A framework for examining climate-driven changes to the seasonality and geographical range of coastal pathogens and harmful algae

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ABSTRACT

Climate change is expected to alter coastal ecosystems in ways which may have predictable consequences for the seasonality and geographical distribution of human pathogens and harmful algae. Here we demonstrate relatively simple approaches for evaluating the risk of occurrence of pathogenic bacteria in the genus *Vibrio* and outbreaks of toxin-producing harmful algae in the genus *Alexandrium*, with estimates of uncertainty, in U.S. coastal waters under future climate change scenarios through the end of the 21st century. One approach forces empirical models of growth, abundance and the probability of occurrence of the pathogens and algae at specific locations in the Chesapeake Bay and Puget Sound with ensembles of statistically downscaled climate model projections to produce first order assessments of changes in seasonality. In all of the case studies examined, the seasonal window of occurrence for *Vibrio* and *Alexandrium* broadened, indicating longer annual periods of time when there is increased risk for outbreaks. A second approach uses climate model projections coupled with GIS to identify the potential for geographic range shifts for *Vibrio* spp. in the coastal waters of Alaska. These two approaches could be applied to other coastal pathogens that have climate sensitive drivers to investigate potential changes to the risk of outbreaks in both time (seasonality) and space (geographical distribution) under future climate change scenarios.

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Introduction

The most recent assessment by the Intergovernmental Panel on Climate Change provided unequivocal evidence for warming of the climate system. Emissions of greenhouse gases from human activities are the highest in history, and have caused unprecedented warming (IPCC, 2014). During the period from 1880 to 2012, mean global land surface air temperatures have increased by 0.85 °C with a greater rate of change in the period from 1970 to present (IPCC, 2014). Similarly, over the last four decades, surface waters of our oceans have warmed at a rate of 0.11 °C per decade, and alterations in precipitation patterns have increased salinity in the Atlantic Ocean and decreased salinity in the Pacific and Southern Oceans (IPCC, 2014). From 1901 to 2010, mean global sea level has risen 0.19 m and the rate of ice loss from glaciers around the

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world has also increased (IPCC, 2014). While much progress has been made in documenting historical changes in climate and generating future climate projections based on various greenhouse gas concentration trajectories, understanding the ecological and human health impacts, especially in coastal systems, and developing strategies for addressing them has (necessarily) lagged behind.

Most assessments of climate change impacts on human health have focused on direct impacts such as the potential for more frequent and severe heat events causing heat stroke, worsening air pollution causing respiratory disease, and more frequent extreme events (e.g., flood, wild fire) causing loss of life (Haines et al., 2006). Of equal concern, but arguably more difficult to predict, are the indirect impacts of climate change, including changes to vector-, food- and waterborne diseases arising from the disruption of natural systems (Hunter, 2003; Noyes et al., 2009; Tirado et al., 2010). Naturally occurring pathogens and harmful algae in coastal environments are very likely to be affected by climate change, resulting in changes in their distribution, abundance, and perhaps virulence or toxicity (Moore et al., 2008; Mahoney et al., 2010; Baker-Austin et al., 2012; Vezzulli et al., 2013). However, the inherent complexity of coastal systems can complicate projections of the pathogen and algae responses. Experts agree that changes are highly likely to occur, but quantitative analyses of the direction, magnitude, and timing of these changes are often lacking (e.g., Anderson et al., 2012). Decision makers responsible for protecting human health need quantitative information on how the risk of illness from coastal pathogens and harmful algae will change in the future, with estimates of uncertainty, to inform the development of preparedness, mitigation, and adaptation strategies.

For some human pathogens and harmful algae in coastal systems, temperature exerts strong constraints on their physiology (e.g., Paerl and Huisman, 2008), controlling their distribution and abundance in space and time. These organisms cannot grow outside of certain temperature windows, and optimal temperatures within the window support proliferative growth. Because changes to temperature in the U.S. and globally are among the most confident projections of climate change with high agreement among climate models in both the direction and magnitude of change (IPCC, 2014; Walsh et al., 2014), the pathogen and algae responses to climate change may have predictable outcomes. Here we evaluate the impacts of climate change on the potential for outbreaks of toxin-producing harmful algae in the genus *Alexandrium* and occurrence and abundance of bacteria in the genus *Vibrio* that threaten human health.

