CHAPTER 8

Disease outbreaks can threaten marine biodiversity

C. Drew Harvell and Joleah B. Lamb

8.1 Introduction

Host–pathogen theory predicts that host-specific pathogens can regulate host population dynamics, whereas multi-host pathogens can cause extreme population impacts, including extinction of susceptible species if they are continuously infected from reservoir species (McCallum and Dobson 1995, McCallum 2012). In this chapter, we focus on global disease outbreaks that have impacted marine communities (Harvell et al. 2002, Burge et al. 2014, Harvell 2019) and pose risks to human health and livelihoods (Daszak et al. 2000). Mass mortality (loss of more than 10 percent of a population) from infectious disease has recently impacted wild marine taxa and habitat-forming taxa such as coccolithophores (Frada et al. 2008), seagrasses (Martin et al. 2016), corals (Harvell et al. 2007), abalone (Crosson and Friedman 2018), sea stars (Montecino-Latorre et al. 2016), urchins (Clemente et al. 2014), marine mammals (Rubio-Guerri et al. 2013), and turtles (Flint et al. 2010).

Since 2013, sea star wasting disease (SSWD), linked to a multi-host sea star-associated densovirus (SSaDV, family Parvoviridae), has caused massive, ongoing mortality, from Mexico to Alaska (Hewson et al. 2014). Over twenty asteroid species have been affected in what is currently the largest documented epizootic of a non-commercial marine taxon (Hewson et al. 2014). Since 1984, an outbreak of withering foot syndrome caused by a rickettsial bacterium has contributed to listing three species of California abalone on the endangered species list (Crosson and Friedman 2018). Beginning in the 1930s, episodes of eelgrass wasting disease, caused by *Labyrinthula zosterae*, have devastated eelgrass beds in the continental USA and Europe (Sullivan et al. 2013, Martin et al. 2016). Reef-building corals around the world are increasingly impacted by infectious diseases caused by a combination of dysbiosis and infectious pathogens.

8.2 Disease outbreaks of threatened foundation, keystone, and ecological engineering species

Single species often have far-reaching impacts on ecosystem structure and functioning, and thereby biodiversity. The most influential species include two kinds. *Foundation species* dominate abundance and biomass within a system, modify the physical environment, and create habitat for many other species (Bruno et al. 2003). *Keystone species* are strong interactors, and thus exert strong impacts disproportionate to their low abundance (Paine 1969). In this chapter, we describe the impacts of disease outbreaks on threatened, foundation, keystone, and ecological engineering species (Figure 8.1), using specific case studies of reef-building corals (Section 8.2.1), sea stars (Section 8.2.2), seagrass (Section 8.2.3), and abalone (Section 8.2.4).

Harvell, C.D., and Lamb, J.B., *Disease outbreaks can threaten marine biodiversity* In: *Marine Disease Ecology*. Edited by: Donald C. Behringer, Kevin D. Lafferty, and Brian. R. Silliman, Oxford University Press (2020).
DOI: 10.1093/oso/9780198821632.003.0008

Figure 8.1 Marine disease threatens biodiversity and key species with regard to ecosystem function, including reef-building corals (top left), seagrass meadows (top right), abalone (bottom left), and sea stars (bottom right). (Photos: M. Primivani, B. Tissot, J. Lamb, and C. Harvell.)

8.2.1 Foundation species: *reef-building corals*

As foundation species, corals have been estimated to support up to nine million marine species, representing one of the most biodiverse ecosystems in the world (Roberts et al. 2002). Since the late 1980s, partly driven by infectious disease, coral cover has decreased by 50–75 percent, jeopardizing associated marine species and the US $375 billion in goods and services coral reefs provide to people each year through fisheries, tourism, and coastal protection (Burke et al. 2011).

When

Outbreaks of coral disease emerged in the 1970s as a significant driver of global coral reef degradation (reviewed in Harvell et al. 2007). Evidence from paleontological monitoring suggests that coral disease epizootics were not as common in the past (Aronson et al. 2003). Lafferty et al. (2004) reviewed modern changes in coral disease over time and found that although bleaching reports did increase over several decades, peaks in infectious disease reports instead corresponded to El Niño events.

Signs and cause

Disease outbreaks have been described across all major ocean basins, with three-quarters of reported diseases estimated globally affecting species in the Caribbean, which is known as a disease "hot spot" (Randall et al. 2014; Harvell 2019). Yet, despite this extensive monitoring and exploration, classical culturing approaches to determine causative agents have been applied to only a few described diseases (Frasca et al. Chapter 11, this volume) that can

repeatedly initiate a consistent disease phenotype, including aspergillosis (causative fungi, *Aspergillus sydowii*), white pox disease (causative bacterium, *Serratia marcescens*), and bacterial bleaching (*Vibrio shiloi*). However, these traditional approaches are arguably challenging when applied to corals (Mera and Bourne 2018).

Documented coral infectious diseases are often multi-host syndromes, enabling them to be unusually destructive. For example, aspergillosis infects six octocoral species (Weil 2004), whereas black band disease (a polymicrobial consortia) has been reported on forty-two coral species in the Caribbean, and on an additional forty coral species from twenty-one genera in the Indo-Pacific (Green and Bruckner 2000) (Figure 8.2).

Infectious agents may spread rapidly in the ocean (McCallum et al. 2003). For example, the coral disease white plague (WP) spread along the coast of Florida at rates of approximating 200 km per year (Richardson et al. 1998). Despite reports of disease significantly impacting corals worldwide, knowledge underlying the distributions, causative agents, and environmental drivers is lacking. Outbreaks of coral diseases stand out as being driven largely by opportunistic agents and a changing environment (Harvell 2019). The dynamics of infectious wildlife diseases are known to be influenced by shifting interactions among the host, pathogen, and other members of the microbiome (Wobeser 2006). This is also a common case for corals (Ainsworth et al. 2010).

Several common Caribbean coral diseases, including yellow-band disease (*Vibrio* consortium and virus-like particles), white pox disease, WP type II (*Aurantimonas coralicida*), and dark-spot syndrome (undetermined causative agent as of 2019), do not display transmission dynamics characteristic of contagious diseases (Muller and van Woesik 2012, 2014, Mera and Bourne 2018), suggesting that intrinsic properties of the holobiont may play a large role in disease initiation and progression. As in some human diseases, it may be that heterogeneous communities of micro-organisms are responsible and act to disrupt microbiome homeostasis (Lamont and Hajishengallis 2015). In these cases, it is important to examine host organismal traits that affect disease susceptibility and environmental thresholds that serve as tipping points for disruption of microbiome homeostasis and disease induction, in addition to focusing on transmission dynamics of pathogens (Burge and Hershberger Chapter 5, this

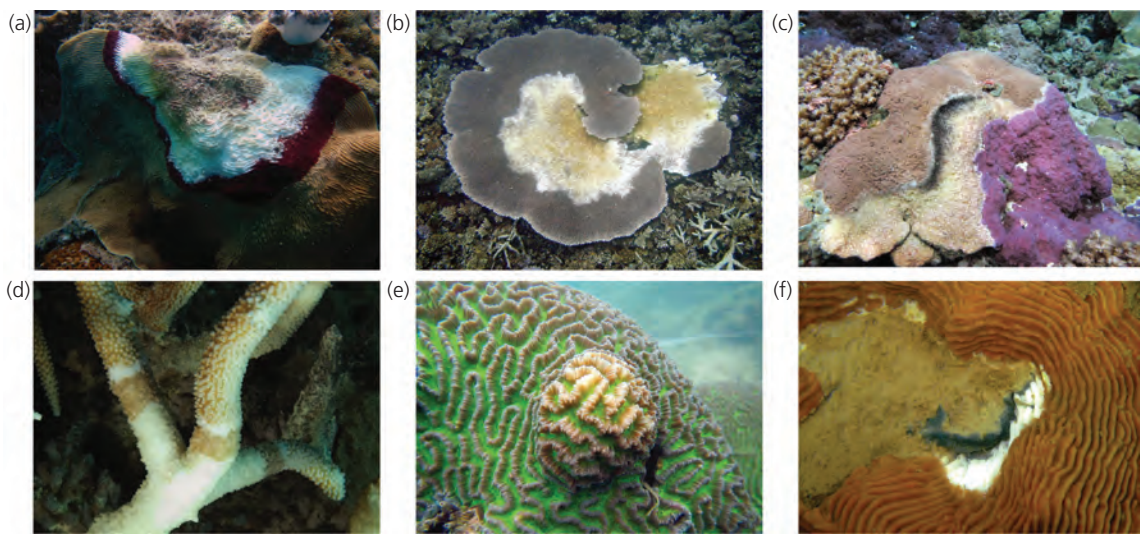

Figure 8.2 Visual characteristics of six coral syndromes commonly affecting reef corals in the Indo-Pacific: (a) black band disease, (b) white syndrome, (c) skeletal eroding band, (d) brown band disease, (e) growth anomaly, and (f) atramentous necrosis. (Photos: J. Lamb and B. Willis.)

volume). Coral host–pathogen work is plagued by a changing and polymicrobial series of pathogenic bacteria, prompting an increasing focus and need to better understand the interplay between the coral microbiome and the environment and the potential role of dysbiosis in triggering outbreaks (Zaneveld et al. 2017).

