species or as subspecies, as "ESA species", to distinguish them from species in the taxonomic sense. Not included in these are the 33 entities that NOAA lists as Species of Concern, which are defined as species, subspecies or population groups about which NOAA has concerns regarding status and threats, but for which there is insufficient information to support listing under the ESA.

In all there are 153 listed ESA species that occur partially or wholly in U.S. waters (Appendix 2). These are classified into the four categories of listing status defined in Table 1. The breakdown by major taxonomic group and listing status is shown in Table 2. Eighty-four (55%) of the 153 listed ESA species are corals, including 82 candidate species listed in response to a petition submitted in October 2009. Forty-one fish form the second-largest group of species (27% of the total), with 28 of these consisting of different runs of five Pacific Coast salmonid species.

 Table 1. Listing status definitions. In this table, "species" refers to a species, subspecies or population, and corresponds to the term "ESA species" as used in this report.

 Otatuse
 Definition

Status	Definition
Endangered	A species that is in danger of extinction throughout all or a significant portion of its range.
Threatened	A species that is likely to become endangered within the foreseeable future throughout all or a significant portion of its range.
Proposed	A species found to warrant listing as threatened or endangered and officially proposed as such. NMFS generally has one year to determine whether to list a proposed species as threatened or endangered.
Candidate	A species undergoing a status review following a determination in response to a petition or on NMFS' initiative that listing may be warranted, but which is not yet the subject of a proposed rule.

Totoaba fish (*Totoaba macdonaldi*) reside. Also, once an exotic organism becomes established in a U.S. port area, that port then becomes a potential source area for introducing the organism to other parts of the world via ballast water or by other transport mechanisms. Because these indirect pathways involve at least one additional step beyond the pathways affecting ESA-listed species found in U.S. waters, they are that much less likely, and are not specifically considered further in this report.

Taxonomic Group	Endangered	Threatened	Proposed	Candidate	Total
Cetaceans	10	0	0	1	11
Pinnipeds	2	2	0	2	6
Turtles	5	3	0	0	8
Fish	9	24	4	4	41
Mollusks	2	0	0	0	2
Corals	0	2	0	82	84
Plants	0	1	0	0	1
Total	28	32	4	89	153

 Table 2. ESA species under NOAA's jurisdiction that occur in U.S. waters, by taxonomic group and listing status.

 Source: NOAA 2010a.

From their habitat descriptions, ESA species can be classified as occupying marine, marine and estuarine, or marine, estuarine and freshwater habitats (Table 3). None of the listed species under NMFS' jurisdiction that occur in U.S. waters are found only in estuarine or fresh waters; however, 108 (71%) are exclusively marine. Considered by habitat occurrence, all of the 153 ESA species occur in marine waters at some times or for some of their life stages, 45 (29% of the total) occur in estuarine waters at some times, and 36 (24% of the total) occur in fresh waters at some times (Table 4). These patterns of habitat occurrence will affect a species' exposure to pathogens released in ballast water which, depending on shipping routes and ballast management practices, may be variously derived from or released into marine, estuarine or fresh waters.

Taxonomic Group	Marine	Marine & Estuarine	Marine, Estuarine & Freshwater	Total
Cetaceans	10	0	1	11
Pinnipeds	2	2	0	6
Turtles	2	6	0	8
Fish	4	2	35	41
Mollusks	2	0	0	2
Corals	84	0	0	84
Plants	0	1	0	1
Total	108	9	36	153

 Table 3. ESA species under NOAA's jurisdiction that occur in U.S. waters, by taxonomic group and habitat classification.
 Sources: CBD 2009; NOAA 2010a,b.

Taxonomic Group	Marine	Estuarine	Freshwater
Cetaceans	11	1	1
Pinnipeds	6	0	0
Turtles	8	6	0
Fish	41	37	35
Mollusks	2	0	0
Corals	84	0	0
Plants	1	1	0
Total	153	45	36

 Table 4. ESA species under NOAA's jurisdiction that occur in U.S. waters, by taxonomic group and habitat occurrence.

 Sources: CBD 2009; NOAA 2010a,b.

ESA species can also be classified by the coastal region of the U.S. in which they are found (Table 5, Appendix 3). Cetacean and sea turtle ESA species are found in all regions. Pinniped ESA species occur mainly in Alaska and on the West Coast, with one species in Hawaii. Most ESA fish species (33 (80%) of the ESA fish species) are found on the West Coast (primarily various runs of salmonids and some rockfish species), with a few ESA fish species occurring in Alaska, on the East Coast and in the Gulf of Mexico, but none in the more tropical waters of the Caribbean, Hawaii and the Pacific Islands. The coral ESA species mainly occur in the Pacific Islands (71 species (85%)), with a smaller number (7-10 species per region) in Hawaii and in the Caribbean, Gulf of Mexico and East Coast regions; none occur on the West Coast or, of course, in Alaska. The two ESA mollusk species (both abalone) are found only on the West Coast, and the sole plant species (a seagrass) is found only in Florida on the East Coast. These different regions are exposed to different volumes of ballast water discharge from different source regions, which affects the risk to the different species groups of encountering ballast water-introduced pathogens (see the section on Ballast water pathways below).

Table 5. ESA species under NOAA's jurisdiction that occur in U.S. waters, by taxonomic group and region. The Caribbean region includes Puerto Rico, the U.S. Virgin Islands and Navassa Island; the Hawaii region includes the Hawaiian Islands and Midway Island: the Pacific Islands region includes Guam, the Northern Mariana Islands, American Samoa, Johnston Atoll, Wake, Howland, Baker and Jarvis islands, Palmyra Atoll and Kingman Reef. Sources: CBD 2009; NOAA 2010a,b.

Taxonomic Group	East Coast	Gulf of Mexico	Caribbean	Alaska	West Coast	Hawaii	Pacific Islands
Cetaceans	6	4	4	7	7	5	4
Pinnipeds	0	0	0	4	2	1	0
Turtles	5	5	6	2	6	5	4
Fish	5	3	0	2	33	0	0
Mollusks	0	0	0	0	2	0	0
Corals	9	7	9	0	0	10	71
Plants	1	0	0	0	0	0	0
Total	26	19	19	15	50	21	79

Impacts of pathogens on naive hosts

Parasites or pathogens often have a greater impact on populations that lack prior exposure to them (referred to as naive host populations). This is a well-known effect in human epidemic disease (*e.g.* Tauxe *et al.* 1995), and is often cited as a dominant factor in the decimation of aboriginal populations soon after European contact and the introduction of novel diseases (Crosby 1972, 1986; Cook 1978; Cronon 1983). There are many documented examples among plants and animals, including marine mammals (Kennedy 1998; Australia DAFF 2000), fish (Hoffman 1970; Bauer & Hoffman 1976; Combes & Le Brun 1990; Kennedy 1994; Nielsen 1999; Mo 1994; Ashworth 1994; Walker & Winton 2010) and mollusks (Culver & Kuris 1999; Burreson *et al.* 2000).

The enhanced pathogenic impact generally occurs because the naive host lacks defenses, such as an effective immunological response, although there may also be behavioral or other adaptations in the host that reduce the incidence or severity pathogenic impact where there has been a long association with a pathogen. In some cases, there may also be a greater impact on naive hosts because some pathogens evolve to become less damaging to their host populations over time, which may enhance the potential for effective transmission and long-term persistence (Fenner & Myers 1977; Anderson & May 1982).

The implication for this review is that bacteria or viruses introduced into a new region could have substantial impact on naive hosts encountered there, even if they have little or no pathogenic effect on related host organisms in their native regions.

Antibiotic resistance

Distinct from concerns about the known pathogenicity of imported bacteria, or the introduction of novel genotypes that may prove to be pathogenic to naive hosts, is the potential for ballast water to introduce antibiotic-resistant forms. Some recent studies have documented the common presence of antibiotic-resistant bacteria in ships' ballast tanks (Thomson et al. 2003; Goodrich 2006; Thomson 2009). Bacteria can carry antibiotic-resistant genes either on chromosomes, or on heritable, non-chromosomal bodies called plasmids. In the latter case two bacteria considered to have the same genotype (*i.e.* identical chromosomal DNA) may nonetheless have differing resistance to antibiotics. Plasmids can also be transferred between bacteria by a process called horizontal gene transfer, with some plasmids (conjugative plasmids) being more likely to transfer than others. Thus, even if bacteria introduced in ballast water have the same genotype as bacteria that were already present in the receiving waters, they could still pose a risk if the introduced bacteria have greater antibiotic resistance, Furthermore, the mixing of bacteria from the world's harbors via ballast transport increases the risk that bacteria with plasmids promoting antibiotic resistance will come into contact with and transfer these plasmids to pathogenic bacteria (F. Dobbs, pers. comm.). In a review of emerging cetacean diseases, Van Bressem et al. (2008) have expressed concern about "the world-wide dissemination of ... antibiotics-resistant marine bacteria through water ballast."

Transport of bacteria, viruses and other pathogenic microbes in ballast water

Although most of the studies on organisms transported in ballast water have focused on multi-cellular organisms (primarily zooplankton) or on phytoplankton (primarily diatoms and dinoflagellates), there is nonetheless good documentation of a large number and diversity of other microbial organisms, including bacteria and viruses, being collected from ballast tanks at the ends of voyages (*e.g.* see Table 1 in Drake *et al.* 2001; and Drake *et al.* 2007). For example, Galil & Hulsmann (1997; see also Hulsmann & Galil 2001) identified 198 living protozoan species in 82 heterotrophic genera collected from water and sediments in the ballast tanks of 17 cargo vessels arriving at Israeli ports in 1996, including flagellates (Euglenozoa, Cryptomonadea, Prymnesiomonadea, Choanoflagellata, Heterokonta, Dinoflagellata and others), ciliates (Karyorelictida, Spirotrichea, Litostomatea, Phyllopharyngea, Oligohymenphorea) and pseudopodial organisms (Gymnamoebea, Heterolobosea, Filosea, Granuloreticulosea, Heliozoa, Labyrinthulea and others). Most nanoflagellates, heliozoans and other organisms smaller than 5-10 µm were not identified.

The transport of toxic dinoflagellates in ballast tanks has received particular attention. Approximately 60 marine dinoflagellates are known to produce substances that are toxic and sometimes fatal to humans or animals (Doblin & Dobbs 2006). Some of these form cysts that can remain dormant and viable for months or even years, and such cysts have been found in the sediments in ballast tanks at up to 22,500 per gram of wet sediment (Hallegraeff & Bolch 1992; Hamer *et al.* 2000, 2001). There is good evidence that some toxic dinoflagellates have been introduced into new regions of the world in ballast discharges (Hallegraeff *et al.* 1995; McMinn *et al.* 1997; Hallegraeff 1998; Lilly *et al.* 2001; Dobbs & Rogerson 2005; Drake *et al.* 2007). *Pfiesteria piscicida* and *P. shumwayae*, dinoflagellates that have been implicated in numerous fish kills, were found in one of four vessels sampled on arrival in Chesapeake Bay or the Great Lakes (Doblin *et al.* 2004; Drake *et al.* 2005) and in about 10% of the tanks sampled for residual ballast water on NOBOB vessels (vessels that declare "no ballast on board" but that typically have relatively small volumes of ballast water remaining in their tanks) arriving at ports in the Great Lakes in 2001-2002 (Johengen *et al.* 2005). Aguirre-Macedo *et al.* (2008) found bacteria that are known coral pathogens in ballast discharges near a coral reef in the Gulf of Mexico.

A series of studies carried out on vessels arriving in Chesapeake Bay and the Great Lakes have enumerated the number of bacteria and virus-like particles (VLPs) in ballast water, in residual water at the bottoms of ballast tanks after they are emptied, in the pore water of sediments collected from the bottoms of ballast tanks after they are emptied, and in biofilms (organic matrices that form on submerged surfaces) on the sides of ballast tanks (Table 6). These studies have been carried out in bulk carriers and coal carriers (colliers) arriving in Chesapeake Bay, and in NOBOB vessels arriving at ports in the Great Lakes. They include vessels arriving from both foreign and domestic ports, and ballast tanks that both had and had not undergone ballast water exchange at sea.

These studies reported mean concentrations in ballast water of 8 x 10^8 to 3 x 10^9 bacteria/liter and 7×10^9 to 3×10^{11} VLPs/liter (Table 6). These are reasonably comparable to normal concentrations in Chesapeake Bay of 2-12 x 10⁹ bacteria/liter and 3-140 x 10⁹ VLPs/liter, a range of concentrations in the summer in Lake Erie of 1.5-5.5 x 10¹¹ VLPs/liter, typical concentrations in lakes and oceans of 10⁹ bacteria/liter and $10^9 - 10^{12}$ VLPs/liter, and concentrations of bacteria and viruses in coastal waters of $10^6 - 10^{12}$ VLPs/liter. 10¹¹/liter (Wommack & Colwell 2000; Drake et al. 2001; Dobbs & Rogerson 2005; Wilhelm et al. 2006). The concentrations of bacteria and VLPs in residual water in recently emptied ballast tanks were similar to the concentrations reported for filled ballast tanks (Drake et al. 2007; Table 6), but the concentrations in residual water in NOBOB vessels were generally orders of magnitude higher, especially for bacteria (Johengen et al. 2005; Table 6). Sediment pore water in recently emptied ballast tanks generally contained 80-320 times higher concentrations of bacteria and 4-160 times higher concentrations of VLPs than was found in ballast water, depending on the data sets compared (Drake et al. 2007; Table 6). Ballast tank biofilms generally contained 2-8 times higher concentration of bacteria and 2-90 times higher concentration of VLPs than found in ballast water (Drake et al. 2005, 2007; Table 6). The ranges reported for pore water in NOBOB vessels suggest similarly elevated concentrations (compared to ballast water) for VLPs but perhaps not for bacteria (Johengen et al. 2005; Table 6). Ballast tank biofilms generally contained 2-8 times higher concentrations of bacteria and 2-90 times higher concentrations of VLPs than found in ballast water (Drake et al. 2005, 2007; Table 6).

Table 6	Concentrations of	bootorio and	virueee in l	hallaat tanka	n – numbor	of tonka compled
I able b.	Concentrations of	Dacteria anu	viruses iri i	Dallast tallks.	$\Pi - \Pi U \Pi D e \Gamma$	ULIANKS SAMULEU.

Typos of Voyago and Vossol Samplos	E	Bacteria	VLPs		
Types of voyage and vessel Samples	n	#/liter	n	#/liter	
In Ballast Water					
Bulk carriers to Chesapeake Bay (Ruiz et al. 2000)	11	8.3 x 10 ⁸	7	7.4 x 10 ⁹	
Bulk carriers from foreign ports to Chesapeake Bay in 1996-2000 (Drake <i>et al.</i> 2001)	18	1.8 x 10 ⁹	12	1.4 x 10 ¹⁰	
Bulk carriers from foreign ports to Chesapeake Bay, surface samples only (Drake <i>et al.</i> 2005)	18	1.7 x 10 ⁹	12	1.3 x 10 ¹⁰	
Massachusetts to Chesapeake Bay in 2002 (Drake et al. 2005)	4	3.2 x 10 ⁹	4	3 x 10 ¹¹	
Unexchanged ballast water (MEPC 2003)	11	8.3 x 10 ⁸	7	7.4 x 10 ⁹	
Coal carriers or foreign ports to Chesapeake Bay in 1996-2001 (Drake <i>et al.</i> 2007)	53	8 x 10 ⁸	31	1.4 x 10 ¹⁰	
One cargo vessel sampled at 5 Great Lakes' ports in July 2003 (Wilhelm <i>et al.</i> 2006)	5	1.4 x 10 ⁹	5	3.3 x 10 ¹¹	
In Residual Ballast Tank Water					
NOBOB voyages to ports in the Great Lakes in 2000-2002 (Johengen <i>et al.</i> 2005)	75	10 ⁸ -10 ¹²	75	10 ¹⁰ -10 ¹²	
Bulk carriers from foreign or domestic ports to Chesapeake Bay in 2003 (Drake <i>et al.</i> 2007)	13	4.4 x 10 ⁸	13	6.2 x 10 ¹⁰	
In Pore Water of Ballast Tank Sediments					
NOBOB voyages to ports in the Great Lakes in 2000-2002 (Johengen <i>et al.</i> 2005)	73	10 ⁷ -10 ¹¹	73	10 ¹⁰ -10 ¹⁴	
Bulk carriers from foreign or domestic ports to Chesapeake Bay in 2003 (Drake <i>et al.</i> 2007)	12	2.6 x 10 ¹⁰	12	1.2 x 10 ¹²	
In Ballast Tank Biofilms					
Bulk and coal carriers from foreign or domestic ports to Chesapeake Bay or Great Lakes in 2002-03 (Drake <i>et al.</i> 2005, 2007)	3	6.6 x 10 ⁹	5	6.3 x 10 ¹¹	

In general, these studies revealed a wide range in variation in bacterial and VLP concentrations in ballast water, and did not reveal significant differences in concentrations between exchanged and unexchanged tanks (although exchange presumably alters the composition of the organisms; Drake *et al.* 2002). Bacterial concentrations declined during voyages in tanks that did not undergo mid-ocean exchanges, and VLP concentrations declined in tanks with or without exchange (Drake *et al.* 2002, 2007). Ballast tank biofilms generally contained 2-8 times higher concentration of bacteria and 2-90 times higher concentration of VLPs than found in ballast water (Drake *et al.* 2005, 2007; Table 6). Although bacterial and viral concentrations were often found to be considerably greater in residual water, pore water or biofilms than in ballast water, due to the much larger volume of ballast water carried by bulk carriers travelling in ballast the estimated total number of bacteria and viruses carried in the ballast water on a vessel is much greater, by ≈1 to >3 orders of magnitude, than is carried in residual or pore water or biofilms (Drake *et al.* 2005, 2007).

This is presumably also true for most or all other vessel types when travelling in ballast, and these differences are probably even greater for ballast discharges, since in a typical discharge much of the sediment and most of the biofilm probably remains in the ballast tank (Drake *et al.* 2007).

Theoretically, ballast tanks could serve as incubators resulting in increases in certain microbes over the course of a voyage: in darkened tanks phytoplankton should cease photosynthesizing and die, in turn resulting in the starvation and death of zooplankton; the decomposition of these organisms could promote bacterial growth, leading to increased viral replication (Drake et al. 2002). On the other hand some bacteria have antiviral properties, so that increased bacteria growth could lead to declines in virus concentrations, while declines in bacteria could enhance viral survival (Girones et al. 1989). General declines in phytoplankton and zooplankton populations in ballast tanks have been observed during voyages (e.g. Gollasch et al. 2000), but overall increases in bacterial and viral concentrations have not (Drake et al. 2002). Nevertheless, the relationships are complex and it is possible that some species of bacteria or viruses may increase in ballast tanks over voyages even while overall numbers decline. In this regard it is worth considering that many proposed or recently adopted ballast water discharge standards would require removing or killing phytoplankton and zooplankton in ballast tanks at greater rates than they decline naturally due to cessation of photosynthesis, without requiring concomitant reductions in bacteria or viruses, including the discharge standards in the IMO Convention (a proposed international treaty, developed by the International Maritime Organization, which is awaiting ratification by enough member states to go into effect), standards adopted by some states under Section 401 of the Clean Water Act and/or state authority (Illinois, Indiana, Minnesota, New York (Interim Standard), Ohio, Pennsylvania (Interim Standard) and Wisconsin), and the standards proposed for near-term implementation by the U.S. Coast Guard (Notice of Proposed Rulemaking Phase I) (Alpert et al. 2010; Lee et al. 2010). A substantial increase in the number of dead phytoplankton and zooplankton sinking to the bottom of ballast tanks could enhance bacterial and viral populations.

