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Detecting and Attributing Health Burdens to Climate Change

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Background: Detection and attribution of health impacts caused by climate change uses formal methods to determine *a*) whether the occurrence of adverse health outcomes has changed, and *b*) the extent to which that change could be attributed to climate change. There have been limited efforts to undertake detection and attribution analyses in health.

Objective: Our goal was to show a range of approaches for conducting detection and attribution analyses.

Results: Case studies for heatwaves, Lyme disease in Canada, and *Vibrio* emergence in northern Europe highlight evidence that climate change is adversely affecting human health. Changes in rates and geographic distribution of adverse health outcomes were detected, and, in each instance, a proportion of the observed changes could, in our judgment, be attributed to changes in weather patterns associated with climate change.

Conclusions: The results of detection and attribution studies can inform evidence-based risk management to reduce current, and plan for future, changes in health risks associated with climate change. Gaining a better understanding of the size, timing, and distribution of the climate change burden of disease and injury requires reliable long-term data sets, more knowledge about the factors that confound and modify the effects of climate on health, and refinement of analytic techniques for detection and attribution. At the same time, significant advances are possible in the absence of complete data and statistical certainty: there is a place for well-informed judgments, based on understanding of underlying processes and matching of patterns of health, climate, and other determinants of human well-being. https://doi.org/10.1289/EHP1509

Introduction

Detection and attribution of the impacts of climate change on human and natural and managed systems relies on formal scientific methods. These methods are applied to determine whether an aspect of system function has changed since a baseline or reference period, and then to determine whether/how much of that change could be attributed to climate change (Stone et al. 2013). The value of these studies was underscored by the United Nations Framework Convention on Climate Change requirement that signatories to the convention adopt measures to "prevent dangerous anthropogenic interference with the climate system" (UN 1992).

There have been limited efforts to understand the extent to which changes in the current burdens of climate-sensitive health outcomes could be formally attributed to climate change (Cramer et al. 2014). Nevertheless there is strong evidence now that changing weather patterns associated with climate change are shifting the geographic range, seasonality, and intensity of transmission of selected climate-sensitive infectious diseases (Semenza and Menne 2009), and increasing morbidity and mortality associated with extreme weather and climate events (Smith et al. 2014). We now have a much better understanding of the character, timing, and spatial pattern of climate change due to research undertaken over the past several decades (IPCC 2013). Together with demonstrable changes in disease incidence and/or mortality, this means it is now possible, in a few instances, to attribute a portion of current burdens of specific climate-sensitive health outcomes to climate change. Building the evidence-base on detection and attribution (D&A) is the basis for better evidence-based risk management to reduce current and plan for future climate change-related health burdens, and to inform advocacy for actions to mitigate greenhouse gas emissions.

We review detection and attribution methods, discuss their application in health research, provide three case studies selected to illustrate the diversity of issues in this field, and conclude with research and data needs for furthering D&A studies in health.

Background on Detection and Attribution Methods

D&A studies determine *a*) "whether a system is changing beyond a specified baseline that characterizes behavior in the absence of climate change"; and *b*) "whether climate change has contributed substantially to the observed change in a system" (Stone et al. 2013). Because climate is always changing, and because there are many factors that can influence whether an aspect of a health or other system changed over time, with these factors also changing over time, studies establish baselines or reference periods against which change is measured. D&A analyses of impacts ideally isolate the system of interest, such as the constellation of influences on Lyme disease, and then determine whether the observed behavior in the system changes when other factors than climate are removed or held constant to the extent possible. Attribution studies typically focus on whether and to what extent a system has changed in response to observed climate change (Stone et al. 2013).

D&A studies have a long history in climate science in quantifying the extent to which climate change has changed the mean and variability of weather variables (Hegerl and Zwiers 2011). The main approaches to D&A can be categorized into single-step and multi-step studies (Stone et al. 2013).

- **Single-step attribution** uses a single comprehensive statistical model that detects a significant change in the variable of interest and compares the observed change with that expected if climate change had not occurred. This approach is typically used for weather data; for example, temperature and heat-related mortality.
- **Multi-step attribution** links separate single-step approaches that *a*) attribute an observed change in a variable of interest to a change in climate or other environmental variable, and

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b) attribute the change in climate to external drivers (e.g., greenhouse gas emissions). For example, the first step links temperature increases to heat-related mortality. The second step links the temperature increase to anthropogenic greenhouse gas emissions. The assessment of the relationships between climate and the variable of interest may involve a process model or statistical association. This approach has been used for D&A in ecosystem studies (Root et al 2003; Parmesan and Yohe 2003).

