6 Can We Predict Climate-Driven Changes to Disease Dynamics? Applications for Theory and Management in the Face of Uncertainty

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How climate change will affect diseases is rapidly becoming one of the most pressing and challenging questions for epidemiologists and conservationists. Advances in modeling techniques and climate science since publication of the first assessment of global climate change in 1990 have led to increasingly reliable predictions about temperature and precipitation changes (IPCC 2007). Corresponding theoretical developments regarding ecological effects of climate on disease have also occurred, but consensus remains elusive (Wilson 2009). While there is a strong body of theoretical work exploring potential climate-disease interactions, there has been little consideration of the potential synergistic effects of climate change and disease on the resilience of wildlife populations and communities. This will be a key concept for identifying effective management strategies in the face of multiple interacting threats and uncertainty (Hoegh-Guldberg and Bruno 2010). We begin this chapter by highlighting the debate over the role of climate in the spread of disease, using human malaria and amphibian chytridiomycosis as case studies. Next, we discuss the mechanisms through which climate change can alter host-pathogen physiology, distribution, interactions, and evolution, emphasizing empirical examples that illustrate the predominant trends. Finally, we discuss current statistical and empirical methods used to evaluate climate-disease linkages before proposing novel methods for studying, predicting, and managing the problems associated with climate-driven variations in disease.

Complexities of Predicting Climate-Driven Changes in Disease Dynamics

The effects of climate change on the distribution and severity of diseases is currently a source of vigorous debate (Lafferty 2009, Randolph 2009, Wilson 2009, Rohr et al. 2011). Multiple, interacting global change drivers, the complex interaction networks of many infectious diseases, and uncertainties in the specifics of temperature and precipitation predic-

tions preclude simplistic generalizations about disease changes resulting from climate change (Tylianakis et al. 2008, Rohr et al. 2011). Given these complexities, it is not surprising that efforts to identify climate signatures in disease patterns have yielded equivocal results. We illustrate this point with two case studies, one involving a human disease (malaria) and one involving a wildlife disease (amphibian chytridiomycosis).

Early attempts at projecting the consequences of climate change for malaria risk based on biological models of vectors predicted large range expansions for human disease risk, igniting more than a decade of debate on the topic (e.g., Martens et al. 1995). Rogers and Randolph (2000) criticized initial models as overly simplistic and argued that they overestimated future malaria distributions. Using current malaria distributions to statistically model future ranges under climate change scenarios, they predicted little change in malaria risk. Ostfeld (2009), however, pointed out that such forecasts underrepresented the climatic tolerances for malaria because they excluded regions of targeted malaria eradication.

Similar controversies have arisen over the role of climate change in the emergence and spread of *Batrachochytrium dendrobatidis* (*Bd*), a chytridiomycete pathogen that has caused dramatic amphibian population declines and extinctions (Skerratt et al. 2007). To explain the decline of tropical montane frogs, Pounds et al. (2006) proposed the"chytrid-thermal-optimum hypothesis," which suggests that climate-mediated increases in cloud cover shifted temperatures towards the growth-optimum for *Bd*. Lips et al. (2008), on the other hand, found no support for climate-driven *Bd* outbreaks in Central and South America, showing instead that disease patterns were consistent with the epidemic spread of a recently introduced pathogen. An analysis by Rohr et al. (2008) further argued that correlations between temperature and frog declines do not necessarily imply that climate change has caused these species declines.

The case studies of malaria and *Bd* emphasize some of the fundamental problems that plague the debate over climate-driven effects on diseases, particularly those of urgent human health or conservation concern. Given the variety and complexity of disease systems and the uncertainties inherent in making climate predictions, it is prudent to question at what scale we can accurately forecast climate-mediated changes in disease. The answer is vitally important because the success of mitigation strategies ultimately depends on the efficient allocation of limited resources to regions most at risk of disease increases. To assess the feasibility of predicting climate change effects on disease dynamics, we first discuss the mechanisms through which climate change can influence host-pathogen physiology, distributions, interactions, and evolution.

How Does Climate Change Affect Patterns of Disease?