Among wildlife, outbreaks of coral diseases stand out as being driven largely by a changing environment (Raymundo et al. Chapter 9, this volume), particularly warming temperatures (Harvell et al. 2002) but also chronic exposure to pollutants like sewage (Lamb et al. 2017), sediment (Pollock et al. 2014), nutrients (Vega Thurber et al. 2014), and aquaculture (Lafferty et al. 2015). These outbreaks have contributed to losses of coral species and are driving a regime shift and, in some locations, collapse of the coral ecosystem.

Coral injury increases the likelihood of disease development by disrupting immune system function during wound healing processes and providing an entry site for opportunist pathogens (Mydlarz et al. 2006). This has been shown following tissue damage from feeding reef organisms (Aeby and Santavy 2006, Nicolet et al. 2013); the passage of cyclones (Brandt et al. 2013); and anthropogenic activities including high-intensity tourism (Lamb and Willis 2011, Lamb et al. 2014), destructive fishing methods and gear (Lamb et al. 2015, 2016), entanglement with plastic debris (Lamb et al. 2018), and ship groundings (Raymundo et al. 2018).

Impact

An outbreak of white band disease virtually eliminated two dominant reef-building corals, *Acropora cervicornis* and *A. palmata*, on many Caribbean reefs and these corals are now listed on the US Endangered Species List (reviewed in Sutherland et al. 2016). Successive disease outbreaks decreased populations of these two significant reef-building acroporid corals by 95 percent and contributed substantially to observed ecological phase shifts from coral- to algal-dominated reefs (Weil 2004).

Infectious disease is demonstrably pivotal in changing the composition, structure, and function of coral reef communities (Morton et al. Chapter 3, this volume)—for example, by opening up substratum for colonization by less competitive species or triggering a phase shift to algal domination (Aronson et al. 2003). Disease-induced reductions in coral cover may also limit direct competitive interactions between neighboring colonies (Bruno et al. 2007). The loss of coral reef structural complexity associated with anthropogenically driven coral diseases (Lamb et al. 2018) has the ability to reduce the economic productivity of fisheries by up to three-fold (Rogers et al. 2014).

8.2.2 Ecosystem engineering species: *seagrass*

Ecosystem engineers modify environments to create unique habitats, which provide better habitat for biodiversity and improved ecological functions, with services for humans. Globally, seagrass cover has declined by 29 percent from 1879 to 2009, with the rate of loss on the rise at 7 percent per year since 1990 (Waycott et al. 2009). These declines are attributed to anthropogenic and environmental stressors, many of which are also synergistic with disease susceptibility, such as terrestrial runoff, physical disturbance, fisheries activities, algal blooms, and ocean warming (Orth et al. 2006). Eelgrass (*Zostera marina*), a seagrass species which forms extensive coastal meadows throughout temperate waters, is a key ecosystem engineer and foundation species. Here, we review historical and current studies documenting large impacts of disease on seagrass, with huge biodiversity repercussions, given the importance of these meadows for habitat.

When

Outbreaks of eelgrass wasting disease (EGWD) historically caused catastrophic losses of eelgrass beds, including documented losses of > 90 percent along the US and European Atlantic coasts in the 1930s (Short et al. 1988) and in Florida in the 1980s (Martin et al. 2016). EGWD currently affects eelgrass populations in Chesapeake Bay (Short et al. 1988), along the US West Coast (Groner et al. 2014, 2016b, 2018, Dawkins et al. 2018), Florida (Martin et al. 2016), and Europe (Godet et al. 2008). Recent work shows rising levels of EGWD in Washington state, in well-monitored meadows in the San Juan Islands (Groner et al. 2014, 2016a, 2016b, 2018, Dawkins et al. 2018), and in Puget Sound.

Signs and cause

EGWD causes sharp, dark-edged, necrotic lesions on the plant, associated with fungus-like protists in the genus *Labyrinthula*; in eelgrass, the causative agent of EGWD is *Labyrinthula zosterae* (Figure 8.3). Other eelgrass pathogens that are less well studied but of emerging importance are *Phytophora* spp. and *Halophytophora* spp. (reviewed in Sullivan et al. 2018). The presence of *L. zosterae* is confirmed with histology, which visualizes the *L. zosterae* spindle-shaped cells within host tissues and culture (Figure 8.3).

A quantitative polymerase chain reaction (qPCR) assay was designed to quantify *L. zosterae* within plant tissues (using the *L. zosterae* ITS region). Multiple virulent strains of *L. zosterae* exist globally, including both pathogenic and non-pathogenic strains (Martin et al. 2016). Strains of *L. zosterae* with varying virulence have been isolated from the US West Coast (Muehlstein et al. 1991, Dawkins et al. 2018) and more globally (Martin et al. 2016). Cross-infection experiments reveal that *L. zosterae* strains are equally pathogenic to eelgrass hosts on both the US Atlantic and Pacific Coast (Martin et al. 2016). Some *L. zosterae* strains are suggested to have low host specificity and infect multiple seagrass species, including *Posidonia* and *Thalassia* (Martin et al. 2016), and may infect marine algae and other potential reservoirs (reviewed in Bockelmann et al. 2013).

As a widespread opportunist throughout the range of eelgrass (Sullivan et al. 2013, Martin et al. 2016), *L. zosterae* can be present but causes few or no signs of disease (Bockelmann et al. 2013, Martin et al. 2016). Outbreaks of lesions with changes in environmental drivers like temperature and nutrients, and vulnerability of older blades to *L. zosterae* prevalence have been identified in some regions (Groner et al. 2014, 2016a, Jakobsson-Thor et al. 2018). The triggers and biological interactions that lead to epidemics and seagrass wasting in complex field ecosystems remain poorly understood (Martin et al. 2016).

Outbreaks of EGWD in temperate regions are associated with warming temperatures, with highest prevalences within sites during the warmest months of the year (Bockelmann et al. 2013). Temperate *L. zosterae* strains appear to grow optimally at temperatures from 14 to 24 °C, with most catastrophic field outbreaks associated with elevated temperatures in this range (Sullivan et al. 2013). Dosage-controlled laboratory experiments show that *L. zosterae in vitro* cultures grow faster at 18 than 11 °C, and *in vivo*, making larger lesions at 18 than 11 °C (Dawkins et al. 2018). A modelling study simulated observed reductions in eelgrass beds during warm periods and mediated by *L. zosterae* and EGWD (Bull et al. 2012). Thus, warmer water temperatures will likely lead

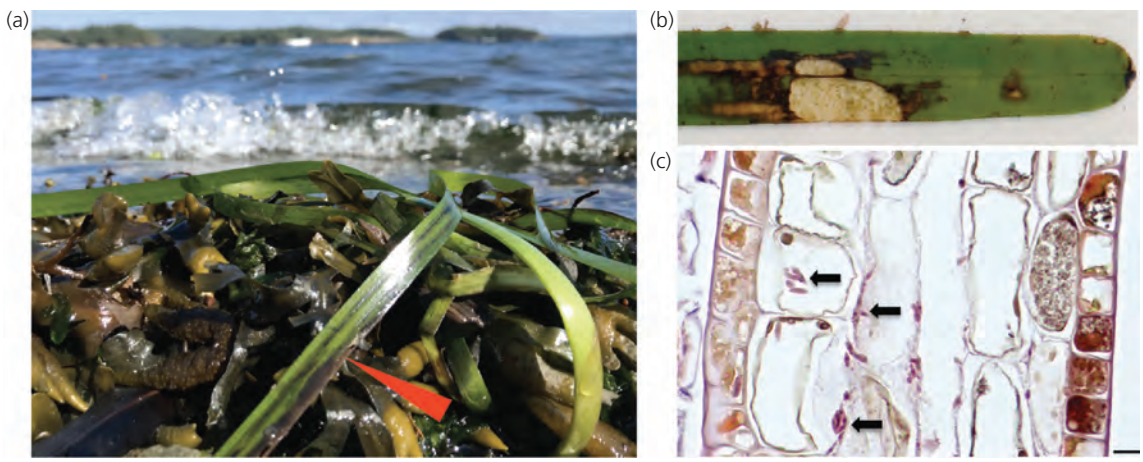

Figure 8.3 Typical signs of EGWD in the field (a and b, red arrow) affecting *Z. marina*. (c) Histological characterization of *Labyrinthula* cells (black arrows). Scale bar = 10 μm. (Photos in a and b: O. Graham and P. Dawkins. Histological section in c from Groner et al. (2014).)

to increased *L. zosterae* transmission and damage to eelgrass health in a warming ocean.

Impact

EGWD has been globally a major factor in the dynamics of eelgrass over the last century (Short et al. 1987, Muehlstein et al. 1991, Sullivan et al. 2013). During the 1930s, eelgrass populations declined drastically and suddenly on both sides of the North Atlantic and in parts of the US Pacific Northwest, giving way to bare sediments or ephemeral algae. *Labyrinthula zosterae* was isolated from diseased plants at that time and suspected as the culprit, along with unusually warm water temperatures in Europe (reported in Sullivan et al. 2013). The 1930s' outbreak reportedly wiped out over 90 percent of eelgrass along the East Coast of North America in 1931–1932, impacting numerous waterfowl species that use eelgrass as habitat and food (reviewed in Sullivan et al. 2013) and effectively killing the fishery for bay scallops. In the 1980s, a similar die-off began in New England, traced to *L. zosterae* (Short et al. 1987, Muehlstein et al. 1991).