In addition, synthesis assessments review and assess large numbers of results that demonstrate the sensitivity of impacts to a change in climatic conditions or other drivers. Through a meta-analysis, health outcomes (e.g., heat-related mortality) described in the existing (peer-reviewed) literature can be correlated with an actual pattern of observed warming. This approach often uses spatial and temporal measures of association. This approach has been used in ecosystem and agricultural detection and attribution studies (Rosenzweig et al. 2008).

Specifying the causal factor to which a change is being attributed is important. Many climate D&A studies focused on expected fingerprints of changes in weather patterns associated with climate change and their associated uncertainties, where fingerprints are metrics or space–time patterns of the response of climate variables to anthropogenic (e.g., greenhouse gas emissions) or natural (e.g., solar radiation changes) forcing. Examples of fingerprints include changes in global mean surface temperature, precipitation, and sea ice extent (IPCC 2013).

In many sectors the paucity of long-run data series leads to a focus on sensitivity to weather (e.g., extreme events). But system responses to long-term change may be different to the responses to acute events. For example, on a time scale of decades, local food production may shift successfully to new heat-tolerant technologies or be abandoned altogether (IPCC 2013). There are few examples of health studies that seek to identify impacts in the long term. One is the report by Bennett et al. (2014) on the shifting balance of winter and summer mortality in Australia between 1968 and 2008 (Bennett et al. 2014).

Applying D&A Methods to Health Outcomes

Detection analyzes data on health and weather/climate to determine whether any change occurred over time, and if so, the probability that this change can be explained by background variability in the system (Stocker et al. 2010). An identified change is considered to have occurred if its likelihood of occurrence due to natural variability is small (e.g., a signal can be detected). Health systems routinely collect and analyze data on a wide variety of health outcomes to chart trends over time and to evaluate the effectiveness of policies and plans to improve population health. Once a trend is detected, then attribution investigates the relative contributions of multiple possibly causal factors. This is not straightforward because many factors may influence the magnitude and pattern of health burdens in a particular region, including the effectiveness of control programs, weather and other environmental variables, sociodemographic change, land use change, trade and tourism, and others (Semenza et al. 2016). Systematic monitoring is required to provide robust estimates of how variables changed over time. Attribution then partitions the reasons for a trend amongst key drivers of the health outcome (e.g., outdoor air quality, smoking habits, and population age structure may be changing simultaneously and each influences mortality rates (compare Prüss-Üstün and Corvalán 2006; Prüss-Üstün et al. 2016).

D&A assumes there is a reference period against which the health data will be compared, taking into consideration that weather and health data are characterized by year-to-year (and shorter-term) variability and longer-term trends. Disease incidence and mortality rates have changed substantially (mostly for the better) over recent decades, which means there is no natural reference period. For example, at the same time as evidence is accumulating that climate change is likely changing the geographic range of the *Anopheles* mosquitoes that can carry malaria, multiple international and national initiatives are reducing the burden of malaria (Smith et al. 2014). Another challenge is that uncertainties in data quality for many climate-sensitive health outcomes increase the further back one goes, but recent periods, those with the best data and therefore potentially the most suitable reference points, are those affected by early impacts of climate change, which means attribution of a climate change effect may be an underestimate of the true impact. In any case, clear specification of the reference period is needed so that estimates of the extent to which changing health burdens could be attributed to climate change can be quantified over time.

In epidemiology, attribution is often described using the population attributable fraction of a risk factor; it is the proportional reduction in deaths or cases of disease that would occur if exposure to this factor were removed or reduced to an alternative exposure distribution (Prüss-Üstün and Corvalán 2006; Prüss-Üstün et al. 2016). Calculating the population attributable fraction requires data on the prevalence of exposure to the risk factor within the population of interest, and the relative risk of the health outcome associated with each level of exposure.

However, exposures to weather and climate are different than typical environmental exposures, which creates several challenges (Bernard and Ebi 2001). Everyone is exposed to weather. Even with most people spending much of their time indoors, virtually the entire population is affected (potentially) by the consequences of changing weather patterns, such as increases in the frequency and intensity of heatwaves. But this exposure is not the same for everyone—vulnerability mapping shows that particular locations and population groups have higher levels of exposure to, for example, higher ambient temperatures than the average for a region or to greater risks for flooding (e.g., Reid et al. 2009). Another complexity is the lack of a well-defined reference period. Climate change has been changing weather and climate patterns for longer than there are quality health data sets in most regions, thus it is often not possible to establish what would be a "climate normal" for health detection and attribution studies before anthropogenic climate change. Autonomous adaptation (e.g., adaptation in response to experience of climate and its effects, without a specific focus on addressing the risks of climate change) also affects trends in some climate-sensitive health outcomes (e.g., Åström et al. 2016; Todd and Valleron 2015).