Physiological Changes

Climate change can influence the physiology of hosts, vectors, and pathogens in different ways, introducing intriguing shifts in disease patterns. Nonlinear responses of pathogens to rising temperature could have a major impact on their abundance. In one example, recent warming shifted the development time of arctic nematode larvae from two years to a single season, thereby increasing the infection risk experienced by musk oxen (Kutz et al. 2005). If warming temperatures consistently accelerate the development of parasites more than that of their hosts, climate change could dramatically increase parasite abundance and host infection. Alongside changes in mean temperature, shifts in climate variability will also affect disease dynamics by changing pathogen development rates or host immune responses relative to constant temperatures (Paaijmans et al. 2009, Rohr and Raffel 2010).

Climate change will alter mortality rates as well as developmental rates, however, and the balance between these changes for hosts, vectors, and pathogens will influence disease severity in a system (figure 6.1). In temperate zones, warmer winters could enhance the overwintering survival of some pathogens and vectors (Harvell et al. 2002, Canto et al. 2009), but higher metabolic rates and temperatures that exceed thermal tolerance limits can also reduce vector and parasite survival (Lafferty 2009, Snall et al. 2009). Nor will the effects of climate change on disease necessarily be consistent across the distribution of a pathogen. For instance, elevated precipitation can reduce water salinity, and therefore the survival of *Vibrio* bacteria, in mesic areas while increasing cholera risk in drier areas, possibly due to lower water availability and increased concentration of the pathogen in available water sources (Pascual et al. 2002).

A final complication of physiological influences on disease patterns is the influence of climate on host immunity, particularly for ectothermic species. Warming temperatures may either increase or decrease host immunity (e.g., Harvell et al. 2002, Canto et al. 2009). Other climatic changes, such as prolonged drought or increased atmospheric carbon dioxide concentrations, can also alter host resistance to pathogens (Garrett et al. 2006). These observations collectively suggest that the net effect of climate change on disease will depend on how the physiology of different hosts, vectors, and pathogens, responds to temperature and precipitation changes.

Range Shifts

Climate models predict a greater rise in minimum temperatures than in maxima, such that temperatures may be more likely to approach the ther-

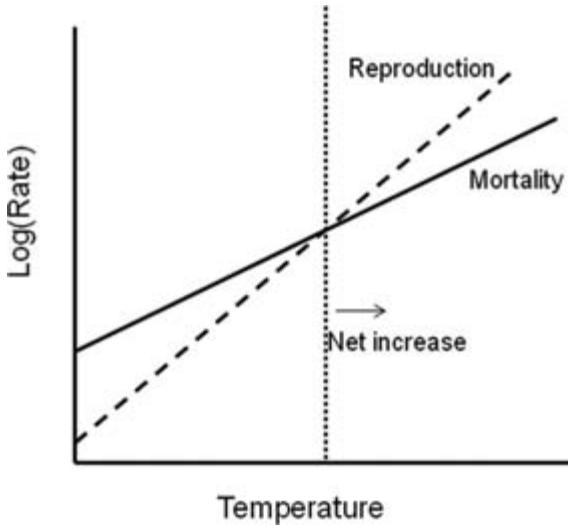

Figure 6.1. Hypothetical trade-offs between temperature-dependent growth and mortality rates of a pathogen. As temperatures approach a pathogen's thermal optimum, the reproductive rate (*dashed line*) may increase more quickly with temperature than the mortality rate (*solid line*). In this scenario, increasing the temperature past the point where the two lines intersect (*dotted line*) will result in a net increase in pathogen populations. If the slopes of these two lines are reversed, as might happen when temperatures approach the thermal maximum, pathogen spread will decline.

mal optima of many organisms, thus leading to predictions that diseases will expand their ranges as temperate areas warm (Ostfeld 2009). Many plant and animal pathogens and vectors may shift poleward in latitude or upward in elevation with climate change (e.g., Pascual et al. 2006; figure 6.2). For example, bluetongue virus has spread northward into Europe since 1998, likely as a result of northward expansion of its vector and increased overwinter virus persistence (Purse et al. 2005). However, many organisms face barriers to dispersal and physiological limitations that prevent range expansions (Root et al. 2003, Lafferty 2009). For instance, Randolph and Rogers (2000) projected a net range reduction of tick-borne encephalitis (TBE) in Europe owing to its dependency on infected nymphal ticks feeding in close proximity to larval ticks—an event that only occurs in particular climatic conditions. Poleward movements of pathogens and vectors could have a strong effect on the immunologically naïve host populations they encounter, regardless of whether pathogens quantitatively expand their ranges. For instance, if malaria shifts its distribution upwards in elevation, it will move into the most populous regions of Africa and South America such that a net decrease in range could still translate into an increase in human impact (Pascual and Bouma 2009). An elevational increase in avian malaria in Hawaii could have devastat-

ing effects on highly susceptible native bird populations (Atkinson et al. 2009). Proactive disease regulation measures (e.g., mosquito control) should be considered for areas where the latitudinal and elevational boundaries of pathogens seem to be determined by climatic factors rather than dispersal barriers.