In both *Z. marina* (eelgrass) and *Thalassia testudinum* (turtle grass), wasting disease has caused mass die-offs at regional to pandemic scales (reviewed in Sullivan et al. 2013). Although Puget Sound eelgrass beds are recorded as stable overall (Shelton et al. 2017), some monitored beds recently disappeared (Wyllie-Echeverria and Harvell, pers. obs.), while other beds declined between 2013 and 2017 (Eisenlord and Harvell, unpublished data). Changes in eelgrass bed size and density likely have several causes; however, our recent data from the San Juan Islands suggest that high EGWD prevalence may be causing declines in bed density (Groner et al. 2016a).

8.2.3 Keystone species: *sea stars*

Keystone species are defined as those that play a disproportionate role in their community relative to their abundance (Paine 1969, Power et al. 1996). In this section, we report on the large impacts to ecologically pivotal sea stars and eighteen other species from a multi-host disease epidemic, and the resulting cascading ecosystem changes.

When

Large numbers of *Asterias forbesi* sea stars died on the northeast coast of the USA beginning in 2011. By 2013, sea stars in over twenty species died catastrophically along the US West Coast, first noticed in British Columbia and the Olympic peninsula. After 2017, SSWD was observed in Asia (Hewson et al. 2018).

The first reports on the West Coast were for ochre sea stars (*Pisaster ochraceus*) from Washington state in June 2013 and sunflower sea stars (*Pycnopodia helianthoides*) from British Columbia, Canada, in August 2013. By late fall 2013, reports of dying sea stars with lesions in upwards of fifteen species were reported from parts of California, Washington, and British Columbia. Summer 2014 was a time of huge mortality across the range from southern California to Alaska (Miner et al. 2018). Previous outbreaks of SSWD have been reported in the northeast Pacific, California, and northern New England since the 1970s (Eisenlord et al. 2016); however, these earlier SSWD outbreaks involved single species in localized areas. In addition to a virus-sized fraction, the 2013–2015 SSWD epidemic has been linked to an increase (Eisenlord et al. 2016, Miner et al. 2018, Harvell et al. 2019) or decrease (Menge et al. 2016) in sea temperature, while host immunity (Fuess et al. 2015), genetics (Wares and Schiebelhut 2016), and a suite of other host or environmental factors are likely involved.

Signs and cause

Infected sea stars develop lesions in the dermis that increase in depth and diameter, dissolving tissue from the outside in (Figure 8.4). One or all arms then detach from the central disc as individuals die, often leaving only white piles of ossicles and disconnected limbs. SSWD signs included lesions through the dermal wall into the coelom on the star dorsal surface, gonads and other internal organs spilling out, and arms detaching. These signs differ from previous reports of sea star wasting in causing catastrophic mortality of top-condition, reproductive sea stars and not a gradual wasting. Vast populations died simultaneously, causing intertidal and subtidal areas to be strewn with dead and dying sea stars and detached, moving arms, sometimes containing ripe gonads.

Figure 8.4 Images of (a) healthy and abundant populations of ochre sea star (*Pisater ochraceus*) before an outbreak of SSWD. Healthy sea stars develop (b) initial curling of arms, (c) development of dermal lesions, (d) loss of arms from central disk, and (e) extensive tissue necrosis and death. (Figure from Eisenlord et al. (2016).)

Sea star mortalities during this event were linked to a sea star-associated densovirus (SSaDV, family Parvoviridae), based on evidence provided by experimental challenge studies with the sunflower sea star and a metagenomic analysis of field and laboratory samples (Hewson et al. 2014). Inoculation experiments confirmed a viral-sized fraction as causative for at least one species, the sunflower sea star, in Washington state, and metagenomics suggested the densovirus as the potential virus, present in *Pycnopodia helianthoides*, *Pisaster ochraceus*, and *Evasterias troscheli* along its geographic range (Salish Sea to southern California) when surveyed in 2013–2014 (Hewson et al. 2014). (Bucci et al. 2017). Inoculation trials were not successful in producing disease signs in any species (Hewson et al. 2018).

Redesigned qPCR primers support an association between asteroid densovirus load (as measured by the WAaDs primer and probe set) and signs of SSWD only in *Pycnopodia helianthoides*, but not in either *Pisaster ochraceus* or *E. troscheli*. Surveys in 2016 showed highest loads of WAaDs in *Pycnopodia helianthoides* and *Pisaster brevispinus* and presence of lower levels of WAaDs in non-symptomatic species of the genera *Crossaster*, *Pteraster*, and *Henricia* (Hewson et al. 2018).

Impact

The outbreak caused strong declines in at least five species (*Pisaster ochraceus*, *Pisaster brevispinus*, *E. troscheli*, *Pycnopodia helianthoides*, and *Solaster stimpsoni*), with impacts on the remainder of poorly studied subtidal sea stars being unclear (Eisenlord et al. 2016, Montecino-Latorre et al. 2016, Harvell et al. 2019). The intertidal *Pisaster ochraceus* and *E. troschelli* declined precipitously in the summer of 2014 at all sites from California to Alaska. The impacts of this disease outbreak reduced populations of multiple species and extirpated at least two (*Pisaster ochraceus* and *Pycnopodia helianthoides*) from some geographic regions in the southern part of their range (Miner et al. 2018, Harvell et al. 2019). In Washington state, *Pisaster ochraceus* (Figure 8.4) declined by over 70 percent between 2014 and 2015, and *Pycnopodia helianthoides* declined over 90 percent for much of their range south of Alaska (Harvell et al. 2019). The epidemic continued in fall 2018, with lesioned sea stars in multiple species still present, although at a very reduced level (Harvell 2019).

Ochre sea stars are keystone species, and sunflower sea stars are pivotal predators (Burt et al. 2018, Harvell et al. 2019) and are likely keystones in some portions of their range. Ochre sea stars are capable of controlling populations of mussels and clams; sunflower sea stars control populations of green and purple sea urchins and clams in some parts of their range. The largest impacts of sea star removal observed are large outbreaks in populations of sea urchins in central California and southern British Columbia, which in turn are devastating kelp beds. Recent surveys document massive declines in California and British Columbia kelp beds (Schultz et al. 2016), driven by urchin increases and overgrazing. In 2017, there was some recovery of ochre sea stars and bouts of significant recruitment at multiple northern sites (Eisenlord, Winningham, Harvell, pers. com.). Data for populations of all subtidal sea stars are poor, except for the most common, the sunflower sea star (Figure 8.5). Citizen science diver data and National Oceanic and Atmospheric Administration (NOAA) trawl data show that sunflower sea star populations had not recovered in 2017 (Harvell et al. 2019). Early observations suggested the sunflower sea star was the most susceptible of the Asteroid species. This wide host range pathogen is currently endangering southern populations of this species, with well-studied confirmation of little or no recovery observed from southern California through British Columbia.

The SSWD outbreak that started in 2013 is considered the largest disease outbreak of marine wildlife, affecting well over twenty species and with an initial range from Mexico to Alaska and recent possible spread to Asia (Hewson et al. 2018), which would qualify it as a global pandemic. Taura syndrome of shrimp is a geographically larger and longer running outbreak, but since it affects predominantly farmed species, it is not considered a disease of wildlife (Lafferty et al. 2015).

The coelomocytes of sunflower sea stars inoculated with a viral-sized fraction from sick sea stars mounted an impressive immune response, showing potential for immune capability (Fuess et al. 2015). Ochre sea star populations show some imprint of selection, in possible association with SSWD, with the frequency of heterozygous EF1α in *Pisaster ochraceus* and transcriptomic analyses of EF1α mutants suggesting that these individuals have a greater cellular response to temperature stress (Chandler and Wares 2017). Moreover, differential survival and genetically based resistance of surviving adults and new recruits follows the epidemic (Schiebelhut et al. 2018).

Warm temperature anomalies between 2014 and 2016 likely fueled larger impacts from this epidemic. In laboratory experiments, ochre sea stars died at a faster rate, and in field populations, they had a higher risk of disease at warmer temperatures (Eisenlord et al. 2016). Similarly, populations of ochre sea stars in warmer parts of the range died sooner and have failed to return, compared to more northern locations