Three Case Studies of D&A of the Health Risks of Climate Change

Within this context, we explore three case studies to highlight different approaches to attributing some of the current burden of climate-sensitive health outcomes to climate change. The studies are concerned with heatwave deaths, emergence of Lyme disease in Canada, and emergence of vibrio infections in northern Europe. In different ways, the studies complete the requirements of D&A to show that climate change is already adversely affecting human health. Other examples include cold-related mortality in England, Wales, and Australia; pollen production; changes in the geographic range of tick-borne encephalitis, plague, and tularemia; and malaria (summarized by Cramer et al. 2014). The following examples are purposely not exhaustive and should be considered illustrative only. Exploration of specific case studies highlights the diversity of methods used.

Approaches to Estimating the Number of Heatwave Deaths Attributable to Climate Change

Background

There is robust evidence that *a*) climate change is affecting the frequency, intensity, and duration of heatwaves (IPCC 2013); and *b*) exposure to high ambient temperatures is associated with excess morbidity and mortality (e.g., Gasparrini et al. 2015). Therefore, following multi-step attribution, recent assessments concluded that climate change is affecting heat-related mortality. For example, while noting there are multiple social, environmental, and behavioral factors that influence heat-related mortality, Cramer et al. (2014) concluded that climate change has contributed to increased heat-related mortality in recent decades in Australia, England, and Wales, with medium confidence (Cramer et al. 2014).

Because few of the individuals who die during heatwaves are diagnosed as suffering from heat exposure, impact studies typically calculate excess mortality at the level of populations. The effects may be substantial: tens of thousands of excess deaths occurred during the European heatwave of 2003 and the Russian heatwave of 2010 (Robine et al. 2008; Shaposhnikov et al. 2014). Although some of the deaths would have occurred anyway during or shortly after a heatwave (mortality displacement), the lack of a substantial compensating undershoot in mortality in subsequent months and years suggests most of the lost person-time was a genuine heatwave effect (e.g., Robine et al. 2008).

Estimating how the change in exposure to heatwaves affects health requires considering other variables that influence heat-related morbidity and mortality such as age, poverty, education, living alone, race/ethnicity, preexisting medical conditions (diabetes, renal disease, CVD), etc., and how these factors changed over time.

Different approaches can be taken to estimate what proportion of deaths during a heatwave could be attributed to climate change as opposed to natural climate variability. As heatwaves outside recent historic experience increase, with higher probabilities that climate change was a major contributor to their occurrence, then the proportion of heatwave deaths attributed to climate change would be expected to increase.

Approaches to Attributing Heatwave-Related Deaths to Climate Change

Attributing a proportion of deaths during a heatwave to climate change requires multiple steps, taking into account that natural climate variability and anthropogenic climate change jointly contribute to the occurrence and intensity of a heatwave. Event attribution is a growing field in climatology that determines whether (and to what extent) an individual event was influenced by anthropogenic forcing of the climate system (Easterling et al. 2016; NAS 2016; Stott et al. 2016). Primary approaches include using the observational record to determine the change in probability or magnitude of an event (e.g., Stott et al. 2004; Schär et al. 2004) and using model simulations to compare the the probability of an event occurring with and without anthropogenic climate change (e.g., Hoerling et al. 2013). These provide slightly different information for use in estimating the number of deaths during a heatwave that could be attributed to climate change.

Without using event attribution, a simple approach to attributing heatwave-related deaths to climate change would be to estimate the shift in the distribution of heatwaves over the last few decades by intensity, duration, or frequency (Murray and Ebi 2012). All deaths occurring in heatwaves above an *a priori* threshold, such as the top 5% or 1%, could then be attributed to climate change.

A more conservative approach that could be based on event attribution would be to assume that climate change increased ambient temperature during a heatwave (e.g., that the heatwave would have occurred anyway, but the temperature was higher than would have happened without climate change). Then the attributable deaths would be those due to the additional temperature. However, estimating this fraction is not straightforward. Questions include how to estimate the temperature increase due to climate change; one approach is to assume the temperature increase during the heatwave is the same as the increase in regional mean temperature. Sensitivity analyses can be used to estimate uncertainty around the numbers of deaths attributed to climate change. There is no standard approach to estimating the number of deaths at the tail of the distribution, in part because there are few data points to allow robust quantification. Deaths could be estimated assuming a linear relationship between temperature and mortality, or it could be assumed that the increase in mortality per degree is greater with extreme temperature; the approach taken will yield very different results (Rocklöv and Ebi 2012).