Based on sampling data, shipping data and temperature tolerances, Drake *et al.* (2007) estimate that each year around 10²⁰ bacteria and viruses are released in ballast discharges at the Port of Hampton Roads and survive in Chesapeake Bay. Although there is little information available on actual or possible bacterial or viral introductions in coastal waters (see discussion below), Ruiz *et al.* (2000) and Drake *et al.* (2001) concluded—based on the ballast tank concentrations, biological capacities (including asexual reproduction, high intrinsic growth rate, and dormant resting stages) and environmental tolerances of many bacteria and viruses—that invasions may nonetheless be relatively common, though unrecognized.

Bacteria or viruses could potentially be transported along with ballast water in a variety of media or modes, some of which have been mentioned. They may be carried in the ballast water itself, including residual water in nominally empty tanks, which may be fresh, brackish or salt; in sediments in the bottom of the tank, either in pore water or associated with sediment particles, in biofilms on the walls of the tanks; or carried in or

on other organisms. The fraction surviving the voyage will depend on the particular bacteria or virus, the specific mode of travel, the length of the voyage, the temperature of the water, and other factors. Appendix 4 shows some typical data on survival times and rates for some pathogenic fish viruses in few different media, illustrating some of these differences. Studies on the persistence in aquatic environments of human or animal bacterial and viral pathogens have established the potential for longer survival of the pathogen at lower temperatures (Gerba 2007; Sinclair et al. 2008), if sediment or organic material is present (Gerba & Schaiberger 1975; Gerba & McLeod 1976; Lipson & Stotzky 1984; Clarke et al. 1998; Gerba 2007), and in biofilms (Alam et al. 2007), and the same principles can be seen in the data on fish viruses (Appendix 4). For example, survival is longer at lower temperatures for VHSV in sea water (Parry & Dixon 1997; Mori et al. 2002; see also Hawley & Garver 2008) and fresh water (Mori et al. 2002), for IHNV in sea water (Toranzo & Hetrick 1982), for ISAV in sea water (MacLeod et al. 2003), and for SAV in both fresh water and sea water (Graham et al. 2007); and several viruses are stable for long periods in mud or clay (Ahne 1982; Yoshinaka et al. 2000) or in enriched water (VHSV-Kocan et al. 2001). There is also evidence that some fish viruses survive longer in sterilized water (KHV in fresh water-Shimizu et al. 2006; ISAV in sea water at 15°C-MacLeod et al. 2003; SAV in sea water-Graham et al. 2007), which may be due to the elimination of bacteria with antiviral properties (Toranzo & Hetrick 1982; Girones et al. 1989; Shimizu et al. 2006). Different viruses or different strains of viruses can have substantially different abilities to survive in water or mud (e.g. IPNV vs. VHSV, PFRV & SVCV–Ahne 1982; different freshwater European VHSV isolates–Parry & Dixon 1997; but smaller differences between European and North American marine VHSV isolates-Parry & Dixon 1997; Winton et al. 1991). Differences in genotypes may account for some of the large differences in survival in different studies under nominally similar test conditions (e.g. the VHSV data in Appendix 4).

Bacterial or viral pathogens may also be carried in or on their hosts in ballast water. Among the groups of organisms that include NOAA ESA species—cetaceans, pinnipeds, sea turtles, fish, two mollusks, corals and one plant—transport in the host is most likely for pathogens of fish, some of which can infect fish species or life stages (larval or juvenile) that are small enough to survive passage through and transport in a ships' ballast water system. Mollusks and corals are transported in ballast tanks almost entirely as larvae (the exceptions being the possible but probably rare transport of small, post-larval specimens on small floating algae or debris; and transport of the few mollusk species that are planktonic as adults which, being only distantly related to the abalone ESA species, are less likely to host pathogens that can infect them). Since most invertebrate pathogens are thought to be hosted by juvenile or adult rather than larval life stages, the transport and introduction of mollusk or coral pathogens in mollusk or coral specimens carried in ballast tanks is unlikely. It might be possible for a pathogen capable of infecting the one ESA plant species to be carried in a small piece of floating plant material carried in ballast water.

Some bacterial pathogens have been found on a variety of taxonomically diverse alternative hosts, which could include small organisms that are commonly transported in ballast waters. In addition, some bacterial or viral pathogens may occur routinely or

incidentally on the outer surfaces of invertebrates, which may serve as mechanical vectors³. For example, it has been shown that the bacterium Vibrio cholerae attaches to the chitinous body parts of copepods and other crustaceans (Huq et al. 2001; Lipp et al. 2002), is found in association with other planktonic invertebrates including larval stages (Martinelli Filho et al. 2010), and attaches in abundance to the mucilaginous outer sheaths of some phytoplankton (Hug et al. 2001; Lipp et al. 2002). Copepods and phytoplankton are common and often abundant in ballast water (e.g. Carlton & Geller 1993; Subba Rao et al. 1994; Ruiz & Hines 1997; Cohen 1998; MEPC 2003), and associating with these organisms is thought to facilitate V. cholerae's transport in ballast water and possibly its capacity to subsequently infect a host (Colwell 1996; Lipp et al. 2002).⁴ Although there is generally less information on such associations by animal pathogens, several ectoparasites of fish are known to transmit viral fish pathogens, including fish lice (isopods), copepods and leeches (Ahne 1985; Mulcahy et al. 1990; Nylund et al. 1994; PAHW 2007; Overstreet et al. 2009), and nematode and trematode parasites of sea lions as well as turtle leeches are suspected of transmitting pathogenic viruses between their hosts (Van Bressom et al. 1999; Greenblatt et al. 2004). Recently, the fish pathogen VHSV was found in benthic amphipods in the Great Lakes (M. Faisal pers. comm.; see also Kipp & Ricciardi 2006 regarding possible survival of VHSV in invertebrates in the bottom of culture ponds). Carried in or on invertebrates or algae (whether serving as hosts or as mechanical vectors), some bacteria and viruses may survive and remain infective for long periods of time, while also being buffered against changes in water chemistry and other environmental conditions (for example, see Hug et al. 2001; Lipp et al. 2002). These circumstances would presumably facilitate transport in ballast water, and by concentrating the pathogen may possibly increase the chance of infecting a host after discharge from a ballast tank.

I found four examples—involving one bacterium and three viruses—that may represent introductions of these microbes by ballast water. *Vibrio cholerae* is the bacterium that causes human cholera. The world experienced six pandemics of cholera between 1817 and the 1920s. In 1961, after a nearly 40-year hiatus, a seventh pandemic began in Indonesia. It spread through Southeast Asia and to the Indian subcontinent by the mid-1960s, reached Africa in 1970, and spread through Africa and the Middle East in the 1980s (Colwell 1996; Den Enden Erwin 2004). In 1990-1991 cholera broke out on the coast of Peru and spread epidemically throughout Latin America. The same strain of *V. cholerae* that caused the Latin American epidemic was discovered by USFDA in fish and oysters in Mobile Bay, Alabama in 1991 and 1992 (DePaola *et al.* 1992; CDC 1993). The USFDA subsequently found the same strain in the ballast water (and on some ships also in the bilge, fire main or sewage water) of 5 out of 16 ships arriving in

³ A mechanical vector, also called a paratenic host or a transport host, is an organism that can convey a pathogen to a new host but is not essential to the development of the pathogen.

⁴ By attaching to invertebrates or phytoplankton, microbial pathogens may be able to achieve concentrations on these individual substrata that approach or exceed an infective dose, with a greater likelihood of infecting a host than if they were dispersed though the water column. There can be as many as 10^4-10^6 *Vibrio cholerae* cells attached to a single copepod, while an infectious dose, based on human volunteer studies, is only 10^3 cells (Colwell 1996; Lipp *et al.* 2002). Thus Lipp *et al.* (2002) report that in areas without proper sanitation, filtering drinking water through a cloth, which removes copepods but not individual *V. cholerae* cells, can reduce the incidence of cholera infection by approximately 50%.

the U.S. from ports in Latin America (McCarthy et al. 1992; McCarthy & Khambaty 1994). Researchers reported an "alarming number" of culturable V. cholerae in these samples, estimated at 10⁹/liter or greater (McCarthy & Khambaty 1994). They concluded that the South American toxicogenic strain of V. cholerae was introduced into U.S. Gulf Coast waters by cargo vessels, probably in ballast water, and that cargo vessels may also have initially introduced the strain into South America from Asia. Subsequent reviewers have generally supported the conclusion that ballast water introduced the toxicogenic strain of V. cholerae into Gulf Coast waters (Drake et al. 2001, 2007; Dobbs & Rogerson 2005; Tibbetts 2007); but are not in agreement regarding its initial arrival in South America, with opinions ranging from statements that it was introduced in ballast water (Epstein et al. 1993; Ditchfield 1993; Epstein 1995; Tibbetts 2007; Aguirre-Macedo et al. 2008; this was also reported to be the view of the Pan American Health Organization—Anderson 1991) to statements that it was not (Colwell 1996; Lipp et al. 2002). My view is that the data supporting ballast water introduction into Gulf waters are compelling, but that ballast water remains one possible vector among several for the initial introduction to South America, with the available data being inadequate to resolve this.

Infectious Salmon Anemia Virus (ISAV) was first isolated from farmed Atlantic salmon in Norway in 1984, and has since been reported elsewhere in Europe, in the Northwest Atlantic and in Chile (PAHW 2007). ISAV is relatively stable outside its host and may remain infective in water for weeks or more (MacLeod et al. 2003; PAHW 2007). Murray et al. (2002) investigated the regional pattern of ISAV spread to Atlantic salmon farms in Scotland and the Orkney and Shetland islands in 1998-1999, across >850 km of coastline, and concluded that the virus' spread to several of the farms was not due to either transfers of fish or to diffusive spread by currents, wild fish, fish parasites or seabirds, but rather was associated with the movement of well boats, which transport fish, equipment and supplies to or from salmon farms. Excluding a few sites where infection was clearly caused by transfers of fish from known infected sites, there was a highly significant relationship between well boat visits and infection status ($r^2=0.66$, p=0.000004). Multivariate analysis showed that site infection was related to the number of harvest visits and not to fish transfer visits or visits for general work or to deliver supplies. In harvest visits, well boats arrived from a fish processing center carrying ballast that was loaded near the center, discharged the ballast near the salmon farm, loaded fish from the farm, and returned to the processing center. At the processing center, salmon were held in net pens before slaughter, and the processing plant discharged effluent from that was not fully disinfected. Thus, a well boat leaving on a harvest visit would ballast with water that could contain ISAV from either the penned salmon or from the plant effluent, which would then be transported to and released near a salmon farm. An alternative explanation to ballast water is that some infected fish or fish detritus could remain in a boats' wells or in its pumps or pipes after salmon are delivered to the harvest station, which could then be discharged by some mechanism while loading salmon at the next farm. Thus, this is a possible and perhaps probable case of the successful transfer of a pathogenic fish virus in ballast water, presumably with an initially high concentration of the virus, to infect other sites across distances of up to several hundred kilometers. Given the relative stability of this virus in sea water,

especially when water temperatures are low (MacLeod *et al.* 2003), this may indicate a potential for considerably longer-distance introductions in ballast water, especially if vessels load ballast near infected fish processing plants or fish farms.

Another possible example of a virus introduced in ballast water is the recent discovery of Viral Hemorrhagic Septicemia Virus (VHSV) in the Great Lakes (Lumsden 2005; Elsayed et al. 2006), which has resulted in several large fish kills involving a variety species (Lumsden 2005; Groocock et al. 2007; CFSPH 2010). Different researchers and agencies have suggested, argued or concluded that VHSV arrived in the Great Lakes either in ballast water (Whelan 2007; Michigan Sea Grant 2007; Michigan DNR 2009; M. Faisal, pers. comm.; G. Whelan pers. comm.), in migrating fish (M. Bain pers. comm.), in ballast water or migrating fish (Elsayed et al. 2006; Kipp & Ricciardi 2006; Wisconsin DNR 2007; NPS 2008; New York Invasive Species Clearinghouse 2008), in migrating fish or birds (J. Casselman pers. comm.) or in migrating fish, ballast water or frozen bait (Illinois - Indiana Sea Grant 2007). VHSV occurs in four distinct genotypes, with Types I, II and III found in Europe and Type IV reported from western North America and Asia (Nishizawa et al. 2002; Hedrick et al. 2003; Einer-Jensen et al. 2004; Snow et al. 2004; PAHW 2007). After the discovery of and sequencing of VHSV from the Great Lakes, Type IV was subdivided into Type IVa, occurring on both sides of the North Pacific, and Type IVb, from the Great Lakes (Elsayed et al. 2006). Further genetic analysis revealed that the VHSV that had been found in a few fish on the northwestern Atlantic coast (New Brunswick and Nova Scotia) were also apparently Type IVb (Olivier 2002; Gagne et al. 2007; Winton et al. 2008), suggesting that the Atlantic Coast is the likely source for the introduction of VHSV into the Great Lakes (Elsayed et al. 2006; Kipp & Ricciardi 2006; Winton et al. 2008). Because the genetic diversity of the VHSV found in the Great Lakes is extremely limited (Winton & Batts 2007; Winton et al. 2008), some researchers have argued that it was probably introduced very recently, most likely sometime in the five years before the first record of VHSV in the Great Lakes in 2003 (Winton et al. 2008; Michigan DNR 2009; J. Winton, pers. comm.). Other evidence supporting a very recent introduction includes VHSV's high degree of virulence to a wide variety of fish species in the Great Lakes (Lumsden 2005; APHIS 2006; Groocock et al. 2007; PAHW 2007; Getchell 2007; CFSPH 2010) suggesting the sudden exposure of a novel pathogen to a naive community of fish (Winton & Batts 2007; Winton et al. 2008; J. Winton, pers. comm.), the absence of records of VHS prior to 2003 (Elsayed et al. 2006; Winton et al. 2008), and its apparent progressive spread from the lower Great Lakes to the upper lakes (Table 7; M. Faisal, pers. comm.). However, other researchers have argued, based on recent documentation of VHSV's wide distribution in the Great Lakes, that it had been present and widespread in the Great Lakes for a significantly longer period, that the lower-to-upper lake progression of discovery is an artifact of where and when sampling was conducted, and that the sudden occurrence of mass mortalities in different species must have a cause other than recent introduction (Bain et al. 2010; M. Bain, pers. comm.).

Table 7. Spread of records of VHSV in the Great Lakes. Sources: Bain *et al.* 2010; G. Whelan, pers. comm.

Year	Extension of Range of Records
2003	Lake St. Claire
2005	Downstream: to Lake Ontario (Bay of Quinte)
2006	Downstream: to St. Lawrence River. Upstream: to Lake Huron (Thunder Bay and Swan River).
2007	Upstream: to Lake Michigan (Sturgeon Bay and Algoma)
2008	Upstream: to Lake Michigan (Milwaukee Harbor)
2009	Upstream: to Lake Superior (Paradise and Apostle Islands)

Questions about the source and timing of introduction bear on assessments of the probable vector. The predominant fish species migrating from coastal waters into the Great Lakes is the American eel, Anguilla rostrata, and VHSV has been found in the European eel, A. anguilla (Castric et al. 1992). However, the number of eels migrating into the Great Lakes has declined precipitously in recent decades (Casselman 2003; J. Casselman pers. comm.). If migrating fish are the vector, and the introduction is recent, why did VHSV arrive now when it hadn't arrived during the preceding decades and centuries of eel migration into Lake Ontario? If transport in the water or sediment in ballast tanks is the vector, the virus could probably survive the short voyage from the Atlantic Coast to the Great Lakes well enough (Parry & Dixon 1997; Mori et al. 2002; CFSPH 2007: Appendix 4), but delivering enough of a virus in ballast discharges to produce sufficient concentrations in the receiving waters to infect a susceptible fish host would be very challenging. On the other hand, transport of the virus in small fish⁵ or invertebrates⁶ within ballast tanks might be considerably more likely to deliver an infective dose (e.g. Colwell 1996; see discussion above). Despite the interest and importance of determining when and how VHSV arrived in the Great Lakes, the question does not yet appear to have been investigated thoroughly; my sense from these inquiries is that a more complete compilation and analysis of the available data could help resolve this. In the meantime, ballast water remains one of several mechanisms that might be responsible for the introduction of VHSV.

One last example of a possible ballast water introduction of a virus is the discovery of an apparently marine cyanophage in Lake Erie in 2002-2003, primarily in the lake's western basin (Wilhelm *et al.* 2006). A virus capable of lysing a marine cyanobacterium, *Synechococcus* sp. strain WH7803, was collected at numerous sites in the lake even though this cyanobacterium cannot persist in freshwater culture medium representative

⁵ For example VHSV is common in gobies (Groocock *et al.* 2007) and has been found in 3-spined stickleback on both North American coasts (Kent *et al.* 1998; Hedrick *et al.* 2006; Gagne *et al.* 2007); both of these small fish are among the most common types of fish reported from ballast tanks (Wonham *et al.* 2000).

⁶ Invertebrates serving as alternative hosts or as mechanical vectors have not been reported for VHSV, but as discussed earlier there is evidence for this with other marine pathogens including fish viruses (Ahne 1985; Mulcahy *et al.* 1990; Nylund *et al.* 1994), and VHSV has been found in invertebrates in the Great Lakes (M. Faisal pers. comm.).

of Lake Erie and neither it nor any other host has been found in the lake. Furthermore, the Lake Erie cyanophage isolates amplified on *Synechococcus* sp. strain WH7803 did not lyse other marine or freshwater cyanobacteria that they were tested on. The gene sequences from these isolates clustered with other marine virus sequences. Wilhelm *et al.* (2006) suggest that these findings would be explained by the introduction of the cyanophage from the marine environment in ballast water discharges.

Ballast water pathways

The U.S. Coast Guard and the National Ballast Information Clearinghouse (NBIC) assemble nationwide information on the transport and discharge of ballast water from the Ballast Water Reporting Forms filled out by vessels arriving in U.S. ports. The National Invasive Species Act of 1996 (PL 104-332) required vessels to submit these forms starting in 1997. NBIC was established in 1999, and from 1999-2004 collected data that included all commercial vessels that arrived at U.S. ports from outside of the 200-mile Exclusive Economic Zone (EEZ). After June 2004 the data have included all commercial vessels that arrive at a port or place in the U.S. NBIC uses these data to estimate the rate of ballast water exchange and the release of foreign ballast water, and provides periodic reports to the U.S. Congress (NBIC 2008).

The most recent report available from NBIC covers ballast water records for 2004-2005. Tables 8-10 show the estimated annual number of foreign vessels arriving in U.S. waters, the volume of foreign and domestic ballast water discharged in U.S. waters, and the source regions for foreign ballast water discharged in U.S. waters.⁷ "Foreign" and "domestic" have particular idiosyncratic meanings in the NBIC reports and in these tables. "Foreign" refers to vessels arriving in U.S. waters that have traveled in waters outside the U.S. and Canadian EEZs since leaving their last ports, and to the ballast water carried by such vessels. It thus includes vessels traveling between one U.S. Coast (East Coast or Gulf of Mexico) and the other (West Coast or Alaska), or between the U.S. mainland and U.S. island states or territories. It does not include vessels traveling along one coast between U.S. ports or between U.S. and Canadian ports while remaining within the combined EEZs. These vessels are classified as "domestic" which refers to vessels, and the ballast water of vessels, that have not traveled outside the combined U.S. and Canadian EEZs since leaving their last ports. Thus the terms foreign and domestic, in the NBIC reports and in this report when referring to vessel or ballast data derived from NBIC, do not imply anything about the nationality, ownership or registration of a vessel.

⁷ To develop these estimates I adjusted the NBIC figures by dividing both the number of vessel arrivals and the ballast water discharge volumes by the rates of reporting given in Tables 3 and 4 of Miller *et al.* 2007. No rate of domestic reporting is provided for the Guam region in that report so I used the lowest rate reported for any other discharge region (the Caribbean), since Guam had the lowest rate of foreign reporting of all the regions. Rates of reporting were particularly low for domestic vessels in 2004 because domestic vessels were not required to submit Ballast Water Reporting Forms until after June of that year.