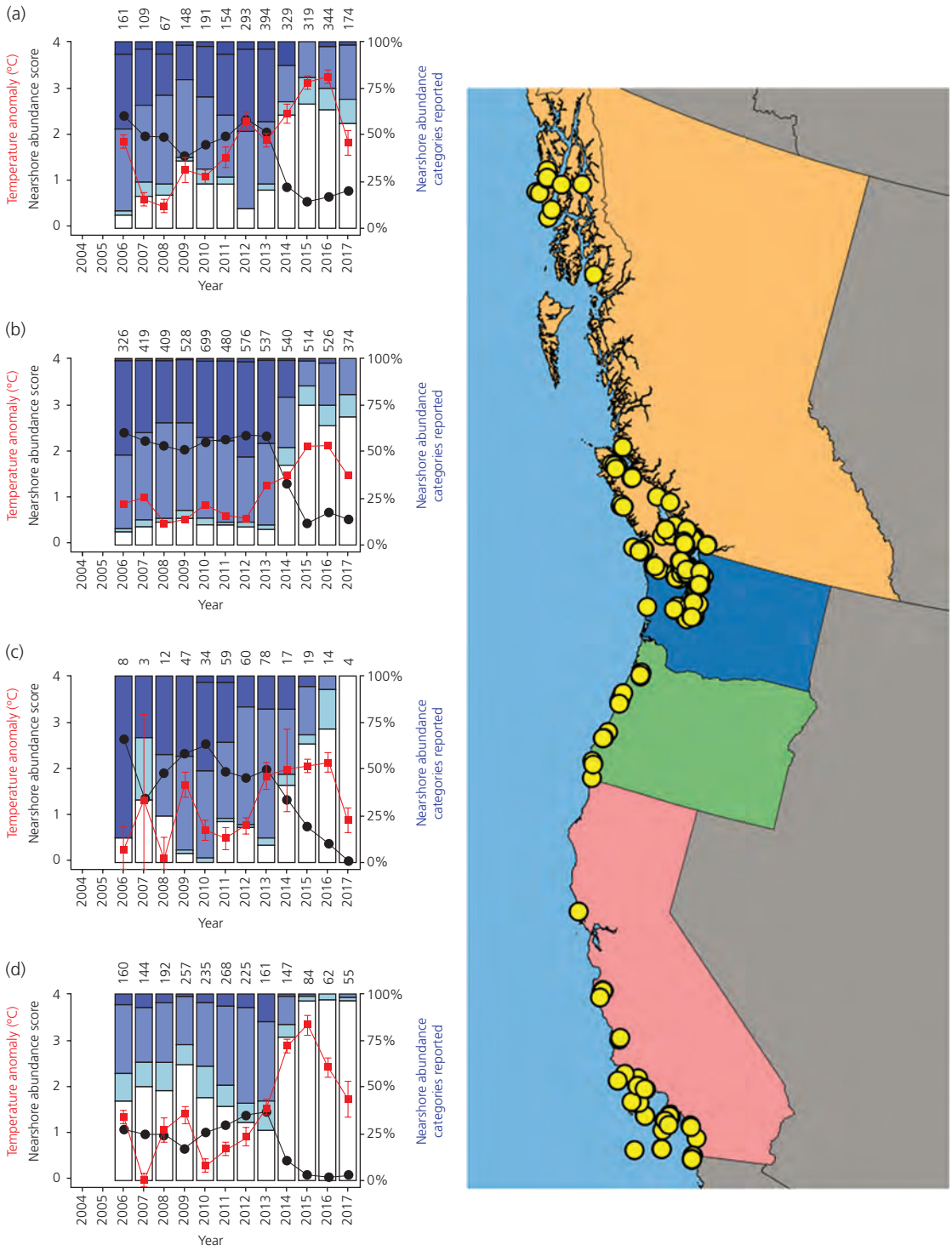

Figure 8.5 Continental-scale decline of sunflower sea star (*Pycnopodia helianthoides*) reported in Reef Environmental Education Foundation (REEF) roving diver surveys from 2006 to 2017. Yellow circles depict locations of surveys; black lines depict annual abundance surveys; red lines depict mean of the maximum temperature anomaly 60 days before each survey in (A) British Columbia, (B) Washington, (C) Oregon, and (D) California. Number of surveys per jurisdiction per year is shown above each plot. (Figure from Harvell et al. (2019).)

(Miner et al. 2018). Timing and extent of mortality of the sunflower sea star was linked with warm temperature anomalies (Harvell et al. 2019). The extent of the 2015–2016 marine heat wave in the Pacific northwest is best measured as a metric called temperature anomaly, which shows the site-specific increase in temperature from a 20-year mean. Analyses of the sunflower sea star decline with both absolute temperature and temperature anomaly show a better fit to the temperature anomaly (Harvell et al. 2019). In one case, higher declines in ochre sea stars were associated with cooler temperatures (Menge et al. 2016). The outbreak has, for now, significantly changed the seascape in ways that can be seen in intertidal and shallow subtidal rocky reefs, with high densities of new sea urchins and widespread urchin barrens (areas of denuded kelp beds). The outbreak has likely changed less-studied, deeper ocean regions due to the widespread disappearance of the sunflower sea star from waters as deep at 1,100 m (Harvell et al. 2019).

This outbreak stands with the abalone withering syndrome (Crosson and Friedman 2018) and amphibian chytrid fungus (Lips et al. 2006) as a stark reminder of the impact a novel, wide-host-range pathogen can have on groups of related species in wild populations (Harvell 2019).

8.2.4 One pathogen, one disease: abalone

Abalone are herbivorous marine gastropods and support fisheries around the world. Before 1980, there were seven species of abalone in California waters and a thriving fishery. In the mid-1980s, a combination of overharvesting, a warm-water El Niño, and a disease epidemic drove declines in California abalone species. Half the species are now under varying levels of endangerment and one is on the verge of extinction. In this section, we review the role of a well-studied multi-host rickettsial bacterium in pushing some of these species to endangerment.

When

Timing, level of impact, and geographic patterns in mortality are best studied for the intertidal black abalone (*Haliotis cracherodii*). Massive die-offs of intertidal black abalone due to withering syndrome were first noted on the Channel Islands off the Californian coast in 1986 (Tissot 1995), and this was thought to be related to starvation due to El Niño. However, the subsequent spread over time suggested an infectious agent (Lafferty and Kuris 1993). By 1992, withering syndrome was observed near Point Conception on the mainland (Altstatt et al. 1996). By 1998, mass mortalities of black abalone due to withering syndrome had occurred throughout southern California (> 90 percent decline in numbers in all size classes) and there was a clear pattern of decline from south to north over time (Raimondi et al. 2002). Mortality rate was later linked to warm temperatures. Abalone continue to die from disease (Crosson and Friedman 2018).

Signs and cause

Withering syndrome is a fatal disease of abalones characterized by a severely shrunken foot. The signs develop slowly and result in the external loss of muscle tone and ability to grip the substrate (Figure 8.6). Histology reveals large inclusions and atrophy of gastro-intestinal tissue and the digestive gland (Crosson and Friedman 2018). Withering syndrome (WS) was eventually confirmed to be caused by infection with a Rickettsiales-like organism (RLO); the causative agent was described and provisionally named "*Candidatus Xenohaliotis californiensis*" (WS-RLO) (Friedman et al. 2000). The WS-RLO is an obligate, intracellular bacterium that infects abalone gastro-intestinal epithelia and disrupts the digestive gland (Figure 8.6). The bacterium is transmitted horizontally via a fecal–oral route, with initial infections located in the posterior esophagus tissue and, to a lesser extent, the intestine of host abalone (Friedman et al. 2002).

Impact

Currently, populations of five of the seven California abalone species are declining and receive varying levels of federal protection, ranging from "Species of Concern," including pinto (*Haliotis kamtschatkana*), green (*H. fulgens*), and pink (*H. corrugata*) abalones, to "Endangered," including white (*H. sorenseni*) and black (*H. cracherodii*) abalones (reviewed in Crosson et al. 2014).

Once a thriving wild and farmed fishery, black and white abalone are endangered in California.

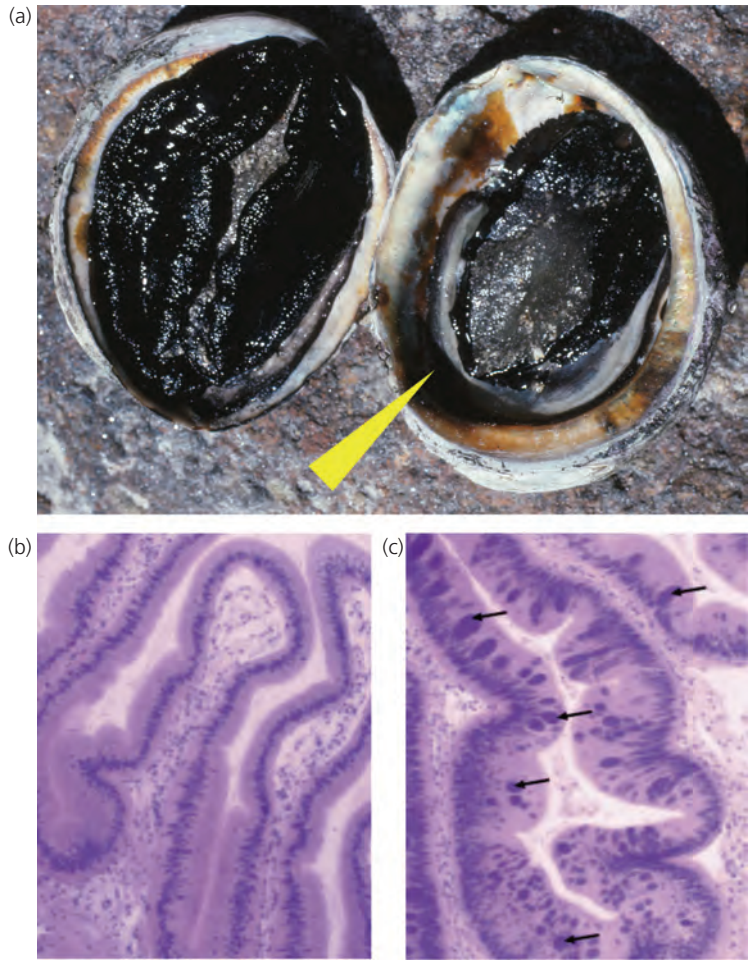

Figure 8.6 Effects of withering syndrome on black abalone (*Haliotis cracherodii*) (a, right, yellow arrow) compared to an uninfected abalone (a, left). (Photo: Jenny Dugan.) Light micrographs of abalone tissues stained with H&E of a normal post-esophagus (b) and a WS-RLO-infected post-esophagus (c), with arrows indicating WS-RLO cytoplasmic inclusions (bacterial colonies). Magnification × 200. (Micrographs from Crosson et al. (2014).)