As the field of event attribution advances, estimates of heat-related mortality could be based on the degree to which the event showed a fingerprint of climate change.

Two recent efforts took different approaches to heat-related D&A, not based on event attribution. A study in Stockholm, Sweden estimated the extent to which mortality due to temperature extremes during the period 1980–2009 could be attributed to climate change based on 1900–1929 baseline temperatures (Astrom et al. 2013). There was an increase in the number of heat extremes (days with temperatures above the 98th percentile of the 1900–1929 distribution) between the reference period ($n = 220$) and the study period ($n = 381$). The increase in daily mean temperatures suggested the increased number of heatwaves were due to climate change. The study concluded that mortality from heat extremes was double what would have occurred without climate change, adjusting for urbanization and the urban heat island effect.

Mitchell et al. estimated the number of deaths during the European heatwave of 2003 that could be attributed to climate change (D. Mitchell, M. Allen, K.L. Ebi, A. Gasparrini, L. Harrington, C. Heaviside, et al., unpublished data, 2015). Thousands of climate simulations of a high-resolution regional climate change generated a comprehensive description of the 2003 heatwave and the role of human influence. Climate change had a highly significant influence on large-scale modes of atmospheric variability. A health impact assessment approach was used to estimate the number of deaths attributed to anthropogenic climate change, using a percent increase in mortality per 1°C increase in maximum apparent temperature (includes temperature and humidity) above city-specific thresholds. The study estimated the risk of heat-related mortality increased about 70% in Central Paris and about 20% in London because of anthropogenic climate change.

Detection of Lyme Disease Emergence in Canada and Its Attribution to Climate Change

Background

The biologies of arthropod vectors and the dynamics of associated vector-borne diseases are intrinsically sensitive to weather, climate, and potentially, climate change (Githeko et al. 2000). Whether or not climate change will have a major impact on the frequency of vector-borne diseases depends on the role of other, climate-independent factors on distribution, abundance, and

activity of the vectors (Reiter 2001). This case study focuses on Lyme disease, a tick-transmitted zoonotic disease caused by the bacterium *Borrelia burgdorferi*, and in particular its emergence in Canada. The natural hosts of both the tick vector and bacterium are wild mammals and birds, and occasionally other taxa, with humans being accidental hosts for the vector and accidental and likely dead-end hosts for the bacterium. In theory, climate can impact Lyme disease risk at three levels, affecting *a*) tick vector distributions and abundance, *b*) *B. burgdorferi* transmission cycle occurrence and efficiency (and thus the proportion of ticks infected), and *c*) the likelihood of transmission to humans.

Lyme disease emerged in North America in the 1970s, and it is thought that this emergence was associated with landscape change driven by socioeconomic factors (migration of rural communities to cities with reforestation of farmland) that in turn allowed abundance of a key animal host of the tick vector of Lyme disease (white-tailed deer) to rebound (Barbour and Fish 1993). This then allowed the tick vector, *Ixodes scapularis*, to expand out of refuges in the northeast (particularly the New England town of Lyme from which Lyme disease gets its name) and the upper Midwest. Lyme disease risk continued to increase and expand its geographic range in the northern United States. Until the early 2000s there was only one known *I. scapularis* population in Canada (at Long Point on the north shore of Lake Erie in Ontario); prior to this time, this was considered the extreme northern outpost of the species. In the early 2000s, studies undertaken to explore what factors may limit the northward geographic spread of the tick (and Lyme disease risk) into Canada revealed that the habitat appeared suitable (Ogden et al. 2006a), with ticks being regularly dispersed into Canada (Ogden et al. 2006c) likely by migratory birds (Ogden et al. 2008a), but that temperature conditions were likely too cold for the ticks in most of Canada (Ogden et al. 2005). For *I. scapularis* in southern Canada, "too cold" essentially means that the temperature conditions across the 2- to 3-y lifecycle of the ticks are too low to allow completion of the lifecycle due to cold temperatures slowing rates of development from one tick lifecycle to the next, rather than direct effects of cold winter temperatures on tick survival. The tick's woodland habitat to some extent protects refuges from the extremes of temperature that limit survival (reviewed by Ogden and Lindsay 2016).

A population model of *I. scapularis* that incorporated known impacts of temperature on the tick was used to predict the geographic occurrence of current climatic suitability, as well as project future climatic suitability in Canada (Ogden et al. 2006b). These tended to corroborate projections based on a statistical "environmental niche" model for this tick (Brownstein et al. 2005). Field studies in 2007 to validate the model predictions detected that incursion of the tick had begun (Ogden et al. 2008b).