Biotic Interactions

Local differences in species' physiological responses to climate change will scale up to influence biotic interactions that can have consequences for disease (Gilman et al. 2010). For instance, climate-driven changes to

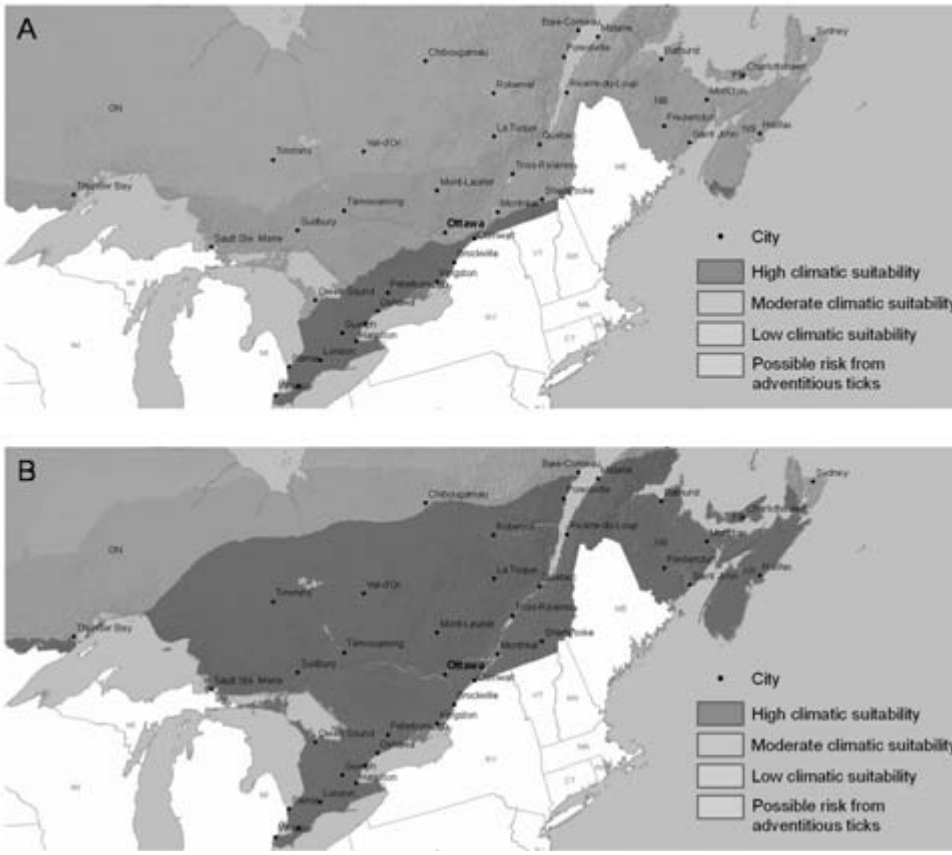

Figure 6.2. Predicted range expansion of the tick vector of Lyme disease, *Ixodes scapularis*, under future projected climate conditions. These risk maps predict the distribution of I. *scapularis* (a) between 2000 and 2019 and (b) between 2080 and 2109. Predictions are based on climate predictions from the CGCM2 model under emissions scenario A2. Figure reproduced with permission from Ogden et al. 2008.