The white abalone was listed as endangered under the Endangered Species Act in 2001. In the most recent surveys by the National Marine Fishery Service, white abalone populations had declined from historic levels of millions to less than 2,500. White abalone are on the verge of extinction. Due to precipitous declines, the black abalone were listed as endangered in 2009. Black abalone are considered locally extinct at most mainland sites south of Point Conception, California. The continued presence in California waters of the rickettsia that causes withering syndrome impedes recovery of these abalone species. The National Marine Fisheries Service is preparing a 5-year review of black abalone and white abalone to determine if anything can be done to save them from extinction. A rickettsia-infecting phage and the existence of resistant individuals provide some hope for the black abalone (Friedman et al. 2014; Little et al. Chapter 4, this volume).

Pinto abalone are the only abalone to the north in Washington and Alaska, regions of historically healthy populations. By 1994, they had declined to the point that the sport fishery closed and they have not recovered. Their populations are so low in the

waters of Washington state that they are listed as a species of concern and have been declared functionally extinct in this locality. Proposals to list the pinto abalone as endangered have been rejected because they thrive in Canada and Alaska and are already protected in Canada. Most of the range for pinto abalone lies north of where temperatures currently cause the rickettsia to be destructive (above 17 °C), so it is unknown to date if disease has had any role in their decline which is largely attributed to overfishing. A recent study revealed extreme temperature dependence in susceptibility for the three species tested and that the white abalone have the greatest susceptibility, followed by the closely related pinto abalone as the most susceptible to the RLO (Crosson and Friedman 2018). Red, black, and pink are the next most susceptible, with green abalone being relatively resistant (Crosson and Friedman 2018). The high susceptibility of the pinto abalone and temperature dependence of the RLO shows a susceptible, at-risk species sitting right on the edge of a temperature-sensitive pathogen's expanding range in a warming ocean.

8.3 Turning the tide: marine biodiversity provides services that influence disease

Disease not only directly threatens biodiversity through reducing vulnerable species, but also indirectly can have cascading impacts through the removal of foundation or keystone species. Foundation species like seagrasses are also ecosystem engineers with potent pathogen-reducing capabilities (Lamb et al. 2017), so their loss through disease outbreaks could amplify disease risk for associated biota. Mechanisms of natural pathogen removal represent a frontier for mitigating disease in the marine environment (Raymundo et al. Chapter 9, this volume).

The oceans have a vast store of novel mechanisms that control pathogenic bacteria, viruses, and parasites. In this section, we briefly describe three scales of pathogen-fighting mechanisms that are currently untapped in today's oceans: at a whole ecosystem level in ecosystems like seagrasses, at the organismal level in the form of invertebrates acting as biofilters, and at the microscopic scale of microbiomes.

The oceans are a microbial soup and this fact overwhelms all others in our consideration of what governs transmission and overall risk of infection for wildlife (Ben-Horin et al. Chapter 12, this volume). A vital component of marine ecosystems are the plants, invertebrates, and microbes that create powerful pathogen bio-filters. Mussels and clams can clean the water and reduce risk of infections propagating to other organisms. Their role in limiting or accelerating the transmission of disease has been largely overlooked. The tricky part is that this same filtration process doesn't always kill infections and can massively concentrate and convey pathogens (Behringer et al. Chapter 10, this volume). For example, clams and mussels can deliver a lethal dose of the pathogen *Vibrio haemolyticus* and *V. vulnificus* to humans (Froelich and Noble 2016). *Vibrio haemolyticus* causes diarrhea and is conveyed to humans by eating infected clams or oysters. *Vibrio vulnificus* is vastly worse and quite simply kills people who eat infected clams or oysters. Unfortunately, both of these are increasing in warming oceans (Baker-Austin et al. 2013). The consequences for human health are likely just the tip of the iceberg in terms of transmission—if humans are being sickened and killed by these bacteria, how are other organisms that eat mussels, clams, and oysters being affected? In our own research during the sea star epidemic, we wondered if sea stars that eat clams and mussels could be exposed to higher doses of the virus-sized pathogen. What other pathogenic micro-organisms are being similarly concentrated and conveyed to other wildlife through these bio-concentrators?

The flip side of bivalve filtration is that they can also clean the water by removing pathogens. In this way, some bivalves may actually protect wildlife from infective doses of disease. For instance, recent laboratory experiments show that oysters can remove infective zoospores of *L. zosterae* from the water and reduce pathogen risk for eelgrass (Groner et al. 2018). Both sides of this coin are illustrated in Figure 8.7, which shows that oysters are a dead-end host that can remove pathogens from the water column and kill them. In this figure, mussels are shown as amplifying infectious bacteria and increasing disease risk if consumed.

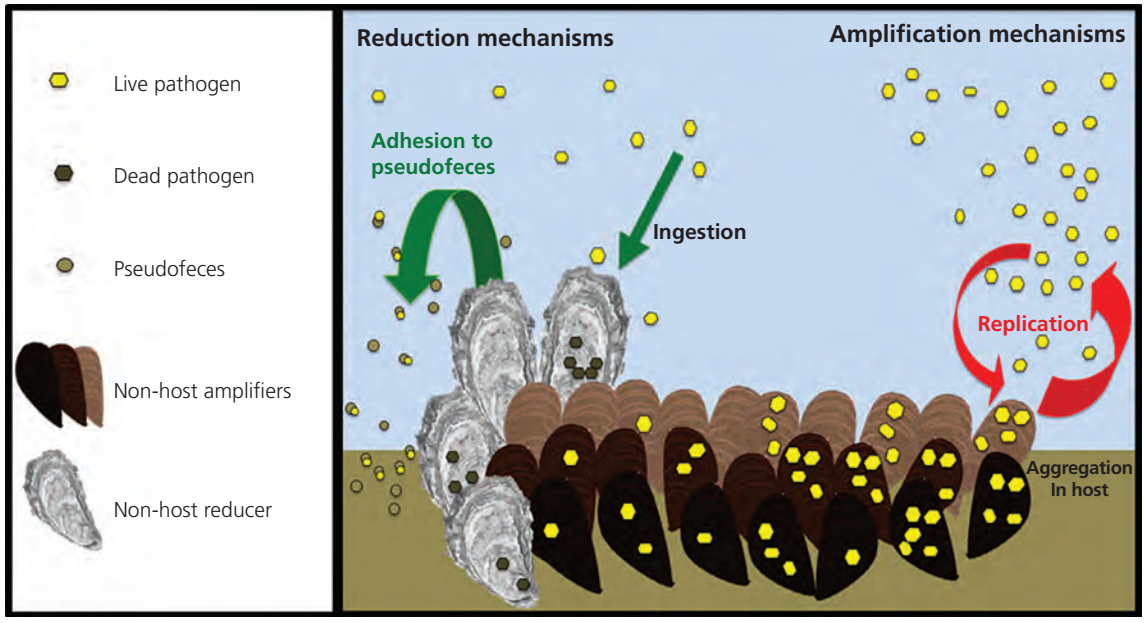

Figure 8.7 Filter feeders can influence pathogen transmission through reduction or amplification. (Figure from Burge et al. (2016).)

At a microbial scale, experimental evidence of chemical and biological pathogen regulation by seagrass and its microbiome has been shown *in vivo*. For example, phytochemicals extracted from seagrass blade tissues of multiple tropical species can kill or inhibit pathogenic bacteria that affect humans, fishes, and invertebrates (Kumar et al. 2008, Mani et al. 2012). Distinct microbial biofilms dominated by diazotrophic epiphytic cyanobacteria on seagrass blade surfaces (Hamisi et al. 2013) and antimicrobial compounds from endophytic fungi found growing within the tissues of several tropical seagrass species (Supaphon et al. 2013) have also been shown to experimentally inhibit multiple fish and human pathogens. In the field, seawater isolated from eelgrass harbors growth-inhibiting bacteria against the toxic dinoflagellate *Alexandrium tamarense* responsible for paralytic shellfish poisoning (Onishi et al. 2014).

The entire seagrass ecosystem could play a pivotal role in the removal of pathogenic bacteria, drawing parallels to literature from constructed wetland vegetation dating back to the 1950s (Wu et al. 2016). Although a seagrass monoculture alone exhibits several physical and biological characteristics of an effective pathogen removal system, an intact seagrass ecosystem comprises a diversity of bivalves, sponges, tunicates, and epiphytic organisms that influence levels of waterborne pathogenic bacteria (Burge et al. 2016). Using amplicon sequencing of the 16S ribosomal RNA gene, the presence of intact seagrass beds resulted in 50 percent reductions in the relative abundance of potential bacterial pathogens capable of causing disease in humans and marine organisms (Lamb et al. 2017). The pathogen-reducing services of seagrass beds extend to wildlife. Field surveys of more than 8,000 reef-building corals located adjacent to seagrass showed two-fold reductions in disease levels compared to paired sites without adjacent seagrass (Figure 8.8).