Detection and Evidence of Climate Associations: The Spatial Pattern

Cramer et al. (2014) concluded that changes in the latitudinal and altitudinal distribution of disease-carrying ticks in North America is consistent with observed warming trends, but evidence was lacking of any associated changes in the distribution of Lyme disease (Cramer et al. 2014).

The evidence for associations of Lyme disease risk in eastern Canada with climate comes from studies of the spatial patterns of tick, pathogen, and human Lyme disease case occurrence. These also served to "detect" the phenomenon of Lyme disease emergence in southern Canada. Temperature increase was considered a key driver of emergence, with this temperature change attributed to climate change (Vincent et al. 2012), while other possible drivers of emergence such as habitat change were ruled out over most of the affected area (Ogden et al. 2014).

The first studies to detect a significant expansion of the range of *I. scapularis* were conducted in 2007 and 2008 (Ogden et al. 2008b; Ogden et al. 2010) and found low abundance of *I. scapularis* at a number of sites in southern Quebec and low prevalence of *B. burgdorferi* in ticks at some of these sites. The spatial pattern of these tick-positive sites at a subprovincial scale was strongly and statistically significantly associated with the predicted numbers for the site based on the site temperature conditions obtained using a simulation model of the tick populations. This analysis accounted for other possible drivers for the emergence of the tick populations including estimated numbers of immigrating ticks, tick host abundance, and clustering/spatial autocorrelation issues. Other studies using the same sites or sampling sites in the region found consistent positive associations between the presence and abundance of *I. scapularis* ticks on animal hosts (rodents and deer) and temperature, accounting for a range of alternative potential drivers for tick occurrence including habitat, rodent host abundance, rodent host species diversity, animal-level variables (e.g., age, sex, reproductive status), deer density, rainfall, and the possibility of spatial autocorrelation (Bouchard et al. 2013a; Bouchard et al. 2013b). Further field surveillance data in eastern Canada supported the importance of temperature in determining the spatial pattern of establishment of *I. scapularis* at a multiprovince geographic scale in eastern Canada (Gabriele-Rivet et al. 2015).

Leighton et al. used passive tick surveillance data (adjusted to improve the geographic specificity in terms of detection of emerging tick populations) (Leighton et al. 2012; Koffi et al. 2012) to identify strong associations between the spatial occurrence of tick populations as well as the speed with which tick populations become established with temperature at a subnational scale. This analysis also accounted for land cover/habitat, rainfall, tick dispersion, and regional variations that may confound associations between the presence of tick populations and temperature.

Evolution of infection prevalence from low to high in tick populations detected in Canada in recent years (Ogden et al. 2010; Ogden et al. 2013a), and patterns of *B. burgdorferi* strain and tick haplotype diversity that suggest population founder events (Ogden et al. 2013b), also support the idea that the establishment of ticks and *B. burgdorferi* transmission cycles are an ongoing, dynamic emergence event.

Studies by Simon et al. suggested that temperature may also determine the geographic pattern of Lyme disease risk in eastern Canada by determining environments suitable for the white-footed mouse (Simon et al. 2014), which is an important reservoir of *B. burgdorferi* in general (Jones et al. 1998), and for strains that cause severe Lyme disease in particular (Mechai et al. 2016).

Together these studies detected the emergence of tick vector populations and Lyme disease risk in Canada in a spatial pattern that was strongly associated with climate—tick populations were more likely to be found in locations with a warmer climate across the multiyear lifecycle of the tick vector. This association accounted for a very wide range of alternative determinants of the observed spatial patterns.

Association of Emergence of Lyme Disease in Canada with Climate Change

There is one long-term passive tick surveillance data set of Lyme disease in Canada, established in the late 1990s between the National Microbiology Laboratory of the Public Health Agency of Canada and provincial public health organization partners. This program involves the voluntary submission of ticks from participating veterinary and medical clinics that obtain the ticks

by examination of, or presentation by, their clients (Ogden et al. 2006c). By careful analysis to relate the number of ticks submitted per unit population to the occurrence of tick populations (Koffi et al. 2012), Leighton et al. estimated how many locations (census subdivisions) in eastern and central Canada contained a tick population in each year from 1991 to 2008 (Leighton et al. 2012). The emergence of tick populations was temporally coincident with warming temperatures in southern Canada and, in particular, temperatures rising above model-derived thresholds for the basic reproductive number (R_0) of greater than 1, that is, above the predicted climatic threshold for tick population persistence (Ogden et al. 2014). Gabriel-Rivet et al. using cumulative field surveillance data from 467 field sites in eastern Canada, showed that this temperature threshold was highly predictive (with a sensitivity of up to 97%) of whether and where tick populations were found in surveillance at a multiprovince scale in eastern Canada (Gabriele-Rivet et al. 2015).