Table 8. Average Annual Number of Foreign Vessels Arriving in U.S. Waters, by Ballast Water Treatment and Discharge Region. Based on 2004-2005 data from Miller *et al.* 2007 (Tables 5a & 5b), adjusted for reporting rates (Miller *et al.* 2007, Table 3). "Pacific Islands" includes Guam and American Samoa. Does not include the Great Lakes, inland waterways and unknown discharge regions.

	Number of Foreign Vessels						
Discharge Region	No Discharge	No Exchange	Some Exchange	Unknown Exchange	Total		
East Coast	14,711	2,130	1,183	103	18,126		
Gulf of Mexico	11,557	1,029	1,965	68	14,618		
Caribbean	4,652	355	391	36	5,433		
Alaska	146	60	138	3	346		
West Coast	6,197	94	1,417	21	7,728		
Hawaii	983	55	47	1	1,085		
Pacific Islands	703	44	22	0	768		
Total	38,947	3,765	5,160	231	48,103		

Table 9. Average Annual Ballast Water Discharge in U.S. Waters, by Ballast Water Treatment and Discharge Region. Based on 2004-2005 data from Miller *et al.* 2007 (Tables 6 & 8), adjusted for reporting rates (Miller *et al.* 2007, Tables 3 & 4a). "Pacific Islands" includes Guam and American Samoa. Does not include the Great Lakes, inland waterways and unknown discharge regions.

	Reported Ballast Water Discharge (1,000 metric tons)								
Discharge Region	Source	No Exchange	Some Exchange	Unknown Exchange	Total				
East Coast	Foreign	2,100	4,781	202	7,083				
	Domestic	9,968	977	648	11,593				
Gulf of Mexico	Foreign	4,148	13,174	403	17,726				
	Domestic	49,754	4,392	3,542	57,689				
Caribbean	Foreign	2,090	4,608	283	6,982				
	Domestic	1,980	117	79	2,177				
Alaska	Foreign	1,812	1,595	95	3,502				
	Domestic	7,902	893	4	8,799				
West Coast	Foreign	638	13,703	225	14,565				
	Domestic	10,035	2,810	179	13,024				
Hawaii	Foreign	220	211	16	447				
	Domestic	45	45	9	100				
Pacific Islands	Foreign	152	149	0	301				
	Domestic	6	3	0	9				
Total	Foreign	11,160	38,222	1,224	50,606				
	Domestic	79,691	9,238	4,461	93,390				

Table 10. Average Annual Foreign Ballast Water Discharge in U.S. Waters, by Ballast Water Source and Discharge Region. Based on 2004-2005 data from Miller *et al.* 2007 (estimated from Figures 17a & 17b), adjusted for reporting rates (Miller *et al.* 2007, Table 3). "Pacific Islands" includes Guam and American Samoa. Does not include the Great Lakes, inland waterways and unknown discharge regions, or 283,000 MT of discharge from unknown sources.

	Sources of Reported Foreign Ballast Water Discharged (1,000 metric tons)										
Discharge Region	Northwest Atlantic Ocean	Southwest Atlantic Ocean	Northeast Atlantic Ocean	Mediterranean & Black Seas	Southeast Atlantic Ocean	Indian Ocean	Northwest Pacific Ocean	Southwest Pacific Ocean	Northeast Pacific Ocean	Southeast Pacific Ocean	Total
E. Coast	2,296	70	2,609	661	52	285	696	14	278	52	7,014
GOM	9,927	72	3,453	1,870	108	388	432		1,151	180	17,582
Caribbean	6,797	17		17			17		167	17	6,931
Alaska	17						3,207		260		3,485
W. Coast	112	56	56	56		168	12,580	56	1,426	56	14,565
Hawaii	62					14	42	39	286	3	446
Pacific Is.						2	86	209	4		301
Total	19,111	214	6,118	2,604	160	858	17,060	317	3,572	308	50,324

Note that these estimates are based on data that are compiled from self-reporting by vessels, with little or no independent verification by the U.S. Coast Guard or other entities.⁸ Studies have shown that vessel self-reporting tends to substantially overstate the fraction of ballast discharge that is exchanged and/or to overstate the completeness of the exchanges that are conducted (Lockwood 1999; Harkless 2003; Lyles 2004; see also Cohen & Foster 2000, footnote 163). Some aspects of the data suggest that in addition the total amount of discharge may be understated. These annual estimates should therefore be considered to have significant uncertainty associated with them, and to probably understate the risk of transporting and releasing coastal organisms into new locations in ballast water.

However, accepting these data as the best currently available, and combining them with information on the distributions of ESA species (Table 5, Appendix 3) and related

⁸ The sole independent verification conducted by federal agencies consists of the U.S. Coast Guard boarding and sampling the salinity in some ballast tanks on some unknown but apparently small number of vessels arriving at coastal ports. If the salinity is too low, the vessel is assumed to not have conducted an exchange of ballast water that meets federal regulations and could be subject to fines or other penalties. However, salinity measurements are only effective at assessing the conduct of mid-ocean exchange in the relatively small number of vessels that load fresh or very low salinity ballast water. For most vessels, salinity measurements are not capable of determining whether a vessel has conducted a ballast exchange that meets regulations. The absence of reliable independent testing, the low legal penalties for inaccurate reporting or intentional falsification of reports, and the paucity of enforcement actions undertaken for inaccurate or false reporting increase the incentives for vessels to under-report discharges and overstate exchanges.

species, allows some comparison of the risks and source areas of risk for different groups of ESA Species. For example, ESA coral species occur in two general regions, the tropical Pacific (Hawaii and the Pacific Islands, with a total of 75 ESA species, four of which are restricted to the Hawaiian Islands and six of which are found in both Hawaii and the Pacific Islands), and the tropical/subtropical Atlantic (a total of nine ESA species found in the Caribbean, the Gulf of Mexico and in the East Coast region in southern Florida; all of these occur in both the Caribbean and Florida, with seven also found in U.S. waters in the Gulf of Mexico and one in southern (non-U.S.) waters in the Gulf of Mexico). In the Hawaii and Pacific Island regions, relatively little foreign ballast water is discharged into U.S. waters (about 0.75 million metric tons (MT) annually), though this is concentrated in a relatively small number of ports. Most of this is derived from the Indo-West Pacific region, with only 62,000 MT coming from the Atlantic. In contrast, the three Atlantic U.S. regions receive nearly 32 million MT of foreign ballast water, of which 1.8 million MT comes from the Indo-West Pacific region. Although this discharge is spread over a larger number or ports and a larger area of coast, including East Coast areas that are too far north to support corals,⁹ it nonetheless appears that, based on ballast volumes, there is greater opportunity for coral diseases to be introduced in ballast water from the Indo-West Pacific into U.S. waters in the Atlantic than from the Atlantic into U.S. waters in the Pacific.

Similarly, the sole ESA plant species, Johnson's seagrass (*Halophila johnsonii*), ranges only from Biscayne Bay, Florida (near Miami) to Sebastian Inlet, Florida, about 200 miles north (NOAA 2010b). Vessels arriving in the Miami area discharge about 1.3 million MT of foreign ballast water each year (based on data in Miller *et al.* 2007). Of the foreign ballast water discharged in the East Coast region, 47% is derived from the Eastern Atlantic (mainly the coast of Europe), 14% from the Indo-West Pacific region and 5% from the Eastern Pacific (Table 10), suggesting ample opportunity to introduce seagrass diseases from other coastal regions of the world. Ballast water source data specific to vessels arriving the Port of Miami could be developed from the NBIC database.

The two ESA mollusk species, white abalone (*Haliotis sorenseni*) and black abalone (*H. cracherodii*), are more-or-less restricted to southern California and Baja California (NOAA 2010b).¹⁰ Within this range, ports in the Los Angeles and San Diego areas receive about 3 million MT of foreign ballast water, or about one-fifth of the foreign ballast water discharged to U.S. West Coast waters. They also receive about 40% of the domestic ballast water discharged to the U.S. West Coast (based on data in Miller *et al.* 2007). About 86% of the foreign ballast water discharged to the U.S. West Coast is derived from the Asian Pacific coast, which is home to several species of *Haliotis* that are not found on the U.S. West Coast (Geiger 1999). This suggests that there is a

⁹ Of the 7 million MT of foreign ballast water discharged by vessels arriving in East Coast waters each year, 1.3 million MT is discharged by vessels arriving at ports in the Miami region (based on data in Miller *et al.* 2007), within or near the range of ESA coral species.

¹⁰ Black abalone are rare north of San Francisco, with a few unconfirmed records in Oregon (NOAA 2010b).

significant risk of introducing abalone diseases into the U.S. range of these two ESAlisted abalone species via ballast water, especially from Asia.

Another major group of ESA species with limited distributions are the pinnipeds, with five ESA species in Alaska and/or on the West Coast and one ESA species in Hawaii (the Hawaiian monk seal). Both Alaska and the West Coast receive substantial discharges of foreign ballast water (3.5 million MT/yr and 14.6 million MT/yr. respectively), primarily from northern Asia (92% and 86%, respectively) (Table 10). There are two species of otariid pinnipeds and five species of phocid pinnipeds that occur in northern Asia (Nagasawa 1999; Trukhin 2009), all which are found in Alaska and three of which occur on the U.S. West Coast (Orr & Helm 1989; NOAA 2010b). However, there are species, subspecies or DPS in Alaska or on the U.S. West Coast that aren't found in Asia, and five of the Asian species, subspecies or DPS aren't found on the U.S. West Coast (Orr & Helm 1989; Stanley et al. 1996; NOAA 2010b). There thus appears to be a significant chance of ballast water transporting pinniped pathogens or strains of pathogens from Asia and releasing them into waters with naive hosts, especially on the West Coast and possibly in Alaska. Hawaii, on the other hand, receives much less foreign ballast water (less than 0.5 million MT/yr), and so there is less opportunity for ballast water to deliver pinniped pathogens. However, since most of that ballast water comes from the northeastern Pacific (64%), which has four species and two subspecies of phocid seals, there may still be a significant risk to the Hawaiian monk seal.

Bacterial and viral threats to ESA-listed species

In general, our knowledge of the diseases of marine and estuarine organisms is quite limited. Much of what we do know is derived from disease outbreaks in animals kept in captivity or used in aquaculture, with less known in many cases about the occurrence of disease in wild populations. Even when diseases are well documented in wild populations, their etiology often remains unknown, and may be viral, bacterial, fungal, protozoan or otherwise in nature. In some cases where pathogenic microbes have been identified in association with disease outbreaks, it is unclear whether the identified pathogens are the primary cause of the morbidity or mortality or represent opportunistic, secondary infections. The life histories of most microbial pathogens are often largely unknown (even for some human pathogens¹¹), and the evolutionary history, biogeography of different genotypes, and the varying virulence of different genotypes to different host species is often complicated and poorly worked out.

Below is a summary of bacterial and viral pathogens known to have affected ESA-listed species or considered to be threats to them, and some bacteria and viruses that have

¹¹ For example, until recently *Vibrio cholerae* was considered to be only a human pathogen with merely incidental occurrence in the environment outside of its host. It wasn't until the late 1970s or 1980s that it was recognized that it has a normal and widespread occurrence as an autochthonous inhabitant of riverine and coastal waters (Lipp *et al.* 2002).

produced disease or mortality in related species. This is not intended to be a complete or exhaustive survey, but rather provides some examples of the types of pathogens that could potentially be transported in ballast water and impact listed species.

Cetacean Pathogens. Most of the cetacean ESA species that occur in U.S. waters have broad distributions and are, as individuals, wide-ranging (NOAA 2010b), which is generally true of whales. This means that species or strains of cetacean pathogens are also likely to be relatively wide-spread, and therefore provide less opportunity for ballast water to introduce a novel pathogen to a naive host population.

Although no ESA-listed cetacean is considered by NOAA to be threatened by disease (NOAA 2010b), bacterial and viral diseases have affected other cetaceans. Bacteria that have been implicated in cetacean diseases and mortalities include species of *Pseudomonas, Erysipelothrix, Klebsiella* and *Brucella*, as well as *Edwardsiella* and *Salmonella* species which may most often affect animals that are already debilitated or stressed from other causes (Moeller 2002; Van Bressem *et al.* 2008, 2009). Pathogens belonging to at least nine virus families have been detected in cetaceans, with species of morbillivirus, poxvirus and papillomavirus having demonstrated a potential to affect population abundance by raising mortality rates or lowering reproductive success (Van Bressem *et al.* 1999, 2008). In general, inshore and estuarine cetaceans may be at greater risk from bacterial or viral disease due to stressful alterations in habitat and environmental conditions, including contamination, vessel interactions, etc. (Van Bressem *et al.* 2009).

Emerging pathogens of major concern for marine mammals are the morbilliviruses. which were discovered in pinnipeds and cetaceans in the late 1980s (morbilliviruses are discussed in further detail in the section on Pinniped Pathogens). Morbillivirus was associated with mass mortalities of striped dolphins in the Mediterranean in 1990-1991 and 2006-2007, of bottlenose dolphins along the U.S. east coast in 1982 and 1987-1988 and in the Gulf of Mexico in 1993-1994, and of long-finned pilot whales in the Mediterranean in 2006-2007 (Barrett et al. 1992, 1995; Lipscomb et al. 1994, 1996; Kennedy 1998; Moeller 2002; Fernandez et al. 2008; Van Bressem et al. 2008), including the loss of possibly >50% of the bottlenose dolphins in inshore waters between New Jersey and Florida in 1987-88 (Lipscomb et al. 1994; Van Bressem et al. 1999, 2008). Kennedy (1998) concluded that morbillivirus mass mortalities "probably resulted from transfer of virus to immunologically-naive populations." Others have noted that the transmission of morbilliviruses under natural conditions is usually restricted to a single mammalian order (Visser et al. 1993c; Osterhaus et al. 1995). Evidence of morbillivirus infection was found in several other dolphin and porpoise species in the Atlantic and Mediterranean, and in short-finned pilot whales in the Atlantic and a fin whale and a minke whale in the Mediterranean (Duignan 1995a,b; Barrett et al. 1995; Gaydos et al. 2004; Wohlsein et al. 2007). These were caused by two distinct viruses or virus strains, named Dolphin Morbillivirus (DMV) and Porpoise Morbillivirus (PMV) (Visser et al. 1993b,c; Osterhaus et al. 1995; De Swart et al. 1995; Moeller 2002; Van de Bildt et al. 2005), with a possible third strain identified in a pilot whale (Pilot Whale

Morbillivirus, or PWMV–Taubenberger *et al.* 2000; Van Bressem *et al.* 2008). Van Bressem *et al.* (1999) concluded that "cetacean morbillivirus induces a serious disease with a high mortality rate [that] may have long-term effects on the dynamics of cetacean populations." Although initially considered to be diseases of the Atlantic Ocean and Mediterranean Sea, cetacean morbillivirus has been detected in other parts of the world, including common dolphins from a mass stranding in southern California and a stranded pygmy sperm whale in Taiwan (Reiderson *et al.* 1998; Van Bressom *et al.* 1998, 2001; Yang *et al.* 2006).

Gaydos *et al.* (2004) assessed the disease threat to the southern resident killer whale population, an ESA species. They listed seven bacterial and three viral or suspected viral pathogens of captive killer whales and a two other bacterial and one other viral pathogen reported in wild killer whales. One of these, consisting of one or more unidentified species of *Brucella* bacteria from the northeastern Atlantic Ocean, was considered to be capable of reducing fecundity in killer whale populations but of low virulence and epizootic potential. Gaydos *et al.* (2004) also considered four additional bacterial and three viral pathogens found in other odontocete species. Both herpesviruses and morbillivirus scored high on virulence and epizootic potential, but only morbillivirus was judged to have a high capacity to affect fecundity.

Pinniped Pathogens. Except for the Hawaiian monk seal (*Monachus schauinslandi*), no ESA-listed pinniped is considered by NOAA to be threatened by disease (NOAA 2010b). NOAA (2010b) lists exposure to disease from human interactions and disease outbreaks as threats to the Hawaiian monk seal. Much of the concern appears to be with the transmission of diseases from terrestrial hosts (leptospirosis, toxoplasmosis, West Nile virus, etc.), but there are also concerns about transmission from northern elephant seals that occasionally visit the islands: three were sighted between 1978 and 2006 (NMFS 2007).

Bacteria causing pinniped disease include *Pseudomonas, Brucella, Edwardsiella* and *Salmonella* species, as well as *Klebsiella* and *Leptospira* in California sea lions and northern fur seals (Moeller 2002; Cameron *et al.* 2008; Zuerner *et al.* 2009; Jang *et al.* 2010). A number of serious viral diseases of pinnipeds have been reported including Sea Lion Hepatitis Virus, Seal Herpesvirus (in harbor seals in Europe and in a California Sea Lion), San Miguel Sea Lion Virus (in sea lions and seals) and Seal Pox (primarily in California and South American sea lions and harbor seals) (Moeller 2002). The reported distributions of many of these pinniped diseases are very restricted; if the distributions of the pathogen strains causing these diseases are similarly restricted. There may be a significant potential for ballast water to carry and release pathogens to waters with naive, ESA-listed hosts. As noted earlier, there is some ballast water carried from the northeastern Pacific region (home to eight otariid or phocid pinniped species, two subspecies and two DPS's that are not found in Hawaii¹²) to Hawaii, home of the endangered Hawaiian monk seal; and a great deal of ballast water is carried from Asia (home to four otariid or phocid pinniped species, one subspecies and one DPS that are

¹² Except for rare visits by northern elephant seals, as noted.

not found on the U.S. West Coast) to the U.S. West Coast¹³, home to the Eastern DPS of the Steller Sea Lion and a population of the Guadalupe Fur Seal, both ESA threatened species. Ballast water transfers of pinniped pathogens into new regions may be facilitated by the common occurrence of some pinniped species in harbor areas (*e.g.* harbor seals, California sea lions), close to areas where ballast water is discharged. For example, for the past twenty years hundreds of California sea lions have occupied floating docks at the northern end of the Port of San Francisco for much of the year (Wikipedia 2010).

As with cetaceans, morbillivirus is an emerging disease concern for pinniped species. Until the late 1980s morbilliviruses were known only from terrestrial animals, where they are the cause of several major diseases including measles in humans, canine distemper in dogs and other carnivores, and rinderpest and peste-des-petits-ruminants virus in ruminants (Barrett et al. 1992; Visser et al. 1993c). In 1988 more than 23,000 harbor seals and grey seals died in an epidemic in northwestern Europe, which killed 50-80% of the harbor seal population in some areas (Osterhaus & Vedder 1988; Barrett et al. 1992; Visser et al. 1993a.c; De Swart et al. 1995; Kennedy 1998; Pomeroy et al. 2005; Harkonen et al. 2006). The epidemic was caused by a previously unknown morbillivirus that was named Phocine Distemper Virus (PDV). Other pinniped species on both sides of the North Atlantic were subsequently found to have been infected by PDV, including harp seal, hooded seal, ringed seal and walrus (Barrett et al. 1995; Nielsen et al. 2000; Harkonen et al. 2006), and a second northern European epidemic in 2002 killed over 30,000 harbor seals (Pomerov et al. 2005; Harkonen et al. 2006). Meanwhile, two or three distinct cetacean morbilliviruses were discovered in dolphins, porpoises and whales starting in 1988, as discussed earlier; and a morbillivirus-caused mortality of thousands of freshwater Siberian seals in Lake Baikal in 1987-1998 which initially was thought to be related to the morbillivirus outbreak in harbor seals in northwestern Europe, instead turned out to be due to Canine Distemper Virus (CDV), probably acquired by contact with domestic dogs or other terrestrial carnivores (Visser et al. 1990, 1993c; Barrett et al. 1992, 1995; De Swart et al. 1995; Mamaev et al. 1996; Kennedy 1998; Kennedy et al. 2000; Harkonen et al. 2006). CDV was apparently also responsible for the death of 10,000 Caspian seals in 2000 (Kennedy et al. 2000: Fuiii et al. 2006).