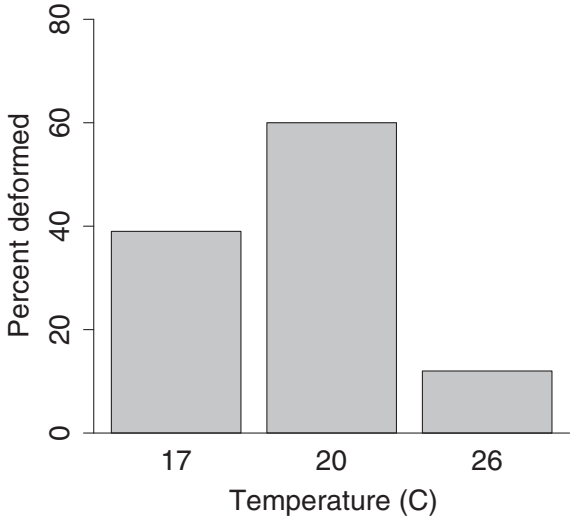

Figure 6.3. A greater percentage of amphibians emerged deformed as a result of infection with the parasite *Ribeiroia ondatrae* at 20° C than at 17 or 26 ° C. This mid-temperature peak in infection likely occurred because although high temperature exacerbated parasites' infectivity, it also reduced tadpoles' vulnerability by causing them to develop more quickly into stages at which they were substantially less likely to become deformed as a result of infection (Paull unpublished data).

host-parasite interactions can affect host pathology. One such example involves the trematode parasite, *Ribeiroia ondatrae*, which sequentially infects snails, amphibians, and birds to complete its life cycle. A laboratory experiment demonstrated that faster parasite development at elevated temperatures increased the pathology experienced by snail hosts infected with *R. ondatrae* by reducing their fecundity (Paull and Johnson 2011). A separate experiment on amphibian hosts showed that temperature-driven increases in parasite infectivity combined with faster development of tadpoles out of vulnerable developmental stages leads to a mid-temperature peak in pathology, measured as the percentage of tadpoles that metamorphose with deformities (figure 6.3). The combination of these temperature-driven changes in host susceptibility, parasite infectivity, and host-parasite reproduction, development and mortality rates across multiple hosts will likely lead to further shifts in the timing and consequence of this host-parasite interaction (Paull and Johnson 2011). Climate change can also shift host-parasite infection dynamics. For example, an analysis of a 30-year dataset of chytrid-diatom dynamics revealed that milder winters reduced chytrid fungal infections of the diatom host *Asterionella formosa* because the diatoms became infected before they bloomed, thus reducing population sizes of both species (Ibelings et al. 2011). Temperature-driven changes in predator-prey relationships can also affect disease transmission. Hall et al. (2006) showed that regulation of fungal epidemics in *Daphnia* by predatory fish may be stronger at warmer temperatures, because the fish respond more strongly to temperature. Climate-driven

changes in the compositions of host and parasite communities will also lead to novel host-parasite interactions. For example, hosts may gain or lose parasites as a result of interspecific differences in movement rates (Garrett et al. 2006, Brooks and Hoberg 2007, Harvell et al. 2009). These novel parasite communities can influence host pathology via competition, facilitation, and predation among different parasite species (Pederson and Fenton 2007). Novel communities could thus result in interactions between parasites that complicate efforts to predict disease patterns.

Evolutionary Responses

Changing climates will shift the selective pressures operating on pathogens and their hosts, thus providing a catalyst for evolutionary change. Pathogens tend to have short generation times and high mutation rates, which facilitate adaption to changing environmental conditions (Koelle et al. 2005). Range shifts may also enhance the evolution and spread of drug-resistant pathogens by aiding host movement and gene flow (Criscione and Blouin 2004, Bonizzoni et al. 2009). Strong selection for use of new hosts by pathogens may lead to disease emergence in previously unaffected populations (Marcogliese 2001, Brooks and Hoberg 2007). A greater understanding of pathogen evolutionary processes can be achieved using a phylodynamic approach to characterize the drivers of pathogen evolutionary dynamics across multiple scales (Holmes and Grenfell 2009). Pathogen evolution and changing climate will stimulate host and vector adaptations as well, although evolutionary constraints may restrict the rate at which this occurs (Austin et al., this volume). Climate is changing at a rate unprecedented in the last 50 million years (IPCC 2007). Adaptation will be constrained in most cases by the rate of microevolution, as well as by antagonistic genetic correlations, which may not proceed at rates fast enough for the predicted pace of climate change (Etterson and Shaw 2001, Visser 2008). While mobile organisms may be able to escape regions of increasing parasitism, those with slow migration rates, such as plants, will be forced to rely more on adaptation to changing threats resulting from pathogens (Garrett et al. 2006). Reductions in plant genetic diversity resulting from local adaptation to rapid climate change could also reduce disease resistance in some populations (Jump and Peñuelas 2005).