In the second step in the D&A of the emergence of Lyme disease in Canada to climate change, Vincent et al. (2012) showed that climate change was responsible for a warming climate in southern Canada. The emergence of tick populations in all regions appeared subsequent to warming increasing temperature conditions such that predicted R_0 is >1, in fact >1.5–2.0 (Ogden et al. 2014; McPherson et al. 2017), which is perhaps more biologically plausible given the likelihood of stochastic fade out of populations when R_0 is close to 1 (Anderson et al. 1992).

Even so, it could be argued that warming in southern Canada and emergence of *I. scapularis* tick populations was just coincidence, and that the process of northward spread of *I. scapularis* tick populations was simply a matter of the tick continuing to more completely fill its ecological niche in North America. However, Leighton et al. provided empirical evidence that during the period of warming, locations acquired tick populations faster the warmer they were, over and above other possible determinants of tick population establishment (dispersal, spatial spread from neighboring locations, habitat, etc.) (Leighton et al. 2012). This empirical information is therefore key to identifying the importance of rising temperatures in the region to the emergence of vector tick populations, as was recognized in (Cramer et al. 2014).

More recently it has become clear that the changing geographic distribution of *I. scapularis* populations is reflected in the geographic pattern in occurrence of Lyme disease cases in eastern and central Canada (Ogden et al. 2015). Furthermore, over recent years the spread of the tick vector has been associated with steadily increasing numbers of Lyme disease cases, confirming that the ecological phenomenon of climate change-driven spread of the tick, accompanied by *B. burgdorferi* transmission cycles, has had clear public health consequences in Canada (Ogden et al. 2014b; Ogden et al. 2015).

The impact of climate change appears to be region-specific (i.e., affecting the northern limit of the range of the tick and pathogen); farther south in the United States, there are more possible alternative drivers for the continued emergence of Lyme disease (Eisen et al. 2015).

Detection of *Vibrio* Emergence in the Baltic Sea and Its Attribution to Climate Change

Background

Vibrio bacteria are typically found in marine environments and can cause foodborne outbreaks and wound infections (Semenza et al. 2012a). Brackish saltwater and elevated sea surface temperature (SST) are ideal environmental growth conditions for certain *Vibrio* species (Semenza et al. 2012b). These conditions can be found during the summer months in estuaries and enclosed water bodies with moderate salinity. *Vibrio* infections seem to be on the increase, particularly in the Baltic Sea in Northern Europe, in line with a projected rise in sea surface temperature (SST) due to climate change (Levy 2015; Vezzulli et al. 2016).

Several species of *Vibrio* are pathogenic, including *Vibrio cholera* (the causative agent of cholera) and noncholera *Vibrio* spp. that includes *V. parahaemolyticus* and *V. vulnificus* (Semenza et al. 2012a). Contamination of raw or undercooked seafood, typically oysters, is the predominant cause the acute gastroenteritis caused by *V. parahaemolyticus*. Although wound infections with *V. parahaemolyticus* also occur, they are less frequent than seafood-borne infections. In fact, *V. parahaemolyticus* outbreaks tend to be clustered along coastal areas in late summer and early fall when SSTs surpassed the threshold of 15°C that favors bacterial replication (Semenza et al. 2012a). Besides oysters and clams, other seafood associated with these outbreaks includes shrimp, crab, squid, mackerel, tuna, and sardines. Recreational water use in areas with high bacterial load or working in affected areas can also result in infections of the eyes, ears, or open cuts and wounds. Subsequent to Hurricane Katrina, 22 *Vibrio* wound infections were reported, 3 caused by *V. parahaemolyticus* and 2 of which were fatal.

V. vulnificus is an even more virulent bacterium that can cause three types of infections (Heymann 2015): *a*) acute gastroenteritis from consuming raw or undercooked shellfish, including oysters; *b*) necrotizing wound infections due to exposure of skin lesions to contaminated marine water (case fatality rate 25%); and *c*) invasive septicemia due to exposure to contaminated food or infection of an open wound (50% case fatality rate). Immunocompromised individuals with chronic liver disease are particularly at risk for developing fatal septic shock from *V. vulnificus* infections.