Several surveys did not find any evidence of exposure to PDV in Pacific Ocean pinnipeds in Alaska (harbor seal, spotted seal, bearded seal, ribbon seal, ringed seal, Steller sea lion and walrus sampled between 1976 and 1999–Osterhaus *et al.* 1988; Calle *et al.* 2002, 2008; Burek *et al.* 2005; Zarnke *et al.* 2006¹⁴) or in British Columbia and the U.S. West Coast (harbor seals sampled between 1992 and 2000–Duignan *et al.* 1995c; Ham-Lamme *et al.* 1999; Hester *et al.* 2004). PDV was believed to be absent from pinnipeds in Pacific waters (Kennedy 1998; Harkonen *et al.* 2006; Calle *et*

¹³ 12.6 million metric tons/year, which is 86% of the ballast water discharged on the U.S. West Coast (Table 10).

¹⁴ Zarnke *et al.* (2006) did record 2 samples as positive for PDV out of 160 harbor seal samples, but considered these to likely be false positives since the antibody titers barely exceeded the minimum threshold.

2002, 2008: Goldstein et al. 2009), and Pacific Ocean pinnipeds were thought to be highly vulnerable to a PDV epidemic due to lack of genetic or acquired immunity (Duignan et al. 1994, 1995c; Ham-Lamme et al. 1999; Calle et al. 2002, 2008)¹⁵. Recently, Goldstein et al. (2009) reported serologic and RNA evidence of PDV in 41 live-captured or dead-collected Alaskan sea otter, including a 300 nucleotide fragment that was identical to an isolate from the 2002 PDV outbreak in European harbor seals and differed from an isolate from the 1998 PDV outbreak at two nucleotide positions. Goldstein et al. (2009) concluded that PDV had been introduced to the Pacific Ocean at least after 2000 and probably after the 2002 epidemic, and had likely been introduced by migrating Arctic or sub-Arctic seals, possibly facilitated by reductions in sea ice in 2004 and 2005. However, Goldstein *et al.* and the other cited authors were apparently unaware of studies published in Japanese journals reporting a high incidence of PDV antibodies in Kuril harbor seals, spotted seals and Steller sea lions on Hokkaido in 1996-1997 (Ohashi & Kai 2000, cited by Fujii et al. 2006), and declining levels of PDV antibodies in Kuril harbor seals on Hokkaido in 1998-2005 (Fujii et al. 2006). Fujii et al. (2006) interpreted these data as indicating an epidemic occurrence of PDV in Japanese pinnipeds before 1998 and sporadic occurrence since. In any event, PDV is apparently now present in both Alaskan and Asian waters, with some potential (as noted above) for transport in ballast water to U.S. West Coast or Hawaiian waters where ESA pinniped species reside that have apparently had no prior exposure to PDV.

Based on *in vitro* tests of blood cells, Osterhaus *et al.* (1992) concluded that Mediterranean monk seals (*Monachus monachus*) were susceptible to some marine mammal morbilliviruses (PDV from seals and PMV from porpoises, but not DMV from dolphins). Visser *et al.* (1993c) suggested that morbillivirus infection posed a serious threat to both Mediterranean and Hawaiian monk seals. In 1997 a disease outbreak killed off 70% of the West African population of Mediterranean monk seals—there were only two populations of Mediterranean monk seals, consisting of about 500 animals in the Mediterranean and about 270 animals in West Africa (Osterhaus *et al.* 1997, 1998; Dhermain 2003). Virus collected from several of the dead seals was identified as a new strain, Monk Seal Morbillivirus (MSMV), which is closely related to DMV (Osterhaus *et al.* 1997). Some researchers, however, concluded that the die-off was due to feeding on fish with accumulated dinoflagellate toxin from a red tide, rather than the morbillivirus (Dhermain 2003).

Sea Turtle Pathogens. Although a number of potentially pathogenic, lesion- or diseaseassociated bacteria (including Vibrio alginolyticus, Aeromonas hydrophila, Flavobacterium, Mycobacterium, Pseudomonas and Salmonella enteridis–Glazebrook & Campbell 1990a,b) and viruses (including Lung-Eye-Trachea Virus, Gray Patch Virus, Loggerhead Genital-Respiratory Herpesvirus and Loggerhead Orocutaneous Herpesvirus–Curry *et al.* 1999, 2000; Stacy *et al.* 2007) have been

¹⁵ "Further studies also must be done to evaluate the potential risk to the harbor seals along the Pacific coast... The only thing protecting Pacific harbor seals at present is the barrier formed by the Arctic...it might only take a single [introduction] event to produce an epizootic as devastating as the recent one in Europe" (Duignan *et al.* 1995c).

reported from captive or wild sea turtles, the main disease concern has been with fibropapillomatosis, which occurs most commonly in green turtles. For example, NOAA (2010b,c) lists fibropapillomatosis in green turtles as the only turtle disease threatening any ESA species, although it also mentions that diseases that affect reef corals indirectly threaten hawksbill turtles. The IUCN (2002) found that fibropapillomatosis threatened 14 out of 34 green turtle populations around the world, including the Florida population. Fibropapillomatosis is characterized by tumors, which are sometimes very large or numerous, both externally on the skin, eyes, oral cavity and carapace (fibropapillomas) and internally on organs (fibromas). These tumors, though considered benign, can interfere with vision, swallowing, breathing and organ function, are a primary cause of strandings in Hawaii and elsewhere, and often result in immunosuppression and secondary bacterial infections (Herbst 1994; Quackenbush *et al.* 1998; Work *et al.* 2003; NOAA 2010c; USGS 2010).

Fibropapillomatosis was first observed in green turtles in the Florida Keys in 1938, and in Hawaii in 1958 (or possibly as early as the 1940s–Williams & Williams 1996), and has become progressively more common and reported more widely (Quackenbush *et al.* 1998; IUCN 2002). It has now been found throughout the greater Caribbean region and in California, Hawaii, Australia, Asia and Africa (Herbst 1994; IUCN 2002). It is most common in green, loggerhead and olive ridley turtles (Herbst 1994; Quackenbush *et al.* 1998; Greenblatt *et al.* 2005), but may occur, at least occasionally, in all sea turtle species (Williams & Williams 2006: questioned by Casey 2006). Since fibropapillomas are easily observed, and sea turtles are highly visible animals that have long been exploited commercially, the lack of earlier records of fibropapillomas suggests that fibropapillomatosis was rare or absent in these regions in the past.

Fibropapillomatosis is generally thought to be caused by a virus that is usually referred to as Fibropapilloma-associated Turtle Herpesvirus (FPTHV).¹⁶ Experiments showed that fibropapillomatosis is transmitted by a filterable agent such as a virus (Herbst 1994), and FPTHV was detected in every fibropapilloma and fibroma tested (Greenblatt *et al.* 2004) at concentrations of at least one copy of viral DNA per cell (Quackenbush *et al.* 1998; Greenblatt *et al.* 2004), which was found to be 2.5-4.5 logs higher than in tumor-free skin from the same animal (Quackenbush *et al.* 2001). However, all efforts to culture FPTHV have been unsuccessful, so the accepted criteria for establishing that a particular microbe is the cause of a disease (known as Koch's postulates) have not been satisfied (Herbst 1994; Work *et al.* 2003, 2009), and there remains some uncertainty whether FPTHV is the cause of fibropapillomatosis.

Quackenbush *et al.* (1998) found three distinct but closely related FPTHV genotypes associated with fibropapillomas in different regions and species, with one genotype in green turtles in Hawaii, another in green and loggerhead turtles in Florida, and a third in olive ridley turtles (probably from the west coast of Central America, though the collection site was not stated). Further work confirmed three genotypes in Australia/Hawaii, Mexico/Costa Rica and Florida/Caribbean regions (Quackenbush *et al.* 2001). Analysis of a larger portion of the genome suggested four or possibly five

¹⁶ It has also been called Chelonid Fibropapilloma-associated Herpesvirus (CFPHV) (Work *et al.* 2009).

genotypes, separated primarily by geography rather than host species, with separate genotypes in the Caribbean (one or two genotypes in green turtles), the American Pacific Coast (green and olive ridley turtles), Hawaii (green turtles) and Australian (green and loggerhead) (Greenblatt *et al.* 2005). On the basis of these global-scale geographic variations in gene sequences, Greenblatt *et al.* (2005) concluded that FPTHV was established in these different regions long before fibropapillomatosis was recognized in the 1930s-1950s.

The regional variation in gene sequence suggest that introductions of FPTHV genotypes between these regions could have impacts on sea turtle populations that are naive to the introduced genotype. Experiments with a different herpesvirus of sea turtles that has been cultured successfully, Lung-Eye-Trachea Virus, found that it remained infective in artificial or natural seawater for over 5 days at 15-23°C (Curry *et al.* 1999, 2000), suggesting that FPTHV might also be stable enough in ballast water to survive relatively short voyages between certain genotype regions, such as between Hawaii and San Diego. Greenblatt *et al.* (2004) examined an array of green turtle parasites and found high loads of FPTHV in marine leeches (*Ozobranchus* spp.), with some sample concentrations indicating nearly 10⁷ copies of FPTHV DNA per leech, suggesting that these may serve as mechanical vectors for the transmission of FPTHV. Transport of FPTHV in leeches in ballast water might thus be a more likely mechanisms for successful ballast water introduction than FPTHV in water.

The regional separation of sea turtle species and breeding populations suggests that other microbial pathogens of sea turtles might also be candidates for ballast water introduction, but these have been received less attention and little is known of regarding the geographic distribution of their genotypes.

Fish Pathogens. Probably more is known about the bacterial and viral pathogens of fish than about the pathogens of other types of ESA species. Nonetheless, NOAA doesn't consider any ESA fish species to be threatened by disease (NOAA 2004, 2005, 2010b). NOAA does note that disease transmission resulting from hatchery introductions may significantly impact West Coast salmonid species (NOAA 2010d); and that while West Coast salmonids are affected by bacterial diseases (Bacterial Kidney Disease, columnaris, furunculosis, redmouth disease) and viral diseases (Infectious Hematopoietic Necrosis and Erythrocytic Inclusion Body Syndrome) that they have coevolved with, there could be greater impacts from introduced pathogens not historically present in a particular watershed (NOAA 1996, 1998, 2004). Similarly, NOAA notes concerns that Atlantic sturgeon could be affected by non-native sturgeon pathogens introduced through aquaculture operations. I briefly review here some of the betterknown bacterial and viral fish pathogens, their occurrence in ESA fish species or related species, their geographic distribution and where available, the geographic distribution of recognized genotypes and factors related to their potential transmission in ballast water. Each of the pathogens discussed here has produced substantial and sometimes largescale mortality in some fish species, often in aquaculture situations but sometimes in

the wild. For reference, the orders, families and genera of ESA fish species are listed in Table 11.

Order	Family	Genus	ESA Species		
Salmoniformes	Salmonidae	Salmo Oncorhynchus Oncorhynchus Oncorhynchus Oncorhynchus Oncorhynchus	Atlantic salmon 9 runs of Pacific Coast Chinook salmon 2 runs of Pacific Coast Chum salmon 4 runs of Pacific Coast Coho salmon 2 runs of Pacific Coast Sockeye salmon 11 runs of Pacific Coast Steelhead Trout		
Acipenseriformes	Acipenseridae	Acipenser	4 sturgeon species		
Scopaeniformes	Sebastidae	Sebastes	3 Pacific Coast rockfish species		
Pristiformes	Pristidae	Pristis	2 sawtooth species		
Gadiformes	Lotidae	Brosme	Cusk		
Clupeiformes	Clupeidae	Clupea	Pacific Herring, Southeast Alaska DPS		
Osmeriformes	Osmeridae	Thaleichthys	Pacific Eulachon, Southern DPS		

Table 11. Orders, families and genera of ESA fish species.

<u>Aeromonas salmonicida subsp. salmonicida</u> is a bacterium that causes the disease furunculosis in salmonid species. It has been isolated from Atlantic, chinook, coho, chum, sockeye salmon, rainbow trout¹⁷, and 10 other salmonid species, including both farmed and wild fish. It has been reported from other freshwater and a few marine species including two gadiforms (Atlantic cod, coalfish), but serious disease problems have been limited to salmon (Kent *et al.* 1998; Raynard *et al.* 2007). Bakke & Harris (1998) noted that the original spread of the disease was "strongly suggestive of an introduced pathogen," probably initially by transfers of live salmonids in aquaculture, with secondary spread by escapes from fish farms and migrations of wild fish. It is now present wherever salmonids occur. Some strains of this bacteria have multiple resistance to antibiotics, indicating that they probably originated on fish farms. The bacterium can persist in the water for some time; it tends to attach to organic matter in sediment, where it may persist for at least 18 months (Enger 1997; Raynard *et al.* 2007, citing Husevag 1994).

<u>Aeromonas salmonicida–atypical strains</u> refers to a non-salmonicida strains of this bacteria, involving at least two apparent subspecies and perhaps more, that are responsible for diseases in a variety of fish species in northern Europe, North America, Japan, Australia and South Africa. Atypical *A. salmonicida* have been isolated from salmonids (Atlantic, coho, chum and sockeye salmon, rainbow trout, and other salmonids), scorpaeniforms (black rockfish (*Sebastes schlegeli*), greenling, sablefish

¹⁷ Rainbow trout and steelhead are the same species, *Oncorhynchus mykiss*; steelhead are the sea-run form.

and lingcod), gadiforms (Atlantic cod, tom cod, haddock) and Pacific herring (Kent *et al.* 1998; Raynard *et al.* 2007).

<u>Listonella (Vibrio) anguillarum</u> may be the most common pathogenic fish bacterium in the world. It causes a vibriosis in fish that has been recognized since 1817. *L. anguillarum* occurs in a wide variety of fish, and is also associated with disease in mollusks and crustaceans. Susceptible species include salmonids (Atlantic salmon and other salmonids) and a gadiform fish (Atlantic cod) (Raynard *et al.* 2007). *L. anguillarum* occurs in several serotypes, which vary among fish species with some serotypes having an apparently narrow host range and others having broad host ranges, and there are genetic differences within serotypes which are sometimes differentiated geographically (Toranzo *et al.* 2005; Raynard *et al.* 2007). Transmission of the disease includes transmission through contact and through food, and the bacterium can reportedly survive for a long time outside its host (Hoff 1989; Raynard *et al.* 2007).

<u>Vibrio salmonicida</u> causes a vibriosis, sometimes called Hitra disease, in farmed Atlantic salmon. It has also been isolated from farmed Atlantic cod (a gadiform fish) and halibut in Europe and Atlantic Canada, but has not been reported from wild fish or from outside the North Atlantic (Raynard *et al.* 2007).

<u>Moritella viscosa (=Vibrio viscosus)</u> is associated with winter ulcer or winter lesions disease in Atlantic salmon, rainbow trout, Atlantic cod (a gadiform fish) and other species in northern Europe. Two distinct genetic subgroups relate appear to be related to origins in Norway and Iceland (Raynard *et al.* 2007).

Renibacterium salmoninarum causes Bacterial Kidney Disease (BKD)¹⁸, which was first described in Atlantic salmon in Scotland in the 1930s. It was subsequently reported in salmonids in the United States including chinook, coho and sockeye salmon and steelhead trout, and is now known from a variety of fish in fresh and salt waters in Europe, North and South America and Asia (NOAA 1996; Raynard et al. 2007). The disease is primarily known from farmed fish, but the bacterium is common in wild salmonids in Alaska and the U.S. West Coast (NOAA 1996; Raynard et al. 2007). Among ESA-listed species, NOAA (1996, citing Foott et al. 1994) reported that steelhead may be able to tolerate *R. salmoninarum* infection better than chinook or coho salmon, but Raynard et al. (2007) stated that chinook and sockeve salmon are considered more susceptible than Atlantic salmon or rainbow trout. Experiments have shown that transmission of R. salmoninarum is possible in Pacific herring and in sablefish, a scorpaeniform fish (Traxler & Bell 1988; Bell et al. 1990; Raynard et al. 2007), and it has been found in Pacific hake, a gadiform (Kent et al. 1998; Raynard et al. 2007). Larval fish can carry R. salmoninarum (Raynard et al. 2007). Although R. salmoninarum isolates are generally similar worldwide, some genetic differentiation has been found (Raynard et al. 2007).

<u>*Piscirickettsia salmonis*</u> was first isolated in 1989, and has been found in Atlantic, chinook, coho and other salmon, in rainbow trout, and in sea bass species in Europe,

¹⁸ BKD has also been called Dee disease, white boil disease and kidney disease (Raynard *et al.* 2007).

Chile and British Columbia (Lannan & Fryer 1994; Raynard *et al.* 2007). *P. salmonis* occurs in at least two genotypes, one that was found in all three regions that the disease has been observed and one that was found in Chile (Fryer & Mauel 1997). Isolates from Ireland may represent additional genotypes (Reid *et al.* 2004). Most rickettsiae are transmitted through alternative hosts, which could be the case for *P. salmonis*; however, it's possible that it may be directly transmitted, as it survives in sea water at 5-15°C for at least 14 days (Lannan & Fryer 1994; Fryer & Mauel 1997). It can also be transmitted to larval fish (Raynard *et al.* 2007).

<u>Epizootic Hematopoietic Necrosis Virus (EHNV)</u> is a ranavirus that was isolated in 1986. It is only known from Australia. It has been found in rainbow trout and redfin perch, and several species have been experimentally infected including Atlantic salmon (by injection) and Mountain galaxias, an osmeriform fish (by immersion) (Langdon 1989; PAHW 2007; OIE 2009). It is weakly infective in rainbow trout but often fatal (OIE 2009). EHNV can survive in water for months (Langdon 1989).

Infectious Hematopoietic Necrosis Virus (IHNV) is a rhabdovirus that causes a disease found primarily in salmonids, including both farmed and wild fish. Naturally infected fish include Atlantic, chinook, coho, chum, sockeye and other salmon, rainbow trout, and other salmonid species, as well as Pacific herring (PAHW 2007). White sturgeon larvae and other fish have been infected experimentally by immersion (PAHW 2007). IHNV was first described in sockeye salmon on the U.S. West Coast in the 1950s. It was reported in Japan in 1971 and later on Russia's Pacific Coast (Rudakova et al. 2007), probably introduced with imported salmon eggs (Nishizawa et al. 2006). It was found from Europe in 1987, thought to have resulted from a single importation of salmon eggs (Enzmann et al. 2005). IHNV has also been reported in the Caribbean (Dominican Republic). Two genotypes have been found on the North American West Coast separated geographically, with one ranging from Alaska to Oregon and the other in southern Oregon and California (PAHW 2007), and different strains of IHNV produce different rates of mortality in their hosts (Garver et al. 2006). It remains infective for up to 2 weeks in sea water, up to 7 weeks in fresh water at 10-15°C, and up to 9 weeks when adsorbed to clay or other substances (Appendix 4). IHNV was also found to be common in ectoparasites of sockeye salmon, including copepods and leeches (and persisted for at least 16 days in leeches), and may prove to be transmitted by them (Mulcahy et al. 1990).

<u>Infectious Pancreatic Necrosis Virus (IPNV)</u> causes an often fatal disease of salmonid species that was first described in 1941, and the virus was isolated in 1972 (Raynard *et al.* 2007). It has been found in Atlantic salmon, rainbow trout and other salmonids, and in various other fish (Raynard *et al.* 2007). It has been spread primarily through transfers of live fish and eggs, and is now found in Europe and the Middle East, the U.S. Atlantic region and New Zealand (Raynard *et al.* 2007). In addition to farmed and wild fish, IPNV has been isolated from water, sediment, birds, scallops, shrimp and other shellfish, which may also contribute to its spread (Cutrin *et al.* 2001). IPNV can accumulate in sediments and shellfish at levels more than two orders of magnitude

greater than those in sea water (Raynard *et al.* 2007). Isolates from the same location often differ in genotype and virulence (Cutrin *et al.* 2001; Shivappa *et al.* 2004).