8.4 Summary

- This chapter highlights the disease threat to ecologically important foundation and keystone species and the resultant disruption to the balance of both tropical and temperate ecosystems.
- Four case histories of disease outbreaks that impact marine biodiversity are reviewed: eelgrass,

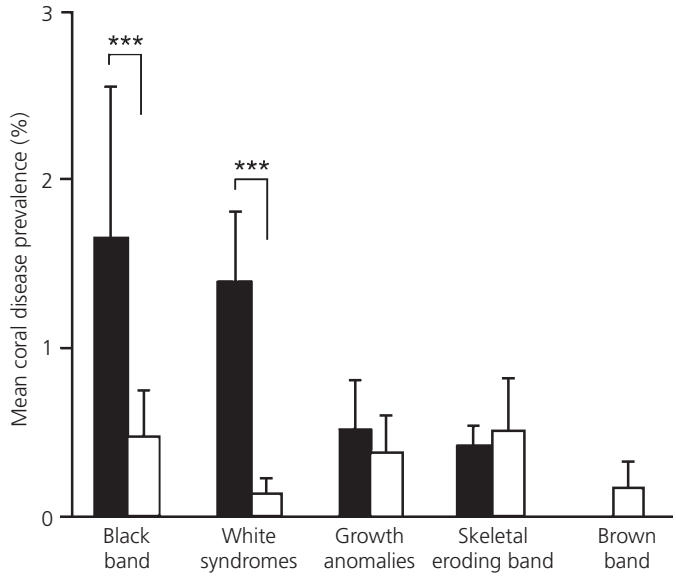

Figure 8.8 Diseases of reef-building corals are lower when adjacent to seagrass meadows. Prevalence (mean and standard error) of coral disease syndromes with adjacent seagrass meadows (white bars) compared to reefs without seagrass meadows (black bars). A total of 8,034 corals were surveyed across four different island reefs in the Spermonde Archipelago, Indonesia. Significant comparisons are indicated by asterisks. (Figure from Lamb et al. (2017).)

corals, sea stars, and abalone. Massive outbreaks in corals, abalone, and sea stars have contributed to imperilment or listing as endangered species.

- Multi-host diseases in all these cases have contributed to extreme population declines and ecosystem destruction or change.
- Vital knowledge gaps for each of the disease outbreak that have imperiled marine biodiversity are reviewed: timing and location of outbreaks, causative micro-organism, and impact of outbreak.
- Infectious diseases pose a great threat to marine biodiversity—directly through the reduction of foundation and keystone species like corals, seagrasses and seastars and indirectly through the disruption in habitat and pathogen-reducing services when foundation species or ecosystem engineers are removed.

8.5 Future directions and priorities for research

- A very poor understanding of host susceptibility to disease and the rates and pathways by which diseases are transmitted in a changing ocean impedes forecasting of outbreaks and management.
- New studies show that marine habitats like seagrass beds have powerful capability to detoxify and reduce pathogenic bacteria. There is a huge knowledge gap regarding which marine habitats provide this service and to what magnitude. Nothing is known about the mechanisms of detoxification and biofiltration. We suggest that the rising tide of marine disease may be alleviated by focused attention on natural services provided by healthy ecosystems.

References

Aeby, G. S., and D. L. Santavy. 2006. Factors affecting susceptibility of the coral *Montastraea faveolata* to black-band disease. Marine Ecology Progress Series 318:103–10.

Ainsworth, T. D., R. V. Thurber, and R. D. Gates. 2010. The future of coral reefs: a microbial perspective. Trends in Ecology & Evolution 25:233–40.

Altstatt, J. M., R. F. Ambrose, J. M. Engle, P. L. Haaker, K. D. Lafferty, and P. T. Raimondi. 1996. Recent declines of black abalone *Haliotis cracherodii* on the mainland coast of central California. Marine Ecology Progress Series 142:185–92.

Aronson, R. B., J. F. Bruno, W. F. Precht, P. W. Glynn, C. D. Harvell, L. Kaufman, C. S. Rogers, E. A. Shinn, Valentine, John F, J. M. Pandolfi, R. H. Bradbury, E. Sala, T. P. Hughes, K. A. Bjorndal, R. G. Cooke, D. McArdle, L. McClenachan, M. J. H. Newman, G. Paredes, R. R. Warner, Jackson, Jeremy B. C, T. P. Hughes, A. H. Baird, D. R. Bellwood, S. R. Connolly, C. Folke, R. Grosberg, O. Hoegh-Guldberg, J. B. C. Jackson, J. Kleypas, J. M. Lough, P. Marshall, M. Nystrom, S. R. Palumbi, J. M. Pandolfi, B. Rosen, and J. Roughgarden. 2003. Causes of coral reef degradation. Science 302:1502–4.

Baker-Austin, C., J. A. Trinanes, N. G. Taylor, R. Hartnell, A. Siitonen, and J. Martinez-Urtaza. 2013. Emerging *Vibrio* risk at high latitudes in response to ocean warming. Nature Climate Change 3:73.

Bockelmann, A.-C., V. Tams, J. Ploog, P. R. Schubert, and T. B. Reusch. 2013. Quantitative PCR reveals strong spatial and temporal variation of the wasting disease pathogen, *Labyrinthula zosterae* in northern European eelgrass (*Zostera marina*) beds. PLoS ONE 8:e62169.

Bucci C., M. Francoeur, J. McGreal, R. Smolowitz, V. Zazueta-Novoa, and G. M. Wessel. 2017. Sea Star Wasting Disease in Asterias forbesi along the Atlantic Coast of North America. PLoS ONE 12(12): e0188523.

Brandt, M. E., T. B. Smith, A. M. S. Correa, and R. Vega-Thurber. 2013. Disturbance driven colony fragmentation as a driver of a coral disease outbreak. PLoS ONE 8:e57164.

Bruno, J. F., J. J. Stachowicz, and M. D. Bertness. 2003. Inclusion of facilitation into ecological theory. Trends in Ecology & Evolution 18:119–25.

Bruno, J. F., E. R. Selig, K. S. Casey, C. A. Page, B. L. Willis, C. D. Harvell, H. Sweatman, and A. M. Melendy. 2007. Thermal stress and coral cover as drivers of coral disease outbreaks. PLoS Biology 5:e124.

Bull, J. C., E. J. Kenyon, and K. J. Cook. 2012. Wasting disease regulates long-term population dynamics in a threatened seagrass. Oecologia 169:135–42.

Burge, C. A., C. Mark Eakin, C. S. Friedman, B. Froelich, P. K. Hershberger, E. E. Hofmann, L. E. Petes, K. C. Prager, E. Weil, and B. L. Willis. 2014. Climate change influences on marine infectious diseases: implications for management and society. Annual Review of Marine Science 6:249–77.

Burge, C. A., C. J. Closek, C. S. Friedman, M. L. Groner, C. M. Jenkins, A. Shore-Maggio, and J. E. Welsh. 2016. The use of filter-feeders to manage disease in a changing world. Integrative and Comparative Biology 56:573–87.

Burke, L. M., K. Reytar, M. Spalding, and A. Perry. 2011. Reefs at Risk Revisited. World Resources Institute, Washington, DC.

Burt, J. M., M. T. Tinker, D. K. Okamoto, K. W. Demes, K. Holmes, and A. K. Salomon. 2018. Sudden collapse of a mesopredator reveals its complementary role in mediating rocky reef regime shifts. Proceedings of the Royal Society B 285:20180553.

Chandler, V. K., and J. P. Wares. 2017. RNA expression and disease tolerance are associated with a "keystone mutation" in the ochre sea star *Pisaster ochraceus*. Peer Journal 5:e3696.

Clemente, S., J. Lorenzo-Morales, J. C. Mendoza, C. López, C. Sangil, F. Alves, M. Kaufmann, and J. C. Hernández. 2014. Sea urchin *Diadema africanum* mass mortality in the subtropical eastern Atlantic: role of waterborne bacteria in a warming ocean. Marine Ecology Progress Series 506:1–14.

Crosson, L. M., and C. S. Friedman. 2018. Withering syndrome susceptibility of northeastern Pacific abalones: A complex relationship with phylogeny and thermal experience. Journal of Invertebrate Pathology 151:91–101.

Crosson, L. M., N. Wight, G. R. VanBlaricom, I. Kiryu, J. D. Moore, and C. S. Friedman. 2014. Abalone withering syndrome: distribution, impacts, current diagnostic methods and new findings. Diseases of Aquatic Organisms 108:261–70.

Daszak, P., A. A. Cunningham, and A. D. Hyatt. 2000. Emerging infectious diseases of wildlife—threats to biodiversity and human health. Science 287:443–9.

Dawkins, P. D., M. E. Eisenlord, R. M. Yoshioka, E. Fiorenza, S. Fruchter, F. Giammona, M. Winningham, and C. D. Harvell. 2018. Environment, dosage, and pathogen isolate moderate virulence in eelgrass wasting disease. Diseases of Aquatic Organisms 130:51–63.

Eisenlord, M. E., M. L. Groner, R. M. Yoshioka, J. Elliott, J. Maynard, S. Fradkin, M. Turner, K. Pyne, N. Rivlin, and R. van Hooidonk. 2016. Ochre star mortality during the 2014 wasting disease epizootic: role of population size structure and temperature. Philosophical Transactions of the Royal Society B: Biological Sciences 371:20150212.

Flint, M., J. C. Patterson-Kane, C. J. Limpus, and P. C. Mills. 2010. Health surveillance of stranded green turtles in southern Queensland, Australia (2006–2009): an epidemiological analysis of causes of disease and mortality. EcoHealth 7:135–45.

Frada, M., I. Probert, M. J. Allen, W. H. Wilson, and C. de Vargas. 2008. The "Cheshire Cat" escape strategy of the coccolithophore *Emiliania huxleyi* in response to viral infection. Proceedings of the National Academy of Sciences 105:15944–9.