In the United States, infection with other *Vibrio* species, besides *V. cholera*, became nationally notifiable in January 2007. A total of 1,252 *Vibrio* infections (excluding toxigenic *V. cholerae* O1 and O139) were reported to CDC in 2014, of which 326 (27%) resulted in hospitalizations, and 34 (4%) in death (CDC 2014). *V. parahaemolyticus* was responsible for almost half of all cases but only 1% of deaths, and *V. vulnificus* was isolated from 10% of the patients, 18% of whom died. Of all these *Vibrio* cases, a third was reported from Pacific Coast states, a quarter from Gulf Coast states, a quarter from Atlantic Coast states and the remaining from noncoastal states. Of the domestically acquired vibriosis cases, a third (402) were non-foodborne (confirmed or probable); of these 79% reported having skin exposure to a body of water within 7 d before illness began, 17% reported contact with marine wildlife, and 17% reported handling seafood (CDC 2014).

In Europe, however, vibriosis is not a notifiable disease (Semenza et al. 2012a). *Vibrio* infections do occur, particularly along the coast of the Baltic Sea, one of the largest brackish inland seas by surface. Open ocean environments do not offer appropriate growth conditions for these bacteria due to the high salt content, low temperature, and limited nutrient content. The salinity of the water in the Baltic Sea is much lower than that of ocean water, due to freshwater runoff from the surrounding shoreline, and due to the shallowness of the sea itself. The Baltic Sea discharges through the Danish straits but a subsurface layer of more saline water moves in the opposite direction. It mixes very slowly with the upper layer, creating a salinity gradient from top to bottom. Thus, the brackish zone of recreational water use constitutes an area of ideal growth conditions for *Vibrio* species during periods of elevated SST. Historically, SST was determined by dipping a thermometer into a container of water that was manually pulled from the sea surface. However, SST

measurements can also be made with satellite by sensing the ocean radiation in two or more wavelengths within the infrared part of the electromagnetic spectrum that can then be empirically related to SST. The rate of SST increase has accelerated over the decades: the warming rate from 1980 to 2010 increased to approximately 5°C (6°C for summer months) per century, a 6-fold increase from the 1854 to 2010 rate (Baker-Austin et al. 2013). The most recent warming seems to represent the fastest warming of a marine environment and can be attributed to global climate change.

Detection and Evidence of Climate Associations

Vibrio bacteria can be analyzed by examining zooplankton from a Continuous Plankton Recorder, an instrument that, when tugged behind ocean vessels, filters plankton over vast areas of ocean. *Vibrio* bacteria attach to such plankton samples and can be tracked over time and space. Over the past six decades, the concentrations of these different *Vibrio* species have increased along with increasing SST (Vezzulli et al. 2016). This experimental evidence not only links multidecadal climatic variability with *Vibrio* abundance, but also with *Vibrio* cases in humans along the coast of the North Atlantic and North Sea. Based on generalized additive models, the SST warming trend is responsible for the long-term increase in *Vibrio* concentration in this large oceanic area, as well as the unprecedented increase in *Vibrio* cases in humans reported from Northern Europe and along the U.S. Atlantic coast (Vezzulli et al. 2016).

Based on a review of the peer-reviewed literature, gray literature, and microbiology laboratories in the Baltic Sea region, 283 *Vibrio* cases were identified in the Baltic Sea region and the Eastern North Sea area between 1977 and 2010 (Baker-Austin et al. 2013). Of these, 272 cases (96%) were from the Baltic Sea area, and most cases reported were *V. vulnificus* and *V. cholerae* (non-O1/O139) wound infections. The vast majority of cases were reported from 1997 onward (234 cases, 85%). The number of cases over this period increased in correlation with temperature increases, with periods of reported infections in close association with the areas of maximum warming. For example, during the summers of 1994, 2003, 2006, and 2010, significant and sustained warm water anomalies were evident across much of the Baltic Sea area and these years corresponded with increases in reported *Vibrio*-associated illness. The relationship between the annual number of human cases of vibriosis and mean summer SST was examined using a generalized linear model. It showed a highly significant association between a mean summer temperature increase and the number of reported human cases of vibriosis: For every increase in the maximum annual SST, the number of observed cases increased 1.93 times (Baker-Austin et al. 2013). Thus, *Vibrio* cases can be attributed to SST increase. When plotted, the number of cases occurring each year was highly aggregated, with only a few cases observed in the majority of years, and only a few years (2003, 2006, and 2010) with an exceptional number of cases.