Infectious Salmon Anemia Virus (ISAV) was first reported in farmed Atlantic salmon in Norway in 1984 (PAHW 2007). It has been isolated from Atlantic and coho salmon and rainbow and brown trout, and in two gadiform and one clupeiform species as well as other fish. In addition, chum salmon have been experimentally infected by injection and another clupeiform, the Atlantic herring *Clupea harengus*, was infected by immersion (Nylund *et al.* 2002; PAHW 2007; Raynard *et al.* 2007). ISAV has been found in northern Europe, in southeastern Canada and northeastern U.S., and in Chile (Murray *et al.* 2002; Cipriano 2002; Raynard *et al.* 2007). There are distinct European and North American genotypes that predate aquaculture, with the Chilean isolate being closely related to the North American (Devold *et al.* 2006; Cipriano 2002; Nylund *et al.* 2003; Raynard *et al.* 2007). The European genotype has been further subdivided into several distinct subgroups (Raynard *et al.* 2007). ISAV can survive in sea water for weeks or longer (MacLeod *et al.* 2003; Appendix 4). It might also be carried in sea lice (Nylund *et al.* 1994).

<u>Koi Herpesvirus (KHV)</u> infects primarily common carp (including varieties such as koi). It has been reported in sturgeon, however the test that was used to determine this cannot distinguish between the mere presence of the virus and its replication in the host fish (PAHW 2007). The disease was first reported in Israel and Germany in 1998 and has spread throughout Europe and to Asia, South Africa and the U.S., mainly through the koi trade (PAHW 2007; OIE 2009). Isolates from different regions of the world are nearly identical, though comparisons of the complete genome revealed some geographic separation into strains (PAHW 2007; Aoki *et al.* 2007; OIE 2009). KHV survives for at most a few days in freshwater or freshwater sediment (Shimizu *et al.* 2006; Appendix 4).

<u>Viral Hemorrhagic Septicemia Virus (VHSV)</u> is a wide-ranging pathogen that has been found in at least 70 different fish species (Skall *et al.* 2005; PAHW 2007). It was first recognized as a disease of farmed rainbow trout in Europe in the 1930s, and the virus was isolated in the 1960s (PAHW 2007). Until 1979, when it was isolated from a wild Atlantic cod, it was considered to be a virus that infected only freshwater fish (Snow *et al.* 2004). In 1988 it was found in chinook and coho salmon in the western U.S., the first records outside of Europe (Brunson *et al.* 1989; Hopper 1989; Winton *et al.* 1991). Over time it was isolated from an increasing number of marine and estuarine fish in Europe, the North Pacific and, in 2000, eastern Canada (Meier *et al.* 1994; Meyers and Winton 1995; Meyers *et al.* 1999; King *et al.* 2001; Brudeseth & Evensen 2002; Hedrick *et al.* 2003; Einer-Jensen *et al.* 2004; Skall *et al.* 2005; Gagne *et al.* 2007) and came to be seen as a virus of marine origin that had recently invaded fresh waters in Europe (Meyers & Winton 1995; Dixon 1999; Einer-Jensen *et al.* 2004; Snow *et al.* 2004). In 2003 VHSV appeared in the Great Lakes (Elsayed *et al.* 2006).

VHSV occurs in four geographically-separated genotypes, with Types I, II and III in Europe and Type IV in North America and Japan (Einer-Jensen *et al.* 2004; Snow *et al.* 2004; PAHW 2007). Type I occurs in five genetic subgroups: one (Type Ib) occurs

mainly in marine fish in the Baltic Sea and North Seas (the latter possibly being migrants from the Baltic), and the other four occur primarily in farmed rainbow trout in different parts of continental Europe (Einer-Jensen et al. 2004; Snow et al. 2004; Skall et al. 2005). These are thought to have been derived from the disease in marine fish, most likely via the practice of feeding marine fish to farmed trout, and to have evolved recently and rapidly in farmed fish (Meyers & Winton 1995; Einer-Jensen et al. 2004). Type II occurs in Baltic Sea marine fish associated with the deep water Eastern Gotland Basin, and Type III occurs in North Sea marine fish and has caused substantial mortalities in farmed turbot in the U.K (Einer-Jensen et al. 2004; Snow et al. 2004). In Europe, disease impacts are mostly restricted to farmed trout and farmed turbot (Einer-Jensen et al. 2004). Type IV occurs in two subgroups, IVa in a variety of marine and salmonid fish in western North America and in farmed flounder and some wild marine fish in Japan and Korea (Meyers & Winton 1995; Nishizawa et al. 2002; Hedrick et al. 2003; Kim & Park 2004; PAHW 2007) and IVb in coastal fish in eastern Canada and a wide variety of freshwater fish in the Great Lakes (Elsayed et al. 2006; Gagne et al. 2007; Winton et al. 2008). VHSV Type IV appears to be nearly avirulent to salmonid species (Meyers & Winton 1995), but there have been mass mortalities in a variety of marine fish in western North America and freshwater fish in the Great Lakes (Meyers & Winton 1995; Meyers et al. 1999; Lumsden 2005; Groocock et al. 2007; CFSPH 2010).

VHSV has been found in Atlantic, chinook and coho salmon, rainbow trout and other salmonids; two scorpaeniform fish, the black rockfish *Sebastes inermis* and the sablefish; many species of gadiform fish including one species of Lotidae (fourbeard rockling *Enchelyopus cimbrius*); several clupeiform fish including Pacific herring; and several osmeriform fish including Pacific eulachon (Brunson *et al.* 1989; Hopper 1989; Meyers *et al.* 1994; Meyers & Winton 1995; Smail 2000; King *et al.* 2001; Hedrick *et al.* 2003; PAHW 2007), and has caused mass mortalities in rainbow trout (VHSV Type I), Pacific herring (VHSV Type IV) and a variety of other marine and freshwater fish (Meier *et al.* 1994; Meyers & Winton 1995; Meyers *et al.* 1999; Skall *et al.* 2005; Lumsden 2005; Groocock *et al.* 2007; PAHW 2007; Kim *et al.* 2009; CFSPH 2010).

There is a great deal of variation in the data on the survival of VHSV in water (Appendix 4), perhaps due to varying capabilities in different genotypes (Winton *et al.* 1991). However, several studies suggest that VHSV can sometimes survive weeks to months in fresh water, and days to weeks in sea water, especially in colder water (Appendix 4). It is not known whether VHSV is ever transmitted through invertebrates serving as alternate hosts or mechanical vectors, but it was recently found to be associated with benthic amphipods in the Great Lakes (M. Faisal pers. comm.).

Clearly there are a variety of serious fish diseases which have either been shown to affect ESA fish species or that may have the potential to do so, based on natural or experimental infection of related species (Table 12). Some of these have been reported to be persistent (capable of surviving for weeks or longer) in fresh water, sea water or sediment, especially at lower temperatures. Many are capable of infecting small fish or larval fish, which may potentially be transported in ballast water. Several also have a

reported association with invertebrates such as leeches, copepods, isopods or amphipods, which similarly have a potential for transport in ballast water.

Table 12. Occurrence of selected bacterial and viral pathogens in orders of ESA fish species. "X" indicates the pathogen occurs in at least one species in the indicated order; bold font indicates that it occurs in an ESA species; square brackets indicate that the records are for experimentally induced infections. The report of KHV in sturgeon might be due to the mere presence of the virus or contamination of the sample, rather than infection.

Pathogen	Salmoniformes (salmon & trout)	Acipenseriformes (sturgeon)	Scorpaeniformes (rockfish)	Pristiformes (sawfish)	Gadiformes (cusk)	Clupeiformes (herring)	Osmeriformes (smelt)
Aeromonas salmonicida subsp. salmonicida	Х				Х		
Aeromonas salmonicida-atypical strains	Х		Х		Х	Х	
Listonella anguillarum	Х				Х		
Vibrio salmonicida	Х				Х		
Moritella viscosa	Х				Х		
Renibacterium salmoninarum	Х		[X]		Х	[X]	
Piscirickettsia salmonis	Х						
EHNV	Х						[X]
IHNV	Х	[X]				Х	
IPNV	Х						
ISAV	Х				Х	Х	
KHV		?					
VHSV	Х		Х		Х	Х	Х

Abalone Pathogens. Among mollusk species, disease outbreaks due to harmful pathogens are probably best documented for oysters, and some of these are believe to have involved introductions of pathogens into new regions, including *Haplosporidium nelsoni* (the cause of MSX disease) in California, eastern North America and Europe (Ford & Haskin 1982; Andrews 1984; Burreson *et al.* 2000; Renault *et al.* 2000; Goulletquer *et al.* 2002; Burreson & Ford 2004), *Bonamia ostreae* in Europe (Van Banning 1987; Cigarria & Elston 1997; Goulletquer *et al.* 2002) and *Perkinsus marinus* (the cause of Dermo disease) in the northeastern U.S. (Ford 1996). These pathogen introductions are generally assumed to have occurred as a result of the transport of oysters, but Burreson & Ford (2004) suggest that *H. nelsoni* spores might have been introduced to western or eastern North America in ballast water, and the same reasoning would apply to the other haplosporidian species. Another group of microbes that have a large impact on mollusks—toxic red tide dinoflagellates that render clams

and mussels unfit for consumption—are believed to have been introduced to some parts of the world via transport in ballast tanks (Hallegraeff & Bolch 1992; Hallegraeff *et al.* 1995; McMinn *et al.* 1997; Hallegraeff 1998; Hamer *et al.* 2000, 2001; Lilly *et al.* 2001).

The molluscan ESA species consist of two endangered abalones, the black abalone *Haliotis cracherodii* and the white abalone *H. sorenseni*, which are largely restricted to California and Baja California (NOAA 2010b). One introduced parasite and one probably introduced bacterial disease have had major impacts on farmed or wild abalone in California in recent decades. The sabellid worm shell parasite, *Terebrasabella heterouncinata*, attacked farmed red abalone, *Haliotis rufescens*, after its introduction in South African abalone, *H. midae*, imported by an abalone farm in the late 1980s (Culver & Kuris 2002; Cohen 2002; Bower 2006). All California abalone farms were affected, some went out of business, and the parasite spread to native gastropods in at least one location necessitating an eradication effort (Culver & Kuris 2000, 2002; Cohen 2002). Although farmed red abalone were the primary species affected, the parasite is capable of infecting most or all California abalone species (Kuris & Culver 1999).

Since 1985, black abalone populations have declined and gone locally extinct in many locations in part due to a wasting disease known as withering syndrome¹⁹, caused by a Rickettsia-like bacterium, Xenohaliotis californiensis²⁰ (Lafferty & Kuris 1993; Friedman et al. 2000; Smith et al. 2003; Bower 2009; NOAA 2010b). At most locations the disease reduced populations by 80% or more, with the greatest reductions in warmer waters (Richards & Davis 1993; Altstatt et al. 1996; Moore et al. 2002; Raimondi et al. 2002; Bower 2009; NOAA 2010b; Smith et al. 2003). NOAA (2010b) lists withering syndrome as a primary factor in the decline of black abalone, and it is the reason that the IUCN lists black abalone as Critically Endangered (Smith et al. 2003). Other abalone can also be affected, including white abalone (Moore et al. 2000; Moore et al. 2002; Burton et al. 2007; OIE 2009). Several aspects of the disease, including its recent appearance and its progressive spread from an initial occurrence in southern California (Lafferty & Kuris 1993; Altstatt et al. 1996; Bergen and Raimondi 2001; Raimondi et al. 2002) strongly suggest that it resulted from an introduced pathogen (Smith et al. 2003), but if so the mechanism of introduction in unknown. All that is known of X. californiensis' potential to survive in water is that it does so long enough to infect other abalone in water-borne transmission studies (OIE 2009). Though all terrestrial rickettsiae are transmitted through alternative arthropod hosts, this may be due to the challenge of bacterial survival and transmission in a terrestrial environment and may not apply to marine rickettsiae (Fryer & Mauel 1997; Moore et al. 2002). X. californiensis was recently found in China and Thailand in native abalone that exhibited no sign of the disease (OIE 2009). If X. californiensis was introduced to southern California, Asia could thus have been the source region, and large quantities of Asian ballast water are discharged to southern California ports (see discussion above under Ballast water pathways).

¹⁹ Also called withering disease, foot withering syndrome and abalone wasting disease.

²⁰ Also sometimes referred to as "*Candidatus* Xenohaliotis californiensis", the use of the term *Candidatus* indicating that the organism is a bacterium that cannot be maintained in a bacteriology culture collection.

Bacterial and viral pathogens of abalone are known from other parts of the world. The bacterium Vibrio harveyi has infected abalone species (Haliotis spp.) in France, Japan and Australia, causing a vibriosis that results in tissue necrosis and death; Vibrio carchariae²¹ is the likely cause of some abalone mass mortalities in Japan and Europe; Vibrio fluvialis II causes blister disease with high mortalities in China (though V. fluvialis is widespread in estuaries around the world); Vibrio parahaemolyticus is associated with mass mortalities of abalone in China: Vibrio alginolyticus causes mass mortalities in larval and post-larval abalone in Baja California and China; and Vibrio splendidus I is associated with abalone disease outbreaks in Australia (Anguiano-Beltran et al. 1998; Cai et al. 2006; Raynard et al. 2007; Bower 2007a, 2010). A Flavobacterium-like bacterium is associated with abalone disease outbreaks in Australia (Raynard et al. 2007) and Klebsiella oxytoca is associated with mass mortalities of abalone in China (Bower 2010). Abalone Viral Ganglioneritis (AVG)²² is caused by Abalone Herpes-like Virus (AbHV) in China, Taiwan and Australia (Chang et al. 2005; Bower 2007b; OIE 2009), and amyotrophia, a fatal wasting disease found in Japan, is believed to be caused by a virus (Bower 2001). Clearly there are a number of serious bacterial and viral diseases of abalone that are present in regions of the world that send substantial quantities of ballast water to California, which could potentially pose a threat to the two species of ESA-listed abalone that reside there.

Coral Pathogens. Coral diseases are a growing threat to coral species around the world. An increasing number of diseases and affected species have been reported since the mid-1990s, along with increases in the range, incidence, prevalence and mortality rates of these diseases (Bruckner 2009; CBD 2009; NOAA 2010e). There are over 30 named coral diseases in the Caribbean and at least seven major diseases and about 30 additional "conditions" characterizing compromised health in scleratinian corals in the Indo Pacific (Bruckner 2009). However, these diseases are still poorly understood: they are often difficult to distinguish, their etiology is frequently unknown, and their development may be complexly related to a variety of factors including pollution, sedimentation, ultraviolet radiation and water temperature. There has been a rapid emergence, wide distribution and high level of virulence of coral diseases in the Caribbean region since the 1970s, producing most of the world's records of coral disease even though most of the corals are in the Indo-Pacific, so that the Caribbean has been considered the world's main "hot spot" for coral disease (Bruckner 2009). This would suggest a greater risk of introducing coral disease from the Atlantic into the Pacific than in the reverse direction; on the other hand, for ballast water discharged into U.S. waters, the greatest transfer of ballast water is from the Pacific into the Atlantic (as discussed earlier under Ballast water pathwavs).²³

²¹ *V. carchariae* may possibly be a junior synonym of (that is, the same species as) *V. harveyi* (Raynard *et al.* 2007; Bower 2010).

²² Also reported as "crack-shell disease".

²³ Of course, corals in U.S. waters can be put at risk by coral diseases introduced into nearby non-U.S. waters, and it is not known whether the *total* volume of ballast water transported between tropical regions is greater in the direction from the Indo-Pacific to the Atlantic or from the Atlantic to the Indo-Pacific. The U.S. discharge data collected by the U.S. Coast Guard is insufficient for addressing this.

NOAA (2010b) lists disease as the main cause of the decline of elkhorn coral Acropora palmata and staghorn coral Acropora cervicornis, the two threatened ESA species, and the listing petition for the 82 additional Candidate species (CBD 2009) argues that "the increase in disease outbreaks and the rapid emergence of new diseases in recent years represents an ever-growing threat to all species of corals." The information provided in NOAA's species descriptions and in the listing petition indicate substantial documented disease impacts on at least 4 Caribbean ESA species; notable susceptibility to disease in all 9 Caribbean ESA species, in 3 of 9 Hawaiian ESA species²⁴, and in 44 of 66 Indo-Pacific ESA species; resistance to disease in 5 Indo-Pacific ESA species; and hampered ability to recover from disease in 3 Caribbean, 1 Hawaiian and 26 Indo-Pacific ESA species (Table 13).²⁵ Both the incidence of many coral diseases and/or their impacts appear to increase with water temperatures (Rosenberg & Ben-Haim 2002; Patterson et al. 2002; Cervino et al. 2004, 2008; Bruno et al. 2007; Hall-Spencer et al. 2007; CBD 2009; NOAA 2010f) and with coral bleaching (which weakens corals and may reduce their ability to resist or recover from disease, and is itself related to water temperatures) (Brant & McManus 2009; Croquer & Weil 2009; CBD 2009). Although disease impacts are high at many disturbed sites, disease has also spread to reefs in unpopulated areas (Bruckner 2009; NOAA 2010e).

The causative agents of most coral diseases are unknown (Cervino et al. 2004; Barash et al. 2005; Bruckner 2009; Sussman 2009). However, some of the most important coral diseases appear to be caused by one or more bacteria or cyanobacteria. In some cases (e.g. some of the "band" diseases), the disease is characterized by a microbial consortium consisting of a bacteria-dominated community, many or most of whose members are different from the microbe species found in the surrounding water, in healthy coral tissue or on dead coral skeletons (Frias-Lopez et al. 2002). These microbes are formed into a microbial mat (the "band") that migrates over the coral surface at rates that may exceed several millimeters per day, destroying coral tissue by exposing it to the anoxic, sulfide-rich basal region of the mat, and leaving dead coral skeleton behind. In such cases of polymicrobial disease, where the disease properties emerge synergistically from the community of microbes, it can be extremely difficult to determine which members of the community (which can include hundreds of species) are the actual "cause" of the disease (Frias-Lopez et al. 2004; Cooney et al. 2002; Barneah et al. 2007; NOAA 2010f). Over the past decade there has been considerable work on the bacterial communities of corals and the role of bacteria in coral disease, but very little work on viruses associated with corals (Rosenberg et al. 2007). I briefly review some of the more important coral diseases that are thought to be caused by bacteria.

²⁴ Five of the nine Hawaiian ESA coral species are also found in other parts of the Indo-Pacific region (see Appendix 3).

²⁵ Note that these data may be incomplete in various ways. Many of the species descriptions did not mention disease, which could mean that there are no disease impacts or threats to the described species, or that there's no information, or the information may not have been reported. Some species may be so rare and so immediately threatened by other stressors that disease is not currently important, even though it might become very important if the other stressors were controlled. On the other hand, some statements about susceptibility may be speculative, based on the susceptibility of other species in the genus or on the described species' geographic or habitat range.

Table 13. Impacts from, susceptibility to, and recovery from disease for ESA coral species, based on NOAA's online species descriptions and the listing petition for 82 candidate species. Indicates the predominant reported condition for each genus in each region. Source: CBD 2009; NOAA 2010b; summarized from Appendix 5.