Harmful algal blooms (HABs) are becoming increasingly frequent in U.S. coastal waters and some have expanded into new geographic locations (e.g., Tester et al., 1991; Campbell et al., 2010; Nishimura et al., 2013), consistent with an apparent worldwide trend (Hallegraeff, 1993, 2010; Van Dolah, 2000; Lewitus et al., 2012). Some harmful algae produce toxins that cause disease in humans that contact them. Paralytic shellfish poisoning (PSP) is perhaps the most widespread of the HAB-related diseases (Erdner et al., 2008) and is caused by potent neurotoxins that are produced by dinoflagellates in the genus *Alexandrium*. The toxins accumulate in filter feeding shellfish when *Alexandrium* bloom and human consumption of contaminated shellfish can cause PSP, characterized by gastrointestinal and neurological symptoms. In severe intoxications, muscle paralysis can develop and death can occur (Quayle, 1969; Kao, 1993). In Puget Sound, Washington State, *Alexandrium* blooms have increased in geographic scope since the 1950s (Trainer et al., 2003) and it is very likely that the 20th century warming trend contributed to the increasing trend in shellfish toxicity (Moore et al., 2011). The timing of blooms is sensitive to weather and climate variations, with toxic blooms largely driven by warm air and water temperatures (Moore et al., 2009).

Puget Sound strains of *Alexandrium* grow over a range of temperatures from ∼7 to 24 °C, with optimal growth occurring at temperatures between ∼10 and 21 °C (Bill et al., submitted for publication). Temperatures exceeding 13 °C have been associated with increased risk of Puget Sound shellfish being contaminated with toxins produced *Alexandrium* (Nishitani and Chew, 1984). The species of *Alexandrium* thought to be responsible for blooms in Puget Sound has historically been identified as *Alexandrium catenella*; however, the name *Alexandrium fundyense* has recently been proposed to replace all Group I strains of the *Alexandrium tamarense* species complex that includes *A. catenella* (John et al., 2014).

Cases of *Vibrio* related illness have increased in the U.S. over the past decade (Newton et al., 2012). *Vibrio* are gram negative, flagellated bacteria that serve as functional members of the natural heterotrophic community in coastal waters. They freely associate with a variety of biotic and abiotic surfaces including water, sediment, fish, shellfish, algae, and zooplankton (Depaola et al., 1994; Maugeri et al., 2006; Turner et al., 2009; Johnson et al., 2010). Several species of *Vibrio* are known to cause illness in humans, with symptoms ranging from skin irritation and gastroenteritis, to bullous lesions, septicemia and mortality. Principal among these are strains of *Vibrio cholerae*, *Vibrio vulnificus*, and *Vibrio parahaemolyticus*. *V. cholerae*, the causative agent of cholera, is endemic to US coastal waters, but nearly all cases of toxigenic 01 and 0139 serotypes are associated with foreign travel (CDC_COVIS, 2014). Some non 01 and 0139 serotypes however, are diarrheagenic and are isolated in 5–10% of reported *Vibrio* related illnesses (Newton et al., 2012). *V. parahaemolyticus* and *V. vulnificus* are associated with the majority of the estimated 80,000 illnesses annually in the US (Scallan et al., 2011).

Temperature strongly controls *Vibrio* growth, generally being inhibitory <10 °C and optimal at ∼37 °C (Martinez-Urtaza et al., 2010). As such, it is highly likely that warming of our coastal oceans will accelerate the spread of *Vibrio* to northern latitudes, where the warming effect is projected to be most pronounced. In the past decade alone, outbreaks have been documented in Alaska, Spain, Europe, and north Atlantic states of the U.S. and correlatively linked to warming trends (González-Escalona et al., 2005; McLaughlin et al., 2005; Baker-Austin et al., 2012; García et al., 2013; Martinez-Urtaza et al., 2013). For example, Baker-Austin et al. (2012) recently provided statistical evidence of the relationship between sea surface temperature (SST) and increasing illnesses in the Baltic. In Alaska, a 2004 outbreak of *V. parahaemolyticus* among cruise ship passengers was associated with an anomalous SST event pushing warm waters into Prince William Sound (McLaughlin et al., 2005). In the Chesapeake, several statistical models have been developed relating SST and other variables