Current Methods for Studying Climate-Driven Changes in Disease

Current techniques for forecasting the influence of climate change on disease risk include correlative studies along temporal and spatial climate gradients, synthetic meta-analyses, predictive models, and experimental

investigations. We discuss the relative merits and weaknesses of each technique before suggesting novel strategies that can enhance their implementation. Because of the urgency of the problem, the complexity of host-parasite-climate systems, and the paucity of baseline data for most diseases, a combination of approaches is likely to generate the most reliable results for forecasting.

Statistical approaches attempt to link temporally or spatially variable climatic patterns with disease incidence. These approaches take two main forms: tests for connections between regional warming trends and disease, and correlations between the El Niño Southern Oscillation (ENSO) or North Atlantic Oscillation (NAO) indices and disease. Studies linking disease incidence to ENSO or NAO indices can be useful for forecasting disease severity up to a year in advance (Chaves and Pascual 2006). Interpreting the results requires some caution, however, as such models often lack mechanistic components, and correlations involving large-scale, monotonic increases in both variables can be misleading (Rohr et al. 2008). Other intrinsic factors, such as changes in the number of immune hosts, could cause cyclical changes in disease, underscoring the need to consider the relative importance of extrinsic climatic forcing as opposed to internal drivers (Dobson 2009, Harvell et al. 2009).

Meta-analyses and other synthetic approaches can distill large-scale patterns from the synthesis of numerous small-scale experiments or surveys. By quantitatively summarizing current knowledge, meta-analyses have provided compelling evidence to support theoretical predictions about biotic responses to climate change (e.g., Parmesan and Yohe 2003, Root et al. 2003). Meta-analyses can be problematic, however, because working with published data can introduce bias (e.g., null results often go unpublished) or nonindependent studies into the analysis (Lei et al. 2007). While these problems can be minimized with a careful literature selection process, the results typically do not mechanistically explain patterns and mask the variability among studies that is essential for fine-scale prediction (Lei et al. 2007).

There are two main types of bioclimatic models: mechanistic models, which use physiological parameters to infer changes to disease distributions, and statistical models, which use the climatic parameters associated with the current range of the disease to forecast future range shifts (Jeschke and Strayer 2008). The utility of bioclimatic models lies in their ability to generate quantitative hypotheses about disease shifts resulting from climate change that can be used in directing management efforts (Jeschke and Strayer 2008). Many bioclimatic models, however, depend

on assumptions that are frequently violated, such as the assumption that species ranges are not limited by dispersal or biotic interactions, and that a species' genetic climate tolerance does not vary through space or time (Peterson and Shaw 2003, Jeschke and Strayer 2008, Gilman et al. 2010, Brodie et al., this volume). Incorporating other aspects known to influence disease risk, such as anticipated changes in host population size or limitations to dispersal will strengthen the predictive power of such models (Peterson and Shaw 2003).

Carefully designed experiments provide the most mechanistic evidence of how climate affects disease dynamics. While short-term laboratory studies are typically limited to one component of a complex disease system, they help clarify the mechanisms underlying climate-disease interactions and can be used to parameterize mechanistic predictive models. For example, Terblanche et al. (2008) experimentally measured the thermal tolerance of tsetse flies, which are vectors for human and animal trypanosomiases, and inferred that future warming would exceed their upper thermal limits and lead to a reduction in their geographic range. Field experiments are needed to explore the effects of climate change on disease in a more realistic larger-scale context. For instance, field studies that examine elevated temperatures of plant-pathogen systems generally find that pathogens respond uniquely to the warming treatment, with some increasing in number and others decreasing (e.g., Wiedermann et al. 2007), thus suggesting that large-scale patterns may not be fully elucidated by smaller single-system experiments.

Where Do We Go from Here? Predicting and Mitigating the Effects of Climate Change on Disease

It is critical that we focus attention on developing more quantitative predictions, greater mechanistic understanding, and explicit management advice regarding the effects of climate on disease. Here, we summarize novel strategies in the areas of *modeling*, *empirical research*, and *disease management*, which can be used in conjunction with existing tools to provide an informative framework for mitigating the effects of climate change on disease. Although forecasts about climate-driven changes in disease dynamics will always be plagued by the complexity of the issue, unpredictable stochastic forces, and variation in disease response across scales, a greater mechanistic understanding of the processes involved, including more cross-disciplinary research, and a focus on climate-sensitive aspects of disease transmission (figure 6.4) will enhance our ability to respond to changing disease risks.