Genus	Number of Species	Documented Population Impacts	Generally Susceptible	Generally Less Susceptible	Generally Slow to Recover				
CARRIBEAN SPECIES									
Acropora	2	Х	Х		х				
Agaricia	1		Х		Х				
Montastraea	3	Х	Х						
Dendrogyra	1		Х						
Dichocoenia	1		Х						
Mycetophyllia	1	Х	Х						
HAWAIIAN SPECIES (SOME ALSO OCCUR IN THE INDO-PACIFIC REGION)									
Acropora	1		Х		Х				
Montipora	3								
Leptoseris	1		Х						
Cyphastrea	2								
Porites	1		Х						
Psammocora	1								
INDO-PACIFIC SP	ECIES								
Acropora	21		х		х				
Anacropora	2		Х		Х				
Astreopora	1		Х		Х				
Isopora	2		Х		Х				
Montipora	5		Х						
Leptoseris	1		Х						
Pachyseris	1								
Pavona	5								
Barabattoia	1		Х						
Caulastrea	1								
Acanthastrea	4		Х						
Pocillopora	2		Х						
Seriatopora	1		Х						
Galaxea	1								
Alveopora	3			Х					
Porites	3		Х						
Turbinaria	4		Х						
Euphyllia	3								
Physogyra	1								
Pectinia	1								
Heliopora	1								
Millepora	2			Х					
Black Band Disease was first reported in Belize and Florida in 1972, and subsequently spread throughout the western Atlantic (UNEP 2010). It was reported in the Indo-Pacific in 1985, in the Red Sea in 1988, and on the Great Barrier Reef in Australia in 1994 (Rosenberg & Ben-Haim 2002; Sussman 2009; UNEP 2010). It affects a wide variety of species including 26 scleratinean corals, 1 hydrozoan and 6 gorgonians in the western Atlantic, and 49 species in 19 genera in the Indo-Pacific and Red Sea, most commonly on acroporid and faviid corals (Bruckner 2009). Black band disease results from a microbial mat that moves in a narrow band across coral colonies at rates of 3-10 mm/day. This mat has been described as having three functionally dominant components: gliding cyanobacteria dominated by *Phormidium corallyticum*²⁶, which provide the structure and movement; sulfide-oxidizing bacteria dominated by Beggiatoa spp.; and at the base of the mat, sulfate-reducing bacteria dominated by Desulfovibrio spp. (Ducklow & Mitchell 1979; Ruetzler & Santavy 1983; NOAA 2010f). More recent research, however, has suggested a different picture, in which some of the initial identifications may be wrong and the actual dominant microbes are a more complicated mix of cyanobacteria and other bacterial forms, along with large numbers of gram negative bacteria amounting in all to over 500 species of bacteria, which moreover may vary in composition or dominant species in different locations (Cooney et al. 2002; Frias-Lopez et al. 2002, 2003, 2004; Rasoulouniriana et al. 2009; Sussman 2009), or may change in composition over time as some corals develop resistance to some agents (Sussman 2009). Sussman (2009) considered the guestion of whether Black Band Disease is endemic in its widespread locations or introduced to some, and concluded that there is as yet insufficient genetic information to determine this.

<u>Red Band Disease</u> is also believed to be caused by a cyanobacterial mat (Bruckner 2009; UNEP 2010). It occurs in two forms (or perhaps as two different diseases). Type I (RBD-I) was first reported in the 1980s in Belize and has since been found in five genera of corals and sea fans (*Gorgonia*) throughout the Caribbean (Bruckner 2009; UNEP 2010). Type II (RBD-II) has only been found in a single location in the Bahamas, in six genera of corals (Bruckner 2009; UNEP 2010).

<u>Yellow Band Disease</u>²⁷, also known as Yellow Blotch Disease, was first reported in the Florida Keys in 1994, and has now been found throughout the western Atlantic where it affects corals in the *Montastraea annularis* complex and *M. faveolata* (Dona *et al.* 2008; UNEP 2010; NOAA 2010e,f). It has also occurred at various sites in the southwestern Pacific and the Philippines on *Diploastrea heliopora*, *Herpolitha* spp. and *Fungia* spp. corals since at least 2005 (Cervino *et al.* 2008; Dona *et al.* 2008). Tissue loss from yellow band disease is slower than in black band disease, progressing at a rate of around 0.2-0.3 millimeters per day (Cervino *et al.* 2004; Rosenberg *et al.* 2007; NOAA 2010f). Recent studies suggest that yellow band disease is caused collectively by strains of four or five species of *Vibrio* bacteria: *Vibrio harveyi*, *V. proteolyticus*, *V. rotiferianus* and *V. alginolyticus*, plus an unidentified *Vibrio* that could be either a new species or a subspecies of *V. alginolyticus* (Cervino *et al.* 2004, 2008). When all four

²⁶ Recently renamed *Geitlerinema* sp. (Sussman 2009).

²⁷ A distinct coral disease, also called Yellow Band Disease, has been reported in Turbinaria, Porites, Cyphastrea and Acropora species in the Arabian Gulf (Bruckner 2009).

Vibrio species together were applied to healthy coral, Yellow Band lesions appeared; when the Vibrios were applied singly or in twos or threes, some paling but no lesions appeared (Cervino et al. 2004, 2008). The bacteria primarily attack the symbiotic zooxanthellae algae in coral tissues, and only secondarily affect the coral tissues themselves (Cervino et al. 2004, 2008; Dona et al. 2008). Cervino et al. (2008) suggest that Yellow Band Disease may have been introduced into the Pacific by unknown means.²⁸ Since the *Vibrio* strains that appear to be the cause of Yellow Band Disease may be closely related to strains that have caused mortalities in the Pacific oyster Crassostrea gigas and other invertebrates (Cervino et al. 2008), introduction with transfers of live shellfish in aquaculture is one possible mechanism. Vibrio species are also transported in ballast water, sometimes in large numbers (McCarthy & Khambaty 1994; Ruiz et al. 2000; Drake et al. 2005), perhaps primarily attached to the chitinous shells of copepods and other crustaceans that are common in ballast water (Hug et al. 2001; Lipp et al. 2002), so transport in ballast water may be another possible mechanism. A marine worm serves as a reservoir and vector of another Vibrio that is a coral pathogen, V. shiloi (Sussman et al. 2003), and this suggests another possible medium for transport in ballast water.

<u>White Plague Type II</u> was discovered in sea fans in the Florida Keys in 1995, ultimately affecting dozens of coral species in the western Atlantic (Richardson *et al.* 1998; Denner *et al.* 2003; Cervino *et al.* 2004; Bruckner 2009). The disease progresses over the coral surface at a very rapid rate of up to 20 mm per day (NOAA 2010f). The disease is caused by a bacterium that was initially described as "*Sphingomonas*-like" or "a possibly novel species of *Sphingomonas*," but was eventually determined to be a member of a new genus, *Aurantimonas coralicida* (Denner *et al.* 2003). Aguirre-Macedo *et al.* (2008) reported finding "*Sphingomonas* White Plague Type II" in ballast water discharged near a coral reef in the Gulf of Mexico, but since this identification was based on morphology and did not reference Denner *et al.* 's (2003) description of *A. coralicida*, it's not clear to me whether Aguirre-Macedo *et al.* 's *Sphingomonas* is in fact the bacterium that causes White Plague Type II.

Two other types of White Plague have also been described in the Caribbean, Type I which was first reported in Florida in 1975, and Type III which was first reported in 1999 (Bruckner 2009; UNEP 2010; NOAA 2010f). The causative agents of these other White Plague types are not known.

<u>White Plague-like Disease</u> was found in the Gulf of Aqaba in the Red Sea in 2002, primarily affecting the major reef-building genera *Favia* and *Goniastrea* (Barash *et al.* 2005; Rosenberg *et al.* 2007). The disease is caused by the bacterium *Thalassomonas loyana* (Thompson *et al.* 2006) in combination with an unidentified extracellular

²⁸ "The data provided here shows that the YBD of the Indo-Pacific and Caribbean are identical at the morphological and cellular levels and seem to be caused by a consortium of *Vibrio* species. To speculate how part of this bacterial consortium was found in distant and separated geographic locations such as the Pacific and Caribbean, is beyond the scope of this study; however, it certainly is an interesting topic that involves ongoing research" (Cervino *et al.* 2008, at page 11).

virulence factor contained in a 0.2 µm filtrate of water collected near a disease coral (Barash *et al.* 2005).

<u>White Pox Disease</u>, also known as Patchy Necrosis Disease, Necrotic Patch Syndrome and Acroporid Serratiosis, was discovered in the Florida Keys in 1996 on the ESA species elkhorn coral (*Acropora palmata*), the only species it is known to affect (Patterson *et al.* 2002; NOAA 2010e). It has since been observed throughout the Caribbean (Patterson *et al.* 2002; Bruckner 2009). White Pox is cased by a common mammalian intestinal bacterium *Serratia marcescens*, which can also live independently in soil or water (Patterson *et al.* 2002; Sutherland & Ritchie 2005; Rosenberg *et al.* 2007), and has also been found in ballast water discharged near a coral reef in the Gulf of Mexico (Aguirre-Macedo *et al.* 2008). It is pathogenic to a variety of organisms including mammals, birds, fishes, insects and plants (Sutherland & Ritchie 2005). It may have been released to marine waters in sewage discharges (Sutherland & Ritchie 2005; NOAA 2010e,f).

Bacterial Bleaching was first observed in the Mediterranean in Oculina patagonica in 1995, and shown to be caused by the bacterium Vibrio shiloi (Kushmaro et al. 1996, 2001; Ben-Haim et al. 1999). Bacterial bleaching was then reported in Pocillopora damicornis in Zanzibar in the Indian Ocean and in the Red Sea in 2001, where it is caused by Vibrio corallilyticus (Ben-Haim & Rosenberg 2002; Ben-Haim et al. 2003a). A recent study shows that acute coral tissue loss classified as White Syndrome at three Pacific Ocean locations is also caused by V. corallilyticus (Sussman et al. 2008). Sussman (2009) considered the question of whether coral-pathogenic strains of V. *corallilyticus* are endemic throughout the Indo-Pacific or whether they may have been recently introduced to parts of this range, and concluded that there is as yet insufficient genetic information to determine this. If they are introduced, a possible mechanism could be shellfish transfers for aquaculture, since V. corallilyticus has been reported in larval oysters in England (Ben Haim et al. 2003b; Sussman 2009). On the other hand, the records of Vibrio species in ballast water (McCarthy & Khambaty 1994: Ruiz et al. 2000; Drake et al. 2005), the propensity for Vibrio species to attach in high numbers to copepods and other invertebrates that are abundant in ballast water (Hug et al. 2001; Lipp et al. 2002), and the occurrence of at least Vibrio species in small invertebrates that may act as both disease reservoirs and as vectors for transport in ballast water (V. shiloi in the marine fireworm Hermodice carunculata—Sussman et al. 2003), suggest that ballast water is also a possible transport mechanism.

In recent decades there has been a confusing proliferation of coral diseases and syndromes involving the loss of coral tissue and the destruction or ejection or symbiotic zooxanthellae, which have had devastating effects of coral populations and coral reef structures, initially concentrated in the Caribbean region but increasingly reported from other parts of the world. Many of these are caused or are suspected of being caused by bacterial agents (Table 14). In five cases causation has been demonstrated by fulfillment of Koch's postulates (White Pox and White Plague Type II in the Caribbean, White Plague-like disease in the Red Sea, and bacterial bleaching in the Mediterranean Sea and in the Indo-Pacific region). In other cases, where a microbial consortium or a non-culturable bacterium may be the cause of disease, fulfilling Koch's postulates may be infeasible or impossible, and other approaches are being developed to determine etiology (Sussman *et al.* 2008; Sussman 2009). It is generally accepted that Yellow Band Disease is caused by a consortium of *Vibrio* bacteria, and that Black Band Disease is caused by members of a highly complex microbial consortium, though which members is unclear. For several other diseases there is an association between disease lesions and concentrations of certain bacterial species (Table 14), suggesting that these bacteria contribute to the disease, although they could also be opportunistic attackers of coral tissue that has been weakened by disease. *Vibrio harveyi*, or bacteria

Disease	Location	Coral Hosts	Agent(s)	Reference			
DISEASES CAUSED BY BACTERIAL AGENT(S)							
White Pox	Caribbean	Acropora palmata	Serratia marcescens	Patterson <i>et al.</i> 2002			
White Plague Type II	Caribbean	many species	Aurantimonas coralicida	Denner <i>et al.</i> 2003			
White-Plague-like disease	Red Sea	<i>Favia</i> spp., <i>Goniastre</i> a spp.	Thalassomonas loyana	Thompson <i>et al.</i> 2006			
Bacterial Bleaching	Mediterranean Sea	Oculina patagonica	Vibrio shiloi	Kushmaro <i>et al.</i> 1996			
Bacterial Bleaching; White Syndrome (part)	Indo-Pacific	several species	Vibrio coralliilyticus	Ben Haim <i>et al.</i> 2003a; Sussman <i>et al.</i> 2008			
DISEASES PROBABLY CAUSED BY BACTERIAL AGENT(S)							
Black Band Disease	Caribbean, Indo-Pacific	many species	bacterial consortium	Frias-Lopez <i>et al.</i> 2003, 2004			
Yellow Band Disease	Caribbean, Pacific	several species	<i>Vibrio</i> consortium	Cervino <i>et al</i> . 2008			
DISEASES THAT MAY E	BE CAUSED, FAG	CILITATED OR EN	HANCED BY BAC	TERIAL AGENT(S)			
White Band Disease Type II	Caribbean	Acropora spp.	<i>Vibrio harveyi</i> complex	Gil-Agudelo <i>et al.</i> 2006			
Rapid Tissue Necrosis; White Syndrome (part)	Indo-Pacific	Pocillopora damicornis	<i>Vibrio harveyi</i> complex	Luna <i>et al.</i> 2007, 2010			
Dark Spots Disease	Caribbean	several species	<i>Vibrio harveyi</i> complex	Gil-Agudelo <i>et al.</i> 2007			
Red Band Disease	Caribbean	several species	unknown bacteria	Richardson 1992			
Atramentous Necrosis	Great Barrier Reef	Montipora aequituberculata	unknown bacteria	Sussman 2009, citing Bourne 2005			

Table 14. Coral diseases with known or suspected bacterial agents.

very closely related to *V. harveyi*, are implicated in two or three of these²⁹, and other *Vibrio* species are the cause of three additional diseases. Whether viruses are involved in any coral disease is not known, and little studied (Rosenberg *et al.* 2007).

Our very limited knowledge regarding the pathogens that cause coral disease—for most coral diseases these have not even been identified—makes it difficult to assess the potential for ballast water transport. The distribution of coral diseases suggests the possibility that some disease introductions may have already occurred (Cervino *et al.* 2008; Sussman 2009), whether by ballast water or other means. Clearly bacteria, particularly including *Vibrio* species, are transported in ballast water in substantial numbers and have multiple mechanisms for transport in ballast tanks. Whether coral diseases caused by microbial consortiums are capable of being transported to a new region without a coral host—and whether one or all members of a consortium must be introduced in order to initiate disease—is unknown.

Seagrass Pathogens. There is only one ESA seagrass species, Johnson's seagrass *Halophila johnsonii*, which is found only in southeastern Florida from Sebastian Inlet to Biscayne Bay (Kenworthy 1997). Disease is not considered to be a threat to this species (Kenworthy 1997; NMFS 2002; Kenworthy *et al.* 2007; NOAA 2010b). However, male flowers are not known in this species nor have any seeds or seedlings been found, so it is only known to reproduce vegetatively (Kenworthy 1997; Kenworthy *et al.* 2007). The species has low genetic diversity and a high degree of clonality (Freshwater & York 1999; Freshwater 2004; Kenworthy *et al.* 2007), which could make it especially vulnerable to an introduced pathogen.

The literature on seagrass disease is dominated by papers on eelgrass wasting disease, which struck Zostera marina on the U.S. Atlantic coast in the 1930s, eliminating over 95% of the population (Short et al. 1988). It also appeared in Europe and on the U.S. Pacific Coast, showed up in New Zealand in the 1960s, and in Atlantic North America again in the 1980s (Short et al. 1987, 1988; Steele et al. 2005). Eelgrass wasting disease is caused by a marine slime mold, Labyrinthula zosterae (Short et al. 1987; Muehlstein et al. 1988, 1991). A die-off of Thalassia testudinum in Florida Bay in the late 1980s, with the complete loss of T. testudinum from 10,000 acres and substantial reductions over another 57,000 acres, is also thought to have been caused by a Labyrinthula species (Robblee et al. 1991; Steele et al. 2005). The marine fungus Lindra thalassiae causes 'Thalassia disease' on T. testudinum (and also "raisin disease" on the brown alga Sargassum) (Orpurt et al. 1964; Kohlmeyer 1971; Ross et al. 2008). There appear to be no reports of any seagrass diseases caused by bacteria or viruses, although of course these might exist undetected. With no information about such diseases, if they exist, there is little that can be said about the potential for ballast transport. However, it is worth noting that there is some potential for ballast water transport of seagrass diseases within their hosts if small pieces of seagrass are entrained in ballast waters.

²⁹ It is possible that White Band Disease Type II of the Caribbean is the same as some occurrences of the disease that has been called either Rapid Tissue Necrosis or White Syndrome in the Indo-Pacific region.

Conclusions

When naive animal or plant populations are exposed to novel, introduced pathogens, the virulence and impacts of resulting disease can greatly exceed those found in the pathogen's natural host. Our knowledge of the diseases of marine and estuarine organisms is still guite limited, and often predominantly based on species that are maintained in captivity or used in aquaculture. Nevertheless, it is clear that there are many bacterial and viral pathogen strains present in other parts of the world which, if they were introduced into the U.S. ranges of NOAA ESA species and infected those species, could cause them grave harm. As discussed in this report, there are many serious bacterial and viral diseases of cetaceans, pinnipeds, sea turtles, fish and abalone; several devastating bacterial diseases of corals, though no known viral diseases; and apparently no known bacterial or viral diseases of sea grasses (Table 15). Some of the more notable examples are the morbillivirus infections of cetaceans and pinnipeds, emerging diseases whose distributions suggest they are spreading to new regions of the world; fibropapillomatosis of sea turtles, which is believed to be caused by a virus; viral hemorrhagic septicemia of fish, recently introduced into the Great Lakes (possibly in ballast water) where it has caused mass mortalities in numerous fish species; abalone withering syndrome, a primary factor in the decline of the endangered black abalone, which is caused by a bacterium that appears to have been introduced into the black abalone's range; and several bacterial diseases of coral, caused in some cases by single species of bacteria and in others by bacterial consortia. and whose recent emergence and spread may in part be due to introductions.