Association of Emergence of Vibrio Infections in the Baltic Sea with Climate Change: The Spatial and Temporal Pattern

Land and ocean surface temperatures have increased globally by approximately 0.85°C since the late 19th century due to climate change (Hansen et al. 2010). The European marine temperate regions have been disproportionally affected and experienced a disproportionate warming at a rate of 4- to 7-fold the global rate (Reid et al. 2011). Indeed, over the last decades, northern Europe experienced a series of heatwaves, notably in 1994, 1997, 2003, 2006, 2010, and 2014, all of which were associated with a spike of domestic *Vibrio* cases. Of these heatwave years, 2014 was the hottest year in Sweden since observations began in 1860, with a mean annual temperature 0.18°C higher than the preceding record in 1934 (Swedish Meteorological and Hydrological Institute 2014). The highest temperature this century in Sweden was recorded in August 2014. In Finland, 2014 was the second warmest year on record and 1.6°C warmer than the long-term average for the period 1981–2010 (Finnish Meteorological Institute 2015). In July and August 2014, the SST in the northern part of the Baltic exceeded historic records; indeed, in some areas the SST exceeded the long-term average by approximately 10°C. *Vibrio* infections during the summer and autumn of 2014 in Sweden and Finland exceeded the number previously recorded (Baker-Austin et al. 2016). Across the Baltic Sea, 89 cases of *Vibrio* infections were recorded in these two countries alone. Cases were also detected in the north of Scandinavia in the subarctic region that was affected by the 2014 heatwave. The SST anomalies correlated with the spatial and temporal distribution of *Vibrio* cases in Sweden and Finland. A generalized linear model of these data indicated that maximum SST explained a significant amount of the variability in *Vibrio* infections: an increase in the maximum SST resulted in a significant increase in *Vibrio* cases (Baker-Austin et al. 2016).

Based on the expected warming of the Baltic Sea under climate change scenarios the risk of *Vibrio* infection can be projected into the future (Baker-Austin et al. 2013). Based on the risk model constructed for the summer 2006, projections of temperature were applied to estimate the risk of infection for 2050. Based on these models, areas in the Baltic with an elevated risk are projected to enlarge; moreover, the risk of infection is projected to expand farther north and engulf coastal areas with high population densities in the middle and southern part of the Baltic Sea.

Conclusions

The three case studies show it is plausible, in our judgment, that a proportion of the current burden of climate-sensitive health outcomes can be attributed to climate change. The case studies also demonstrate there is at present no standard practice for climate change attribution for health outcomes.

While some deaths during heatwaves are undoubtedly attributable to climate change based on climate change increasing the probability of these events, different approaches can be used to estimate the exact proportion. Attributing deaths above a threshold related to the degree to which climate change increased ambient temperature over recent decades would be a conservative and defensible approach. Sensitivity analyses and assumptions of the linearity of the relationship between temperature and mortality could be used to provide an uncertainty range around the estimated impact.

There is strong evidence that the emergence of tick vectors of Lyme disease in Canada is occurring in a pattern that is determined by climate. There is evidence of a qualitative, indirect nature for an impact of climate change as a driver of this process: tick populations emerged during a time when temperatures rose above biologically relevant thresholds. There is also empirical evidence that during this time, higher temperatures were associated with faster tick population establishment accounting for other possible processes involved in tick population establishment. Therefore, there is indirect evidence that warming in southern Canada, likely associated with climate change, has been one of the forces leading to the emergence of *I. scapularis* populations and this has resulted in a significant public health problem for Canada. More detailed analyses of longer-term surveillance

data are needed to quantify relationships between a warming climate and tick population range spread.

The observed increase in cases of *Vibrio* infections in the Baltic Sea can be attributed to an increase in SST, which in turn can be attributed to global climate change. SST projections into the future indicate that an enlargement of coastal areas that can sustain large *Vibrio* populations also translates into an elevated risk of *Vibrio* infections in this region.

Evidence that climate change is affecting the burden of climate-sensitive health outcomes will continue to emerge as climate change unfolds. How can we gain a better understanding of the size, timing, and distribution of the climate change burden of disease and injury? Reliable long-run data sets, more knowledge about the factors that confound and modify the effects of climate on health, and refinement of analytic techniques for detection and attribution, including greater sharing of knowledge from other sectors, will all be important. So will recognition that significant advances can be made in the absence of complete data and statistical certainty: there is a place for well-informed judgments, based on understanding of underlying processes and close matching of patterns of health, climate, and other determinants of human well-being. This evidence can be used to modify health system policies and programs, to ensure adequate protection for population health today, and can inform iterative risk management to prepare for and more effectively manage future burdens of climate-sensitive health outcomes.

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