Friedman, C. S., K. B. Andree, K. A. Beauchamp, J. D. Moore, T. T. Robbins, J. D. Shields, and R. P. Hedrick. 2000. "*Candidatus Xenohaliotis californiensis*", a newly described pathogen of abalone, *Haliotis* spp., along the west coast of North America. International Journal of Systematic and Evolutionary Microbiology 50:847–55.

Friedman, C. S., W. Biggs, J. D. Shields, and R. P. Hedrick. 2002. Transmission of withering syndrome in black abalone, *Haliotis cracherodii* Leach. Journal of Shellfish Research 21:817–24.

Friedman, C. S., N. Wight, L. M. Crosson, G. R. VanBlaricom, and K. D. Lafferty. 2014. Reduced disease in black abalone following mass mortality: phage therapy and natural selection. Frontiers in Microbiology 5:78.

Froelich, B. A., and R. T. Noble. 2016. Vibrio bacteria in raw oysters: managing risks to human health. Philosophical Transactions of the Royal Society B: Biological Sciences 371:20150209.

Fuess, L. E., M. E. Eisenlord, C. J. Closek, A. M. Tracy, R. Mauntz, S. Gignoux-Wolfsohn, M. M. Moritsch, R. Yoshioka, C. A. Burge, and C. D. Harvell. 2015. Up in arms: immune and nervous system response to sea star wasting disease. PLoS ONE 10:e0133053.

Godet, L., J. Fournier, M. M. van Katwijk, F. Olivier, P. Le Mao, and C. Retière. 2008. Before and after wasting disease in common eelgrass *Zostera marina* along the French Atlantic coasts: a general overview and first accurate mapping. Diseases of Aquatic Organisms 79:249–55.

Green, E. P., and A. W. Bruckner. 2000. The significance of coral disease epizootiology for coral reef conservation. Biological Conservation 96:347–61.

Groner, M. L., C. A. Burge, C. S. Couch, C. J. Kim, G.-F. Siegmund, S. Singhal, S. C. Smoot, A. Jarrell, J. K. Gaydos, and C. D. Harvell. 2014. Host demography influences the prevalence and severity of eelgrass wasting disease. Diseases of Aquatic Organisms 108:165–75.

Groner, M. L., C. A. Burge, C. J. Kim, E. Rees, K. L. Van Alstyne, S. Yang, S. Wyllie-Echeverria, and C. D. Harvell. 2016a. Plant characteristics associated with widespread variation in eelgrass wasting disease. Diseases of Aquatic Organisms 118:159–68.

Groner, M. L., J. Maynard, R. Breyta, R. B. Carnegie, A. Dobson, C. S. Friedman, B. Froelich, M. Garren, F. M. D. Gulland, S. F. Heron, R. T. Noble, C. W. Revie, J. D. Shields, R. Vanderstichel, E. Weil, S. Wyllie-Echeverria, and C. D. Harvell. 2016b. Managing marine disease emergencies in an era of rapid change. Philosophical Transactions of the Royal Society B: Biological Sciences 371(1689).

Groner, M. L., C. A. Burge, R. Cox, N. Rivlin, M. Turner, K. L. Van Alstyne, S. Wyllie-Echeverria, J. Bucci, P. Staudigel, and C. S. Friedman. 2018. Oysters and eelgrass: potential partners in a high pCO_2 ocean. Ecology 99(8):1802–14.

Hamisi, M., B. Díez, T. Lyimo, K. Ininbergs, and B. Bergman. 2013. Epiphytic cyanobacteria of the seagrass *Cymodocea rotundata*: diversity, diel nifH expression and nitrogenase activity. Environmental Microbiology Reports 5:367–76.

Harvell, C. D. 2019. Ocean Outbreak: Confronting the Rising Tide of Marine Disease. University of California Press, Oakland.

Harvell, C. D., C. E. Mitchell, J. R. Ward, S. Altizer, A. P. Dobson, R. S. Ostfeld, and M. D. Samuel. 2002. Climate warming and disease risks for terrestrial and marine biota. Science 296:2158–62.

Harvell, C. D., E. Jordan-Dahlgren, S. Merkel, and E. Rosenberg. 2007. Coral disease, environmental drivers, and the balance between coral and microbial associates. Oceanography 20:172–95.

Harvell, C. D., D. Montecino-Latorre, J. M. Caldwell, J. M. Burt, K. Bosley, A. Keller, S. F. Heron, A. K. Salomon, L. Lee, and O. Pontier. 2019. Disease epidemic and a marine heat wave are associated with the continental-scale collapse of a pivotal predator (*Pycnopodia helianthoides*). Science Advances 5:eaau7042.

Hewson, I., J. B. Button, B. M. Gudenkauf, B. Miner, A. L. Newton, J. K. Gaydos, J. Wynne, C. L. Groves, G. Hendler, and M. Murray. 2014. Densovirus associated with sea-star wasting disease and mass mortality. Proceedings of the National Academy of Sciences 111:17278–83.

Hewson, I., K. S. Bistolas, E. M. Quijano Cardé, J. B. Button, P. J. Foster, J. M. Flanzenbaum, J. Kocian, and C. K. Lewis. 2018. Investigating the complex association between viral ecology, environment, and northeast Pacific sea star wasting. Frontiers in Marine Science 5:77.

Jakobsson-Thor, S., G. B. Toth, J. Brakel, A.-C. Bockelmann, and H. Pavia. 2018. Seagrass wasting disease varies with salinity and depth in natural *Zostera marina* populations. Marine Ecology Progress Series 587:105–15.

Kumar, C. S., D. V. Sarada, T. P. Gideon, and R. Rengasamy. 2008. Antibacterial activity of three South Indian seagrasses, *Cymodocea serrulata*, *Halophila ovalis* and *Zostera capensis*. World Journal of Microbiology and Biotechnology 24:1989–92.

Lafferty, K. D., and A. M. Kuris. 1993. Mass mortality of abalone *Haliotis cracherodii* on the California Channel Islands: tests of epidemiological hypotheses. Marine Ecology Progress Series 96:239–48.

Lafferty, K., J. W. Porter, and S. Fort. 2004. Are diseases increasing in the ocean? Annual Review of Ecology, Evolution, and Systematics 35:31–54.

Lafferty, K. D., C. D. Harvell, J. M. Conrad, C. S. Friedman, M. L. Kent, A. M. Kuris, E. N. Powell, D. Rondeau, and S. M. Saksida. 2015. Infectious diseases affect marine fisheries and aquaculture economics. Annual Review of Marine Science 7:471–96.

Lamb, J. B., and B. L. Willis. 2011. Using coral disease prevalence to assess the effects of concentrating tourism activities on offshore reefs in a tropical marine park. Conservation Biology 25:1044–52.

Lamb, J. B., J. D. True, S. Piromvaragorn, and B. L. Willis. 2014. Scuba diving damage and intensity of tourist activities increases coral disease prevalence. Biological Conservation 178:88–96.

Lamb, J. B., D. H. Williamson, G. R. Russ, and B. L. Willis. 2015. Protected areas mitigate diseases of reef-building corals by reducing damage from fishing. Ecology 96:2555–67.

Lamb, J. B., A. S. Wenger, M. J. Devlin, D. M. Ceccarelli, D. H. Williamson, and B. L. Willis. 2016. Reserves as tools for alleviating impacts of marine disease. Philosophical Transactions of the Royal Society B: Biological Sciences 371:20150210.

Lamb, J. B., J. A. van de Water, D. G. Bourne, C. Altier, M. Y. Hein, E. A. Fiorenza, N. Abu, J. Jompa, and C. D. Harvell. 2017. Seagrass ecosystems reduce exposure to bacterial pathogens of humans, fishes, and invertebrates. Science 355:731–3.

Lamb, J. B., B. L. Willis, E. A. Fiorenza, C. S. Couch, R. Howard, D. N. Rader, J. D. True, L. A. Kelly, A. Ahmad, J. Jompa, and C. D. Harvell. 2018. Plastic waste associated with disease on coral reefs. Science 359:460–2.

Lamont, R. J., and G. Hajishengallis. 2015. Polymicrobial synergy and dysbiosis in inflammatory disease. Trends in Molecular Medicine 21:172–83.

Lips, K. R., F. Brem, R. Brenes, J. D. Reeve, R. A. Alford, J. Voyles, C. Carey, L. Livo, A. P. Pessier, and J. P. Collins. 2006. Emerging infectious disease and the loss of biodiversity in a Neotropical amphibian community. Proceedings of the National Academy of Sciences 103:3165–70.

Mani, A. E., V. Bharathi, and J. Patterson. 2012. Antibacterial activity and preliminary phytochemical analysis of seagrass *Cymodocea rotundata*. International Journal of Microbiological Research 3:99–103.

Martin, D. L., Y. Chiari, E. Boone, T. D. Sherman, C. Ross, S. Wyllie-Echeverria, J. K. Gaydos, and A. A. Boettcher. 2016. Functional, phylogenetic and host-geographic signatures of *Labyrinthula* spp. provide for putative species delimitation and a global-scale view of seagrass wasting disease. Estuaries and Coasts 39:1403–21.

McCallum, H. 2012. Disease and the dynamics of extinction. Philosophical Transactions of the Royal Society B: Biological Sciences 367:2828–39.

McCallum, H., and A. Dobson. 1995. Detecting disease and parasite threats to endangered species and ecosystems. Trends in Ecology & Evolution 10:190–4.

McCallum, H., Harvell C. D, and Dobson A. 2003. Rates of spread of marine pathogens. Ecology Letters 6:1062–7.