It is also clear that bacteria and viruses are routinely present in ballast water in substantial numbers, and that in some cases these include pathogens that can infect the types of animals that comprise NOAA's ESA species. It is less clear whether these pathogens are transported and discharged in ballast water in numbers that could reasonably be expected to result in infections in ESA species. While some bacterial or viral pathogens have substantial capacity to survive outside of their hosts for extended periods in fresh water or sea water, others rapidly decline. However, there are other modes of transport within ballast tanks that would allow more sustained transport of bacterial or viral pathogens. Some pathogens are more stable in sediments or biofilms, which are typically present in ballast tanks. At least some, and possibly many, potential pathogens of ESA species have alternative hosts or mechanical vectors that are small enough to be successfully transported in ballast water, and some main hosts (e.g. of fish pathogens) may also be small enough to travel in ballast tanks. Examples would include the fish virus VHSV which infects (among many other species) gobies and stickleback, which are small fish that are commonly transported in ballast water; and the various species of Vibrio bacteria that cause disease in sea turtles, fish, abalone or corals (Table 15), which are commonly transported in ballast water in concentrated numbers attached to the chitinous shells of copepods or in the mucilaginous sheaths of

Taxonomic Group	Bacterial Pathogens	Viral Pathogens		
Cetaceans	Pseudomonas, Erysipelothrix, Klebsiella, Brucella, Edwardsiella, Salmonella	Dolphin Morbillivirus (DMV), Porpoise Morbillivirus (PMV), Pilot Whale Morbillivirus (PWMV), poxvirus, papilloma virus		
Pinnipeds	Pseudomonas, Brucella, Edwardsiella, Salmonella, Klebsiella, Leptospira	Phocine Distemper Virus (PDV), Monk Seal Morbillivirus (MSMV), Sea Lion Hepatitis Virus, Seal Herpesvirus, San Miguel Sea Lion Virus, Seal Pox		
Turtles	Vibrio alginolyticus, Aeromonas hydrophila, Flavobacterium, Mycobacterium, Pseudomonas, Salmonella enteridis	Fibropapilloma-associated Turtle Herpesvirus (FPTHV), Lung-Eye-Trachea Virus, Gray Patch Virus, Loggerhead Genital-Respiratory Herpesvirus, Loggerhead Orocutaneous Herpesvirus		
Fish	Aeromonas salmonicida subsp. salmonicida & atypical strains, Listonella anguillarum, Vibrio salmonicida, Moritella viscosa, Renibacterium salmoninarum, Piscirickettsia salmonis	Viral Hemorrhagic Septicemia Virus (VHSV), Epizootic Hematopoietic Necrosis Virus (EHNV), Infectious Hematopoietic Necrosis Virus (IHNV), Infectious Pancreatic Necrosis Virus (IPNV), Infectious Salmon Anemia Virus (ISAV), Koi Herpesvirus (KHV)		
Abalone	Xenohaliotis californiensis, Vibrio harveyi, Vibrio carchariae, Vibrio fluvialis II, Vibrio parahaemolyticus, Vibrio alginolyticus, Vibrio splendidus I, Flavobacterium-like bacterium, Klebsiella oxytoca	Abalone Viral Ganglioneritis (AVG), possibly the amyotrophia pathogen		
Corals	Vibrio shiloi, Vibrio coralliilyticus, Vibrio harveyi, Vibrio proteolyticus, Vibrio rotiferianus, Vibrio alginolyticus, Aurantimonas coralicida, Thalassomonas loyana, Serratia marcescens, and the bacteria that cause Black Band, Red Band and Atramentous Necrosis Disease	None known.		
Seagrasses	None known.	None known.		

Table 15. Examples of known or suspected bacterial and viral pathogens of ESA species groups.

phytoplankton, which are themselves often abundant in ballast water. Transported in ballast water in these alternative hosts or vectors, pathogens would be more likely to reach potential hosts in sufficient concentrations to deliver infective doses. As described in this report, there are a few known outbreaks of human or animal disease that may have resulted from the transport of bacterial or viral pathogens in ballast water.

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Appendix 1. ESA-listed species under NMFS' jurisdiction that do not occur in U.S. waters

Habitat: M = Marine, E = Estuarine, F = Freshwater

Sources: NOAA 2010a,b.

Family	Common Name	Scientific Name	Listing Status	Habitat	Range
CETACEANS					
Balaenidae	Southern Right Whale	Eubalaena australis	Endangered	М	Southern hemisphere
Eschrichtiidae	Gray Whale, Western North Pacific DPS	Eschrichtius robustus	Endangered	ME	Western Pacific
Lipotidae	Chinese River Dolphin/Baiji	Lipotes vexillifer	Endangered	F	Yangtze River, China
Phocoenidae	Gulf of California Harbor Porpoise/Vaquita	Phocoena sinus	Endangered	ME	Gulf of California
Platanistidae	Indus River Dolphin	Planista minor	Endangered	EF	Indus River, Pakistan
PINNIPEDS					
Phocidae	Mediterranean Monk Seal	Monachus monachus	Endangered	М	Mediterranean Sea & East Atlantic Ocean
Phocidae	Saimaa Seal	Phoca hispida saimensis	Endangered	F	Lake Saimaa, Finland
Phocidae	Spotted Seal, Southern DPS	Phoca largha	Proposed	М	Northwestern Pacific
FISH					
Sciaenidae	Totoaba	Totoaba macdonaldi	Endangered	ME	Gulf of California

Appendix 2. ESA-listed species under NMFS' jurisdiction that occur in U.S. waters

Habitat: M = Marine, E = Estuarine, F = Freshwater

Sources: CBD 2009; NOAA 2010a,b.

Family	Common Name	Scientific Name	Listing Status	Habitat	Range
CETACEANS					
Balaenidae	Bowhead Whale	Balaena mysticetus	Endangered	М	Arctic
Balaenidae	North Atlantic Right Whale	Eubalaena glacialis	Endangered	М	North Atlantic
Balaenidae	North Pacific Right Whale	Eubalaena japonica	Endangered	М	North Pacific
Balaenopteridae	Blue Whale	Balaenoptera musculus	Endangered	М	worldwide
Balaenopteridae	Fin Whale	Balaenoptera physalus	Endangered	М	Atlantic, Pacific & Southern Oceans
Balaenopteridae	Humpback Whale	Megaptera novaeangliae	Endangered	М	worldwide
Balaenopteridae	Sei Whale	Balaenoptera borealis	Endangered	М	worldwide
Monodontidae	Beluga Whale, Cook Inlet DPS	Delphinapterus Ieucas	Endangered	MEF	Pacific Coast
Physeteridae	Sperm Whale	Physeter macrocephalus	Endangered	М	worldwide
Delphinidae	Killer Whale, Southern Resident DPS	Orcinus orca	Endangered	М	Pacific Coast
Delphinidae	False Killer Whale, Insular Hawaiian DPS	Pseudorca crassidens	Candidate	М	Hawaii
PINNIPEDS					
Otariidae	Guadalupe Fur Seal	Arctocephalus townsendi	Threatened	М	Pacific Coast
Otariidae	Stellar Sea Lion, Eastern DPS	Eumetopias jubatus	Threatened	М	Pacific Coast
Otariidae	Stellar Sea Lion, Western DPS	Eumetopias jubatus	Endangered	М	Western Pacific including western Aleutians
Phocidae	Hawaiian Monk Seal	Monachus schauinslandi	Endangered	М	Hawaii
Phocidae	Ringed Seal	Phoca hispida	Candidate	М	circumpolar north of 35°
Phocidae	Bearded Seal	Erignathus barbatus	Candidate	М	Arctic

Family	Common Name	Scientific Name	Listing Status	Habitat	Range
SEA TURTLES					
Cheloniidae	Green Turtle, Florida & Mexico's Pacific coast breeding colonies	Chelonia mydas	Endangered	ME	Atlantic, Gulf & Pacific Coasts
Cheloniidae	Green Turtle, all other areas	Chelonia mydas	Threatened	ME	worldwide in tropical/temperate waters
Cheloniidae	Hawksbill Turtle	Eretmochelys imbricata	Endangered	ME	worldwide in tropical waters
Cheloniidae	Kemp's Ridley Turtle	Lepidochelys kempii	Endangered	М	Atlantic & Gulf Coasts
Cheloniidae	Loggerhead Turtle	Caretta caretta	Threatened*	ME	worldwide in tropical/temperate waters
Cheloniidae	Olive Ridley Turtle, Mexico's Pacific coast breeding colonies	Lepidochelys olivacea	Endangered	ME	Pacific Coast
Cheloniidae	Olive Ridley Turtle, all other areas	Lepidochelys olivacea	Threatened	ME	worldwide in tropical waters
Dermochelyidae	Leatherback Turtle	Dermochelys coriacea	Endangered	М	worldwide in tropical/temperate waters
FISH					
Salmonidae	Atlantic Salmon, Gulf of Maine DPS	Salmo salar	Endangered	MEF	Atlantic Coast
Salmonidae	Chinook Salmon, California coastal ESU	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Central Valley spring-run	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Sacramento River winter-run	Oncorhynchus tshawytscha	Endangered	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Lower Columbia River	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Upper Columbia River spring-run	Oncorhynchus tshawytscha	Endangered	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Upper Willamette River	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Snake River fall-run	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast
Salmonidae	Chinook Salmon, Snake River spring/summer-run	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast

Family	Common Name	Scientific Name	Listing Status	Habitat	Range
FISH - continued					
Salmonidae	Chinook Salmon, Puget Sound	Oncorhynchus tshawytscha	Threatened	MEF	Pacific Coast
Salmonidae	Chum Salmon, Columbia River	Oncorhynchus keta	Threatened	MEF	Pacific Coast
Salmonidae	Chum Salmon, Hood Canal summer-run	Oncorhynchus keta	Threatened	MEF	Pacific Coast
Salmonidae	Coho Salmon, Central California coast	Oncorhynchus kisutch	Endangered	MEF	Pacific Coast
Salmonidae	Coho Salmon, Southern Oregon & Northern California coasts	Oncorhynchus kisutch	Threatened	MEF	Pacific Coast
Salmonidae	Coho Salmon, Oregon Coast	Oncorhynchus kisutch	Threatened	MEF	Pacific Coast
Salmonidae	Coho Salmon, Lower Columbia River	Oncorhynchus kisutch	Threatened	MEF	Pacific Coast
Salmonidae	Sockeye Salmon, Ozette Lake	Oncorhynchus nerka	Threatened	MEF	Pacific Coast
Salmonidae	Sockeye Salmon, Snake River	Oncorhynchus nerka	Endangered	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Southern California	Oncorhynchus mykiss	Endangered	MEF	Pacific Coast
Salmonidae	Steelhead Trout, South-Central California coast	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Central California coast	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, California Central Valley	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Northern California	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Lower Columbia River	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Middle Columbia River	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Upper Columbia River	Oncorhynchus mykiss	Endangered	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Upper Willamette River	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Salmonidae	Steelhead Trout, Snake River basin	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast

Family	Common Name	Scientific Name	Listing Status	Habitat	Range
FISH - continued					
Salmonidae	Steelhead Trout, Puget Sound	Oncorhynchus mykiss	Threatened	MEF	Pacific Coast
Acipenseridae	Atlantic Sturgeon	Acipenser oxyrinchus oxyrinchus	Candidate	MEF	Atlantic Coast
Acipenseridae	Shortnose Sturgeon	Acipenser brevirostrum	Endangered	MEF	Atlantic Coast
Acipenseridae	Gulf Sturgeon	Acipenser oxyrinchus desotoi	Threatened	MEF	Gulf Coast
Acipenseridae	Green Sturgeon, southern DPS	Acipenser medirostris	Threatened	MEF	Pacific Coast
Sebastidae	Bocaccio, Puget Sound/Georgia Basin DPS	Sebastes paucispinis	Proposed	М	Pacific Coast
Sebastidae	Canary Rockfish, Puget Sound/Georgia Basin DPS	Sebastes pinniger	Proposed	М	Pacific Coast
Sebastidae	Yelloweye Rockfish, Puget Sound/Georgia Basin DPS	Sebastes ruberrimus	Proposed	М	Pacific Coast
Pristidae	Smalltooth Sawfish, United States DPS	Pristis pectinata	Endangered	ME	Atlantic & Gulf Coast
Pristidae	Largetooth Sawfish	Pristis perotetti	Candidate	MEF	Gulf Coast, Central & South America
Lotidae	Cusk	Brosme brosme	Candidate	Μ	Atlantic Coast
Clupeidae	Pacific Herring, Southeast Alaska DPS	Clupea pallasi	Candidate	ME	Pacific Coast
Osmeridae	Pacific Eulachon/Smelt, Southern DPS	Thaleichthys pacificus	Proposed	MEF	Pacific Coast
MOLLUSKS					
Haliotidae	Black Abalone	Haliotis cracherodii	Endangered	Μ	Pacific Coast
Haliotidae	White Abalone	Haliotis sorenseni	Endangered	М	Pacific Coast
CORALS					
Acroporidae	Elkhorn Coral	Acropora palmata	Threatened	М	Caribbean
Acroporidae	Staghorn Coral	Acropora cervicornis	Threatened	М	Caribbean
Acroporidae	Fuzzy Table Coral	Acropora paniculata	Candidate	Μ	Hawaii
Acroporidae	Hawaiian Reef Coral	Montipora dilatata	Candidate	М	Hawaii
Acroporidae	Blue Rice Coral	Montipora flabellata	Candidate	М	Hawaii
Acroporidae	Sandpaper Rice Coral	Montipora patula	Candidate	М	Hawaii
Acroporidae		Acropora aculeus	Candidate	М	Indo-Pacific

Family	Common Name	Scientific Name	Listing Status	Habitat	Range		
CORALS - continu	CORALS - continued						
Acroporidae		Acropora acuminata	Candidate	Μ	Indo-Pacific		
Acroporidae		Acropora aspera	Candidate	М	Indo-Pacific		
Acroporidae		Acropora dendrum	Candidate	М	Indo-Pacific		
Acroporidae		Acropora donei	Candidate	М	Indo-Pacific		
Acroporidae		Acropora globiceps	Candidate	М	Indo-Pacific		
Acroporidae		Acropora horrida	Candidate	М	Indo-Pacific		
Acroporidae		Acropora jacquelineae	Candidate	М	Indo-Pacific		
Acroporidae		Acropora listeri	Candidate	М	Indo-Pacific		
Acroporidae		Acropora lokani	Candidate	М	Indo-Pacific		
Acroporidae		Acropora microclados	Candidate	М	Indo-Pacific		
Acroporidae		Acropora palmerae	Candidate	М	Indo-Pacific		
Acroporidae		Acropora pharaonis	Candidate	М	Indo-Pacific		
Acroporidae		Acropora polystoma	Candidate	М	Indo-Pacific		
Acroporidae		Acropora retusa	Candidate	М	Indo-Pacific		
Acroporidae		Acropora rudis	Candidate	М	Indo-Pacific		
Acroporidae		Acropora speciosa	Candidate	М	Indo-Pacific		
Acroporidae		Acropora striata	Candidate	М	Indo-Pacific		
Acroporidae		Acropora tenella	Candidate	М	Indo-Pacific		
Acroporidae		Acropora vaughani	Candidate	М	Indo-Pacific		
Acroporidae		Acropora verweyi	Candidate	М	Indo-Pacific		
Acroporidae		Anacropora puertogalerae	Candidate	М	Indo-Pacific		
Acroporidae		Anacropora spinosa	Candidate	М	Indo-Pacific		
Acroporidae		Astreopora cucullata	Candidate	М	Indo-Pacific		
Acroporidae		Isopora crateriformis	Candidate	М	Indo-Pacific		
Acroporidae		Isopora cuneata	Candidate	Μ	Indo-Pacific		
Acroporidae		Montipora angulata	Candidate	М	Indo-Pacific		
Acroporidae		Montipora australiensis	Candidate	М	Indo-Pacific		
Acroporidae		Montipora calcarea	Candidate	М	Indo-Pacific		
Acroporidae		Montipora caliculata	Candidate	М	Indo-Pacific		
Acroporidae		Montipora lobulata	Candidate	М	Indo-Pacific		
Agaricidae	Lamarck's Sheet Coral	Agaricia lamarcki	Candidate	М	Caribbean		

Family	Common Name	Scientific Name	Listing Status	Habitat	Range
CORALS - contin	ued				
Agaricidae		Leptoseris incrustans	Candidate	М	Hawaii
Agaricidae		Leptoseris yabei	Candidate	М	Indo-Pacific
Agaricidae		Pachyseris rugosa	Candidate	М	Indo-Pacific
Agaricidae		Pavona bipartita	Candidate	М	Indo-Pacific
Agaricidae		Pavona cactus	Candidate	М	Indo-Pacific
Agaricidae		Pavona decussata	Candidate	М	Indo-Pacific
Agaricidae		Pavona diffluens	Candidate	М	Indo-Pacific
Agaricidae		Pavona venosa	Candidate	М	Indo-Pacific
Faviidae	Boulder Star Coral	Montastraea annularis	Candidate	М	Caribbean
Faviidae	Mountainous Star Coral	Montastraea faveolata	Candidate	М	Caribbean
Faviidae		Montastraea franksi	Candidate	М	Caribbean
Faviidae	Agassiz's Coral	Cyphastrea agassizi	Candidate	М	Hawaii
Faviidae	Ocellated Coral	Cyphastrea ocellina	Candidate	М	Hawaii
Faviidae		Barabattoia laddi	Candidate	М	Indo-Pacific
Faviidae		Caulastrea echinulata	Candidate	М	Indo-Pacific
Meandrinidae		Dendrogyra cylindrus	Candidate	М	Caribbean
Meandrinidae	Elliptical Star Coral	Dichocoenia stokesii	Candidate	М	Caribbean
Mussidae		Mycetophyllia ferox	Candidate	М	Caribbean
Mussidae		Acanthastrea brevis	Candidate	М	Indo-Pacific
Mussidae		Acanthastrea hemprichii	Candidate	М	Indo-Pacific
Mussidae		Acanthastrea ishigakiensis	Candidate	М	Indo-Pacific
Mussidae		Acanthastrea regularis	Candidate	М	Indo-Pacific
Mussidae		Pocillopora danae	Candidate	М	Indo-Pacific
Mussidae		Pocillopora elegans	Candidate	М	Indo-Pacific
Mussidae		Seriatopora aculeata	Candidate	М	Indo-Pacific
Oculinidae		Galaxea astreata	Candidate	М	Indo-Pacific
Poritidae		Porites pukoensis	Candidate	М	Hawaii
Poritidae		Alveopora allingi	Candidate	М	Indo-Pacific
Poritidae		Alveopora fenestrata	Candidate	М	Indo-Pacific
Family	Common Name	Scientific Name	Listing Status	Habitat	Range
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CORALS - continu	ued				
Poritidae		Alveopora verrilliana	Candidate	М	Indo-Pacific
Poritidae		Porites horizontalata	Candidate	М	Indo-Pacific
Poritidae		Porites napopora	Candidate	М	Indo-Pacific
Poritidae		Porites nigrescens	Candidate	М	Indo-Pacific
Siderastreidae	Stellar Coral	Psammocora stellata	Candidate	М	Hawaii
Dendrophyllidae		Turbinaria mesenterina	Candidate	М	Indo-Pacific
Dendrophyllidae		Turbinaria peltata	Candidate	М	Indo-Pacific
Dendrophyllidae		Turbinaria reniformis	Candidate	М	Indo-Pacific
Dendrophyllidae		Turbinaria stellula	Candidate	М	Indo-Pacific
Euphyllidae		Euphyllia cristata	Candidate	М	Indo-Pacific
Euphyllidae		Euphyllia paraancora	Candidate	М	Indo-Pacific
Euphyllidae		Euphyllia paradivisa	Candidate	М	Indo-Pacific
Euphyllidae		Physogyra lichtensteini	Candidate	М	Indo-Pacific
Pectinidae		Pectinia alcicornis	Candidate	М	Indo-Pacific
Helioporidae		Heliopora coerulea	Candidate	М	Indo-Pacific
Milleporidae		Millepora foveolata	Candidate	М	Indo-Pacific
Milleporidae		Millepora tuberosa	Candidate	М	Indo-Pacific
PLANTS					
Hydrocharitaceae	Johnson's Seagrass	Halophila johnsonii	Threatened	ME	Atlantic Coast

* Seven populations of Loggerhead Turtle have been proposed for listing as endangered (Mediterranean Sea, North Indian Ocean, North Pacific Ocean, Northeast Atlantic Ocean, Northwest Atlantic Ocean, South Pacific Ocean and Southeast Indo-Pacific Ocean populations).

Appendix 3. ESA-listed species under NMFS' jurisdiction that occur in U.S. waters, by coastal regions

Regions:	EC = East Coast	GM = Gulf of Mexico	CR = Caribbean	
-	AK = Alaska	WC = West Coast	HI = Hawaii	PI = Pacific Islands

Caribbean region includes Puerto Rico, the U.S. Virgin Islands and Navassa Island.

Hawaii region includes the Hawaiian Islands and Midway Island.

Pacific Islands region include Guam, the Northern Mariana Islands, American Samoa, Johnston Atoll, Wake Island, Howland Island, Baker Island, Palmyra Atoll, Kingman Reef and Jarvis Island.