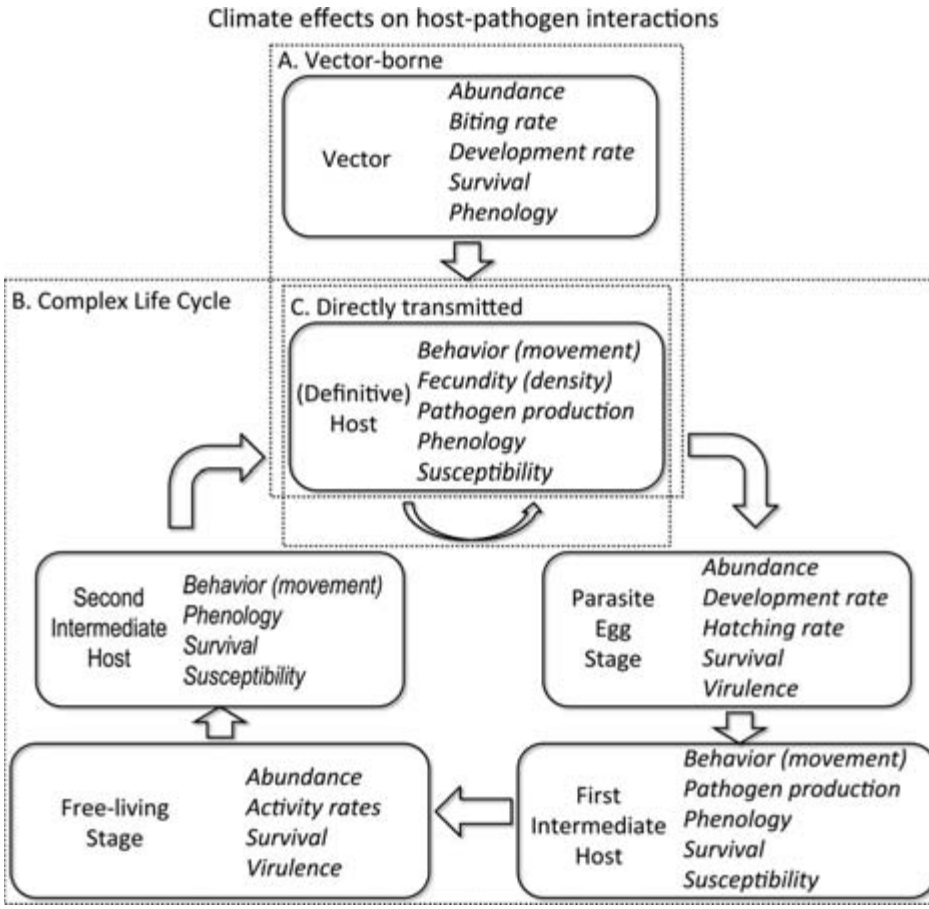

Figure 6.4. Potential direct influence of climate change at different stages of pathogen transmission for hypothetical vector-borne, complex-life-cycle, and directly transmitted diseases. Changes that occur in the dynamics of any disease will be affected by whether the organisms involved are ectothermic or endothermic, as well as by indirect interactions with the community and environment. Attempts to understand climate-driven changes in disease dynamics will be further complicated by evolutionary changes and distributional shifts of hosts, vectors, and pathogens.

Physiology Meets Ecology: Using Novel Modeling Strategies to Enhance Disease Forecasting

Mechanistic models based on physiological parameters of specific host-pathogen systems and regional climate forecasts can facilitate management plans at the local level. Dynamic energy budget (DEB) models describe organismal physiologies in detail, and can be adapted to model interactions between organisms at the population and community levels

(e.g., Kooijman 2001, Vasseur and McCann 2005). Biophysical models have strong predictive power relative to correlative methods because they can detect effects across multiple scales and can distinguish between hypothesized drivers of disease change (Helmuth 2009, Kearney et al. 2009). For example, a biophysical model that incorporated the microclimatic effects of different water storage containers demonstrated that water storage had a larger impact than climate change on the distribution of dengue-carrying mosquitoes (Kearney et al. 2009). Such mechanistic models are rare, however, owing to the increase in parameters that occurs when bioenergetics models are extended to the community level (Vasseur and McCann 2005). In the absence of such detailed physiological data, qualitative predictions about host-parasite interactions can still be made by considering easily measured physiological parameters such as thermal windows, which describe the *range* of temperatures across which an organism can maintain stable performance, and the Q_{10} coefficient, which describes a change in a given physiological *rate* for every 10° C change in temperature. These measures may be useful in predicting the direction of changes in host-pathogen interactions (figure 6.5). An increased emphasis on physiological models for predicting climate-driven changes in biotic interactions within specific disease systems could complement the current use of bioclimatic models to provide a more complete overall picture.