Menge, B. A., E. B. Cerny-Chipman, A. Johnson, J. Sullivan, S. Gravem, and F. Chan. 2016. Sea star wasting disease in the keystone predator *Pisaster ochraceus* in Oregon: insights into differential population impacts, recovery, predation rate, and temperature effects from long-term research. PLoS ONE 11:e0153994.

Mera, H., and D. G. Bourne. 2018. Disentangling causation: complex roles of coral-associated microorganisms in disease. Environmental Microbiology 20:431–49.

Miner, C. M., J. L. Burnaford, R. F. Ambrose, L. Antrim, H. Bohlmann, C. A. Blanchette, J. M. Engle, S. C. Fradkin, R. Gaddam, and C. D. Harley. 2018. Large-scale impacts of sea star wasting disease (SSWD) on intertidal sea stars and implications for recovery. PLoS ONE 13:e0192870.

Montecino-Latorre, D., M. E. Eisenlord, M. Turner, R. Yoshioka, C. D. Harvell, C. V. Pattengill-Semmens, J. D. Nichols, and J. K. Gaydos. 2016. Devastating transboundary impacts of sea star wasting disease on subtidal asteroids. PLoS ONE 11:e0163190.

Muehlstein, L. K., D. Porter, and F. T. Short. 1991. *Labyrinthula zosterae* sp. nov., the causative agent of wasting disease of eelgrass, *Zostera marina*. Mycologia 83(2):180–91.

Muller, E. M., and R. van Woesik. 2012. Caribbean coral diseases: primary transmission or secondary infection? Global Change Biology 18:3529–35.

Muller, E. M., and R. van Woesik. 2014. Genetic susceptibility, colony size, and water temperature drive white-pox disease on the coral *Acropora palmata*. PLoS ONE 9:e110759.

Mydlarz, L. D., L. E. Jones, and C. D. Harvell. 2006. Innate immunity, environmental drivers, and disease ecology of marine and freshwater invertebrates. Annual Review of Ecology, Evolution, and Systematics 37:251–88.

Nicolet, K. J., M. O. Hoogenboom, N. M. Gardiner, M. S. Pratchett, and B. L. Willis. 2013. The corallivorous invertebrate *Drupella* aids in transmission of brown band disease on the Great Barrier Reef. Coral Reefs 32:585–95.

Onishi, Y., Y. Mohri, A. Tuji, K. Ohgi, A. Yamaguchi, and I. Imai. 2014. The seagrass *Zostera marina* harbors growth-inhibiting bacteria against the toxic dinoflagellate *Alexandrium tamarense*. Fisheries Science 80:353–62.

Orth, R. J., T. J. Carruthers, W. C. Dennison, C. M. Duarte, J. W. Fourqurean, K. L. Heck, A. R. Hughes, G. A. Kendrick, W. J. Kenworthy, and S. Olyarnik. 2006. A global crisis for seagrass ecosystems. BioScience 56:987–96.

Paine, R. T. 1969. A note on trophic complexity and community stability. The American Naturalist 103:91–3.

Pollock, F. J., J. B. Lamb, S. N. Field, S. F. Heron, B. Schaffelke, G. Shedrawi, D. G. Bourne, and B. L. Willis. 2014. Sediment and turbidity associated with offshore dredging increase coral disease prevalence on nearby reefs. PLoS ONE 9:e102498.

Power, M. E., D. Tilman, J. A. Estes, B. A. Menge, W. J. Bond, L. S. Mills, G. Daily, J. C. Castilla, J. Lubchenco, and R. T. Paine. 1996. Challenges in the quest for keystones:

identifying keystone species is difficult—but essential to understanding how loss of species will affect ecosystems. BioScience 46:609–20.

Raimondi, P. T., C. M. Wilson, R. F. Ambrose, J. M. Engle, and T. E. Minchinton. 2002. Continued declines of black abalone along the coast of California: are mass mortalities related to El Niño events? Marine Ecology Progress Series 242:143–52.

Randall, C. J., A. G. Jordán-Garza, E. M. Muller, and R. Van Woesik. 2014. Relationships between the history of thermal stress and the relative risk of diseases of Caribbean corals. Ecology 95:1981–94.

Raymundo, L. J., W. L. Licuanan, and A. M. Kerr. 2018. Adding insult to injury: Ship groundings are associated with coral disease in a pristine reef. PLoS ONE 13:e0202939.

Richardson, L. L., K. G. Goldberg, R. B. Kuta, R. B. Aronson, G. W. Smith, K. B. Ritchie, J. C. Halas, J. S. Feingold, and S. M. Miller. 1998. Florida's mystery coral killer identified. Nature 392:557–8.

Roberts, C. M., C. J. McClean, J. E. Veron, J. P. Hawkins, G. R. Allen, D. E. McAllister, C. G. Mittermeier, F. W. Schueler, M. Spalding, and F. Wells. 2002. Marine biodiversity hotspots and conservation priorities for tropical reefs. Science 295:1280–4.

Rogers, A., J. L. Blanchard, and P. J. Mumby. 2014. Vulnerability of coral reef fisheries to a loss of structural complexity. Current Biology 24:1000–5.

Rubio-Guerri, C., M. Melero, F. Esperón, E. N. Bellière, M. Arbelo, J. L. Crespo, E. Sierra, D. García-Párraga, and J. M. Sánchez-Vizcaíno. 2013. Unusual striped dolphin mass mortality episode related to cetacean morbillivirus in the Spanish Mediterranean Sea. BMC Veterinary Research 9:106.

Schiebelhut, L. M., J. B. Puritz, and M. N. Dawson. 2018. Decimation by sea star wasting disease and rapid genetic change in a keystone species, *Pisaster ochraceus*. Proceedings of the National Academy of Sciences 115(27):201800285.

Schultz, J. A., R. N. Cloutier, and I. M. Côté. 2016. Evidence for a trophic cascade on rocky reefs following sea star mass mortality in British Columbia. Peer Journal 4:e1980.

Shelton, A. O., T. B. Francis, B. E. Feist, G. D. Williams, A. Lindquist, and P. S. Levin. 2017. Forty years of seagrass population stability and resilience in an urbanizing estuary. Journal of Ecology 105:458–70.

Short, F. T., L. K. Muehlstein, and D. Porter. 1987. Eelgrass wasting disease: cause and recurrence of a marine epidemic. The Biological Bulletin 173:557–62.

Short, F. T., B. W. Ibelings, and C. Den Hartog. 1988. Comparison of a current eelgrass disease to the wasting disease in the 1930s. Aquatic Botany 30:295–304.

Sullivan, B. K., T. D. Sherman, V. S. Damare, O. Lilje, and F. H. Gleason. 2013. Potential roles of *Labyrinthula* spp. in global seagrass population declines. Fungal Ecology 6:328–38.

Sullivan, B. K., S. M. Trevathan-Tackett, S. Neuhauser, and L. L. Govers. 2018. Host–pathogen dynamics of seagrass diseases under future global change. Marine Pollution Bulletin 134:75–88.

Supaphon, P., S. Phongpaichit, V. Rukachaisirikul, and J. Sakayaroj. 2013. Antimicrobial potential of endophytic fungi derived from three seagrass species: *Cymodocea serrulata*, *Halophila ovalis* and *Thalassia hemprichii*. PLoS ONE 8:e72520.

Sutherland, K. P., B. Berry, A. Park, D. W. Kemp, K. M. Kemp, E. K. Lipp, and J. W. Porter. 2016. Shifting white pox aetiologies affecting *Acropora palmata* in the Florida Keys, 1994–2014. Philosophical Transactions of the Royal Society B: Biological Sciences 371:20150205.

Tissot, B. N. 1995. Recruitment, growth, and survivorship of black abalone on Santa Cruz Island following mass mortality. Bulletin of the Southern California Academy of Sciences 94:179–89.

Vega Thurber, R. L., D. E. Burkepile, C. Fuchs, A. A. Shantz, R. McMinds, and J. R. Zaneveld. 2014. Chronic nutrient enrichment increases prevalence and severity of coral disease and bleaching. Global Change Biology 20:544–54.

Wares, J. P., and L. M. Schiebelhut. 2016. What doesn't kill them makes them stronger: an association between elongation factor 1-α overdominance in the sea star *Pisaster ochraceus* and "sea star wasting disease." Peer Journal 4:e1876.

Waycott, M., C. M. Duarte, T. J. B. Carruthers, R. J. Orth, W. C. Dennison, S. Olyarnik, A. Calladine, J. W. Fourqurean, K. L. Heck, A. R. Hughes, G. A. Kendrick, W. J. Kenworthy, F. T. Short, and S. L. Williams. 2009. Accelerating loss of seagrasses across the globe threatens coastal ecosystems. Proceedings of the National Academy of Sciences 106:12377–81.

Weil, E. 2004. Coral reef diseases in the wider Caribbean, pp. 35–68. In: E. Rosenberg and Y. Loya (eds) Coral Health and Disease. Springer, Berlin.

Wobeser, G. A. 2006. Essentials of Disease in Wild Animals. Blackwell Publishing, Ames, Iowa.

Wu, S., P. N. Carvalho, J. A. Müller, V. R. Manoj, and R. Dong. 2016. Sanitation in constructed wetlands: a review on the removal of human pathogens and fecal indicators. Science of the Total Environment 541:8–22.

Zaneveld, J. R., R. McMinds, and R. V. Thurber. 2017. Stress and stability: applying the Anna Karenina principle to animal microbiomes. Nature Microbiology 2:17121.