Sources: CBD 2009; NOAA 2010b.

Species		Atlantic Ocean			Pacific Ocean			
opecies	EC	GM	CR	AK	WC	HI	ΡI	
CETACEANS								
Bowhead Whale				Х				
North Atlantic Right Whale	Х							
North Pacific Right Whale				Х	Х			
Blue Whale	Х	Х	Х	Х	Х	Х	Х	
Fin Whale	Х	Х	Х	Х	Х	Х	Х	
Humpback Whale	Х	Х	Х	Х	Х	Х	Х	
Sei Whale	Х				Х			
Beluga Whale, Cook Inlet DPS				Х				
Sperm Whale	Х	Х	Х	Х	Х	Х	Х	
Killer Whale, Southern Resident DPS					Х			
False Killer Whale, Insular Hawaiian DPS						Х		
PINNIPEDS								
Guadalupe Fur Seal					Х			
Stellar Sea Lion, Eastern DPS				Х	Х			
Stellar Sea Lion, Western DPS				Х				
Hawaiian Monk Seal						Х		
Ringed Seal				Х				
Bearded Seal				Х				
TURTLES								
Green Turtle, Florida & Mexico Pacific coast breeding colonies	Х	Х	Х	Х	Х			
Green Turtle, all other areas						Х	Х	
Hawksbill Turtle		Х	Х		Х	Х	Х	
Kemp's Ridley Turtle		Х	Х					
Loggerhead Turtle		Х	Х		Х	Х	Х	
Olive Ridley Turtle, Mexico Pacific coast breeding colonies					Х			
Olive Ridley Turtle, all other areas			Х		Х	Х		
Leatherback Turtle	Х	Х	Х	Х	Х	Х	Х	

Oracia		Atlantic Ocean		Pacific Ocean			
Species	EC	GM	CR	AK	WC	ні	ΡI
FISH							
Atlantic Salmon, Gulf of Maine DPS	х						
Chinook Salmon, California coastal ESU					Х		
Chinook Salmon, Central Valley spring-run					Х		
Chinook Salmon, Sacramento River winter-run					Х		
Chinook Salmon, Lower Columbia River					Х		
Chinook Salmon, Upper Columbia River spring-run					Х		
Chinook Salmon, Upper Willamette River					Х		
Chinook Salmon, Snake River fall-run					Х		
Chinook Salmon, Snake River spring/summer-run					Х		
Chinook Salmon, Puget Sound					Х		
Chum Salmon, Columbia River					Х		
Chum Salmon, Hood Canal summer-run					Х		
Coho Salmon, Central California coast					Х		
Coho Salmon, Southern Oregon & Northern California coasts					Х		
Coho Salmon, Oregon Coast					Х		
Coho Salmon, Lower Columbia River					Х		
Sockeye Salmon, Ozette Lake					Х		
Sockeye Salmon, Snake River					Х		
Steelhead Trout, Southern California					Х		
Steelhead Trout, South-Central California coast					Х		
Steelhead Trout, Central California coast					Х		
Steelhead Trout, California Central Valley					Х		
Steelhead Trout, Northern California					Х		
Steelhead Trout, Lower Columbia River					Х		
Steelhead Trout, Middle Columbia River					Х		
Steelhead Trout, Upper Columbia River					Х		
Steelhead Trout, Upper Willamette River					Х		
Steelhead Trout, Snake River basin					Х		
Steelhead Trout, Puget Sound					Х		
Atlantic Sturgeon	Х						
Shortnose Sturgeon	Х						
Gulf Sturgeon		Х					
Green Sturgeon, southern DPS				Х	Х		
Bocaccio, Puget Sound/Georgia Basin DPS					Х		
Canary Rockfish, Puget Sound/Georgia Basin DPS					Х		
Yelloweye Rockfish, Puget Sound/Georgia Basin DPS					Х		
Smalltooth Sawfish, United States DPS	Х	Х					
Largetooth Sawfish		Х					

Oracias	Atlantic Ocean			Pacific Ocean			
Species	EC	GM	CR	AK	WC	HI	Ы
FISH - continued							
Cusk	х						
Pacific Herring, Southeast Alaska DPS				х			
Pacific Eulachon/Smelt, Southern DPS					Х		
MOLLUSKS							
Black Abalone					Х		
White Abalone					Х		
CORALS							
Acropora cervicornis	х		Х				
Acropora palmata	х		Х				
Agaricia lamarcki	х	Х	Х				
Montastraea annularis	Х	Х	Х				
Montastraea faveolata	Х	Х	Х				
Montastraea franksi	Х	Х	Х				
Dendrogyra cylindrus	Х	Х	Х				
Dichocoenia stokesii	Х	Х	Х				
Mycetophyllia ferox	х	Х	Х				
Acropora paniculata						х	Х
Montipora dilatata						Х	
Montipora flabellata						Х	
Montipora patula						Х	Х
Leptoseris incrustans						Х	Х
Cyphastrea agassizi						Х	Х
Cyphastrea ocellina						Х	Х
Porites pukoensis						Х	
Psammocora stellata						Х	
Acropora aculeus							Х
Acropora acuminata							Х
Acropora aspera							Х
Acropora dendrum							Х
Acropora donei							Х
Acropora globiceps							Х
Acropora horrida							Х
Acropora jacquelineae							Х
Acropora listeri							Х
Acropora lokani							Х
Acropora microclados							Х
Acropora palmerae							Х

Spacing	Atla	Atlantic Ocean			Pacific Ocean		
Shecies	EC	GM	CR	AK	WC	HI	ΡI
CORALS - continued							
Acropora pharaonis							Х
Acropora polystoma							Х
Acropora retusa							Х
Acropora rudis							Х
Acropora speciosa							Х
Acropora striata							Х
Acropora tenella							Х
Acropora vaughani							Х
Acropora verweyi							Х
Anacropora puertogalerae							Х
Anacropora spinosa							Х
Astreopora cucullata							Х
Isopora crateriformis							Х
Isopora cuneata							Х
Montipora angulata							Х
Montipora australiensis							Х
Montipora calcarea							Х
Montipora caliculata							Х
Montipora lobulata							Х
Leptoseris yabei							Х
Pachyseris rugosa							Х
Pavona bipartita							Х
Pavona cactus							Х
Pavona decussata							Х
Pavona diffluens							Х
Pavona venosa							Х
Barabattoia laddi							Х
Caulastrea echinulata							Х
Acanthastrea brevis							Х
Acanthastrea hemprichii							Х
Acanthastrea ishigakiensis							Х
Acanthastrea regularis							Х
Pocillopora danae							Х
Pocillopora elegans							Х
Seriatopora aculeata							Х
Galaxea astreata							Х
Alveopora allingi							Х
Alveopora fenestrata							Х

Species	Atlantic Ocean			Pacific Ocean			
Shecies	EC	GM	CR	AK	WC	HI	ΡI
CORALS - continued							
Alveopora verrilliana						Х	Х
Porites horizontalata							Х
Porites napopora							Х
Porites nigrescens							Х
Turbinaria mesenterina							Х
Turbinaria peltata							Х
Turbinaria reniformis							Х
Turbinaria stellula							Х
Euphyllia cristata							Х
Euphyllia paraancora							Х
Euphyllia paradivisa							Х
Physogyra lichtensteini							Х
Pectinia alcicornis							Х
Heliopora coerulea							Х
Millepora foveolata							Х
Millepora tuberosa							Х
PLANTS							
Johnson's Seagrass	Х						

Virus	Temperature	Period	End Status	Source
Viral Hemorrhagic Septi	cemia Virus VHS	6		
fresh water	4°C	5 d	survival	Kipp & Ricciardi 2001
fresh water	4°C	months	0.1% survival	PAHW 2007
fresh water	4°C	up to 28-35 d	survival	Parry & Dixon 1997
fresh water [1]	12°C	1 h	2% survival	Winton <i>et al.</i> 1991
fresh water [2]	12°C	1 h	0.5% survival	Winton <i>et al.</i> 1991
fresh water	15°C	13 d	0.1% survival	Hawley & Garver 2008
fresh water	20°C	≈28 d	0.1% survival	PAHW 2007
fresh water	20°C	60 d	survival	Mori <i>et al.</i> 2002
fresh water	25°C	40 d	survival	Mori <i>et al.</i> 2002
fresh water-filtered	4°C	up to >1 y	infective	Hawley & Garver 2008
tap water	10°C	49 d	survival	Ahne 1982
sea water	4°C	7-21 d	survival	Parry & Dixon 1997
sea water	4°C	up to 25 d	survival	Mori <i>et al.</i> 2002
sea water	4°C	10 mon	infective	CFSPH 2007
3% NaCl solution [1]	12°C	1 h	50% survival	Winton <i>et al.</i> 1991
3% NaCl solution [2]	12°C	1 h	10% survival	Winton <i>et al.</i> 1991
sea water	15°C	4 d	0.1% survival	Hawley & Garver 2008
sea water	15°C	a few days	survival	Mori <i>et al.</i> 2002
sea water	15-20°C	<7 d	survival	Parry & Dixon 1997
sea water-sterile [3]	15°C	0.5 d	50% survival	Kocan <i>et al.</i> 2001
sea water-sterile [3]	15°C	1.5 d	10% survival	Kocan <i>et al.</i> 2001
sea water-sterile [4]	15°C	60 d	survival	Mori <i>et al.</i> 2002
sea water-sterile [4]	20°C	32 d	survival	Mori <i>et al.</i> 2002
sea water-enriched [5]	15°C	4 d	20% survival	Kocan <i>et al.</i> 2001
sea water-enriched [6]	15°C	4 d	≈100% survival	Kocan <i>et al.</i> 2001
sea water-enriched [7]	15°C	15 d	≈100% survival	Kocan <i>et al.</i> 2001
sea water-enriched [7]	15°C	36 d	55% survival	Kocan <i>et al.</i> 2001
mud	4°C	10 d	stable	Ahne 1982

Appendix 4. Some data on the survival of fish viruses in water and mud

[1] European (F1) isolate
[2] Northwestern Pacific (Makah) isolate

[5] 5 μ m-filtered and UV, with 0.1% ovarian fluid added [6] 5 μ m-filtered and UV, with 1% ovarian fluid added

[3] 5 µm-filtered and UV

[4] 0.22 µm filtered

[7] 5 µm-filtered and UV, with culture medium added

[8] 0.45 µm-filtered

Virus	Temperature	Period	End Status	Source
Infectious Haematopietic	Necrosis Virus	(IHNV)		
fresh water	4°C	140 d	0.1% survival	Pietsch <i>et al.</i> 1977
fresh water	15°C	25 d	0.1% survival	Toranzo & Hetrick 1982
fresh water-lake	10°C	49 d	survival	Wedemayer <i>et al.</i> 1978
fresh water-river	15°C	1 d	1% survival	LaPatra <i>et al.</i> 2001
fresh water	20°C	14 d	0.1% survival	Toranzo & Hetrick 1982
distilled water	10°C	14 d	survival	Wedemayer <i>et al.</i> 1978
sea water	15°C	14 d	0.1% survival	Toranzo & Hetrick 1982
sea water	15°C	4 d	0.01% survival	Pietsch <i>et al.</i> 1977
sea water-artificial	15°C	3 d	0.01% survival	Pietsch <i>et al.</i> 1977
sea water	15°C	3 d	survival	Kamei <i>et al.</i> 1987
sea water	20°C	12 d	0.1% survival	Toranzo & Hetrick 1982
sea water-artificial	25°C	2 h	survival	LaPatra <i>et al.</i> 2001
adsorbed to clay	?	up to 63 d	infective	Yoshinaka <i>et al.</i> 2000
Koi Herpesvirus (KHV)				
fresh water	23-35°C	<21 h	infective	Perelberg <i>et al.</i> 2003
fresh water	15-25°C	3 d	≤0.1% survival	Shimizu <i>et al.</i> 2006
fresh water-sterile [8]	15-25°C	>7 d	≈1% survival	Shimizu <i>et al.</i> 2006
sediment	15-25°C	3 d	≤0.1% survival	Shimizu <i>et al.</i> 2006
Infectious Salmon Anem	ia Virus (ISAV)			
fresh water-sterile	4°C	>126 d	detectable	MacLeod <i>et al.</i> 2003
fresh water-sterile	15°C	>126 d	detectable	MacLeod <i>et al.</i> 2003
sea water	4°C	105 d	detectable	MacLeod et al. 2003
sea water	6°C	>20 h	infective	Nylund <i>et al.</i> 1994
sea water	15°C	28 d	detectable	MacLeod et al. 2003
sea water-sterile	4°C	>105 d	infective	MacLeod et al. 2003
sea water-sterile	15°C	>105 d	infective	MacLeod et al. 2003
Pike Fry Rhabdovirus (P	FRV)			
tap water	10°C	70 d	survival	Ahne 1982
mud	4°C	42 d	stable	Ahne 1982
Infectious Pancreatic Ne	crosis Virus (IPN	IV)		
tap water	10°C	>231 d	survival	Ahne 1982
mud	4°C	>210 d	stable	Ahne 1982
Spring Viraemia of Carp	Virus (SVCV)			
tap water	10°C	42 d	survival	Ahne 1982
mud	4°C	42 d	stable	Ahne 1982

[5] 5 μm -filtered and UV, with 0.1% ovarian fluid added

[1] European (F1) isolate[2] Northwestern Pacific (Makah) isolate

[3] 5 μm-filtered and UV [4] 0.22 μm filtered

[6] 5 µm-filtered and UV, with 1% ovarian fluid added [7] 5 μ m-filtered and UV, with culture medium added

[8] 0.45 µm-filtered or autoclaved at 121°C for 15 min.

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Appendix 5. NOAA and Listing Petition comments on disease impacts and threats to ESA-listed coral species

Comments on the 2 Threatened species (*Acropora cervicornis* and *A. palmata*) are summarized from NOAA's online species descriptions (NOAA 2010b); comments on the 82 Candidate species are summarized from the Listing Petition (CBD 2009).

Species	Comments on disease impacts and threats
CARIBBEAN SPECIES	
Acropora cervicornis	Disease is the main cause of decline; low genetic diversity due to asexual reproduction makes recovery from disease difficult.
Acropora palmata	Disease is the main cause of decline; low genetic diversity due to asexual reproduction makes recovery from disease difficult.
Agaricia lamarcki	Threatened by white plague & black band disease; ability to resist and recover from disease is hampered by overlapping colonies.
Montastraea annularis	Threatened by infectious diseases.
Montastraea faveolata	Develops white plague infections after bleaching events.
Montastraea franksi	Threatened by infectious diseases, but more resistant than other <i>Montastraea</i> species.
Dendrogyra cylindrus	Especially sensitive to white plague.
Dichocoenia stokesii	Highly susceptible to white plague, which is a major threat; also susceptible to black band disease.
Mycetophyllia ferox	Localized declines and partial recovery from white plague outbreaks in 1970s-1980s; later outbreaks have been increasingly virulent with significant mortality; also susceptible to black band disease.
HAWAIIAN SPECIES (SO	ME SPECIES ALSO OCCUR IN THE INDO-PACIFIC REGION)
Acropora paniculata	Especially susceptible to disease and slow to recover.
Montipora dilatata	Disease not mentioned.
Montipora flabellata	Disease not mentioned.
Montipora patula	Disease not mentioned.
Leptoseris incrustans	Susceptible to disease.
Cyphastrea agassizi	Disease not mentioned.
Cyphastrea ocellina	Disease not mentioned.
Porites pukoensis	More susceptible to disease than many corals.
Psammocora stellata	Disease not mentioned.

Species	Comments on disease impacts and threats
INDO-PACIFIC SPECIES	
Acropora aculeus	Especially susceptible to disease and slow to recover.
Acropora acuminata	Especially susceptible to disease and slow to recover.
Acropora aspera	Especially susceptible to disease and slow to recover.
Acropora dendrum	Especially susceptible to disease and slow to recover.
Acropora donei	Especially susceptible to disease and slow to recover.
Acropora globiceps	Especially susceptible to disease and slow to recover.
Acropora horrida	Especially susceptible to disease and slow to recover.
Acropora jacquelineae	Especially susceptible to disease and slow to recover.
Acropora listeri	Especially susceptible to disease and slow to recover.
Acropora lokani	Especially susceptible to disease and slow to recover.
Acropora microclados	Especially susceptible to disease and slow to recover.
Acropora palmerae	Especially susceptible to disease and slow to recover.
Acropora pharaonis	Especially susceptible to disease and slow to recover.
Acropora polystoma	Especially susceptible to disease and slow to recover.
Acropora retusa	Especially susceptible to disease and slow to recover.
Acropora rudis	Especially susceptible to disease and slow to recover.
Acropora speciosa	Especially susceptible to disease and slow to recover.
Acropora striata	Especially susceptible to disease and slow to recover.
Acropora tenella	Especially susceptible to disease and slow to recover.
Acropora vaughani	Especially susceptible to disease and slow to recover.
Acropora verweyi	Especially susceptible to disease and slow to recover.
Anacropora puertogalerae	Especially susceptible to disease and slow to recover.
Anacropora spinosa	Especially susceptible to disease and slow to recover.
Astreopora cucullata	Low tolerance or resistance to disease and slow to recover.
Isopora crateriformis	Low tolerance or resistance to disease, and slow to recover due to limited reproduction and dispersal.
Isopora cuneata	Low tolerance or resistance to disease, and slow to recover due to limited reproduction and dispersal.
Montipora angulata	Susceptible to disease, but broad distribution and depth range could provide some resilience at the population level.
Montipora australiensis	Susceptible to disease.
Montipora calcarea	Susceptible to disease.
Montipora caliculata	Susceptible to disease.
Montipora lobulata	Susceptible to disease.
Leptoseris yabei	Susceptible to disease.
Pachyseris rugosa	Disease not mentioned.

Species	Comments on disease impacts and threats
INDO-PACIFIC SPECIES	- continued
Pavona bipartita	Disease not mentioned.
Pavona cactus	Disease not mentioned.
Pavona decussata	Disease not mentioned.
Pavona diffluens	Disease not mentioned.
Pavona venosa	Susceptible to disease.
Barabattoia laddi	Susceptible to disease due to restricted depth range.
Caulastrea echinulata	Disease not mentioned.
Acanthastrea brevis	Disease not mentioned.
Acanthastrea hemprichii	Especially susceptible to disease.
Acanthastrea ishigakiensis	Especially susceptible to disease due to restricted depth range.
Acanthastrea regularis	Especially susceptible to disease due to restricted depth range.
Pocillopora danae	Especially susceptible to disease.
Pocillopora elegans	Especially susceptible to disease.
Seriatopora aculeata	Especially susceptible to disease.
Galaxea astreata	Disease not mentioned.
Alveopora allingi	This genus is thought to be relatively unsusceptible to disease.
Alveopora fenestrata	This genus is thought to be relatively unsusceptible to disease.
Alveopora verrilliana	This genus is thought to be relatively unsusceptible to disease.
Porites horizontalata	This genus is more susceptible to disease than most corals.
Porites napopora	This genus is more susceptible to disease than most corals.
Porites nigrescens	This genus is more susceptible to disease than most corals.
Turbinaria mesenterina	Disease not mentioned.
Turbinaria peltata	Disease not mentioned.
Turbinaria reniformis	Susceptible to disease due to restricted depth range.
Turbinaria stellula	Susceptible to disease due to restricted depth range and distribution.
Euphyllia cristata	Disease not mentioned.
Euphyllia paraancora	Disease not mentioned.
Euphyllia paradivisa	Disease not mentioned.
Physogyra lichtensteini	Disease not mentioned.
Pectinia alcicornis	Disease not mentioned.
Heliopora coerulea	Disease not mentioned.
Millepora foveolata	In Fiji, the genus appears to be resistant to disease.
Millepora tuberosa	In Fiji, the genus appears to be resistant to disease.