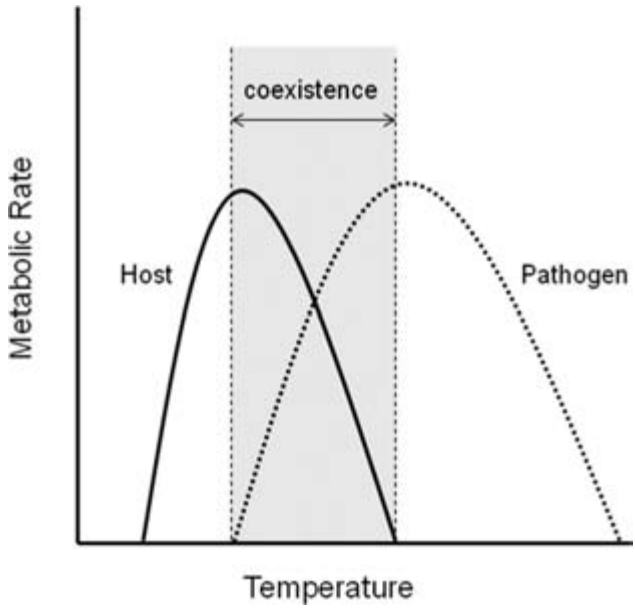

Figure 6.5. Depiction of the thermal tolerance window of a hypothetical host (*solid line*) and pathogen (*dotted line*). The shaded region is the range of temperatures at which the host and parasite can coexist. As temperatures rise they become more favorable for the parasite, thus shifting the character of the relationship.

Experimental Climate Change: Using Novel Empirical Approaches to Address Disease Effects

Empirical research on the linkage between climate and disease has been hindered by the logistical complications of experimentally modifying environmental temperatures. We suggest two forms of empirical study to help advance research on climate change: (1) spatial gradients in temperature and (2) experimental mesocosm and field studies. Because elevation gradients offer a range of climatic conditions over relatively short distances, correlations between climate and disease patterns across differing altitudes will have fewer covariates to influence the results (Fukami and Wardle 2005). Relatively few studies have correlated biotic responses to climate change using available spatial gradients, despite the value of such geographical gradients in temperature for understanding climate-driven changes in disease risk (Hudson et al. 2006, Altizer et al. 2006). Seminatural mesocosm experiments are also an effective way to test theories about climate-driven changes in disease transmission. Designs for large outdoor mesocosms can range from expensive computerized aquatic systems to simple Plexiglas heat-trapping structures in terrestrial or aquatic environments (Liboriussen et al. 2005, Netten et al. 2008). Such use of simplified host-parasite systems can further facilitate experimental testing of hypotheses about disease reactions to climate change. The Arctic is a promising region for such studies, due to its low anthropogenic influence, its low level of biodiversity, and its predicted large climatic shifts (Kutz et al. 2009).

Further study of the direct and indirect climatic drivers, aside from temperature, of disease dynamics is also necessary. Climate change involves alteration of a suite of variables beyond mean temperature, including precipitation, diurnal and seasonal temperature ranges, and the frequency and severity of extreme weather events. For example, in aquatic systems, changes in ice cover, acidification, eutrophication, lake mixing regimes, and ultraviolet exposure will also affect hosts and parasites (Marcogliese 2001). Changes in terrestrial ecosystems are expected in response to climate-driven alteration of snow cover, wildfire disturbance regimes, the frequency of extreme weather events, and carbon dioxide concentrations (Garrett et al. 2006, Schumacher and Bugman 2006, Jentsch et al. 2009). Studies that test factors other than changes in mean temperature and precipitation on disease systems are needed to assess whether climatic variability or indirect drivers may also play a role in disease dynamics.

Technological Advances for Research and Collaboration

Interdisciplinary collaboration will be important in developing novel research methods to explore climate-driven changes in disease. For instance, molecular PCR-based techniques can improve disease surveillance methods (Polley and Thompson 2009). Recent breakthroughs in DNA sequencing techniques will also pave the way for phylodynamic approaches to epidemiology that could provide key insights into evolutionary responses of pathogens to climate change (Holmes and Grenfell 2009). Technological advances in sequencing and identification techniques have also made the direct analysis of paleoparasitological changes associated with changes in paleoclimate data an increasingly useful avenue of research (Dittmar 2009). Geographic information systems (GIS) offer another powerful epidemiological tool that can be used for mapping potential climate-driven changes to disease risk (Ostfeld et al. 2005). For example, remote sensing technology can be used to characterize regions with high disease risk (Glass et al. 2007). Collectively, these tools should be applied toward developing a large-scale, interactive, and publicly accessible database of disease distribution and pathology that would provide an invaluable resource for global-scale analyses of climate-driven changes in disease (Semenza and Menne 2009). Because the study of climate change and disease spans disciplines ranging from atmospheric science to epidemiology, multidisciplinary efforts are key to developing the creative research and data acquisition strategies necessary for effective disease management.

Planning for the Unpredictable: Management and Surveillance Tools

Despite our best efforts to predict disease responses to climate change, the complexities and uncertainties within these systems ensure that ecological "surprises" will occur. Acting in the face of such uncertainties requires effective use of management strategies in combination with enhanced disease treatment and surveillance methods. Managing populations to increase their resilience will be critical given the uncertainties in predicting climate-driven changes to ecosystems (Hoegh-Guldberg and Bruno 2010). To increase the resilience of populations to climate-driven disease susceptibility, managers should focus their efforts on maintaining high genetic and species diversity while reducing other environmental stressors (Evans and Perschel 2009, Hoegh-Guldberg and Bruno 2010). Simple changes in animal husbandry practices, including grazing, housing, and shearing, can also reduce disease risk in domestic animals and the spillover of infections into wildlife populations (Morgan and Wall

2009). In the case of diseases in humans or in threatened or economically valuable species, vaccination against infection may be necessary (Hampson et al. 2009). Flexibility will be a key component of plans for managing climate-driven changes in disease. Adaptive management is one such strategy that involves development of experimental management programs to test alternative hypotheses for effective resource management (Walters and Holling 1990). Another emerging strategy for dealing with stochastic events that cause unpredictable regime shifts is to develop alternative management plans for multiple future scenarios to cope with unexpected changes quickly and effectively (Bennett et al. 2003).

Linking Climate Change, Disease, and Conservation

Ultimately, the success of predictions about climate-disease interactions will be measured by their utility in mitigating the negative consequences of diseases for human and wildlife populations. Although low host population sizes can often reduce disease persistence, diseases can still cause species extinctions by driving populations to unstably small numbers or by residing in reservoir hosts (de Castro and Bolker 2005). Even if a disease does not cause extinction of a particular species, it can lead to genetic homogenization that reduces its ability to cope with other environmental stressors (Smith et al. 2006). An overall assessment of climate-driven changes to disease risk should use these characteristics to determine which diseases are most likely to pose a threat to wildlife populations.

Finally, the conservation of parasites and pathogens themselves may be an appropriate management consideration. Parasites play a vital role in many ecosystems, and their disappearance could have a cascading effect on other processes. Parasites serve as key links in food webs and as regulators of host populations (Dobson et al. 2008). Specialist parasites may have a higher extinction risk, which could allow generalist parasites (typically associated with higher pathological effects) to increase as a result of competitive release (Dunn et al 2009). Parasites and pathogens have a dramatic influence on the health of human and wildlife populations. Changes in their dynamics and abundance will be among the most important consequences of global climate change.

Conclusions

Given the complexities involved in disease dynamics and the uncertainties surrounding climate change predictions, the debate over whether climate change will increase or reduce global disease risk will continue. Diseases and species tend to respond idiosyncratically to climate change,

with range shifts, physiological changes, phenological changes, and evolutionary rates differing among species. Nevertheless, the risk of changing diseases to human health and wildlife conservation is great enough that action is required. Our predictive abilities can be enhanced through biophysical modeling, increased use of experimental manipulations incorporating the direct and indirect effects of climate change, and collaborative efforts that capitalize on recent technological innovations. Our forecasting capabilities may be limited to predicting the general behavior of specific, well-parameterized host-pathogen systems, or to identifying the factors that are important in driving the dynamics of specific classes of pathogens. The best approach for maximizing our predictive capabilities is to combine mechanistic empirical and modeling approaches. The uncertainty arising from the complexities of host-parasite-climate interactions, particularly in conjunction with other global change drivers, underscores the need for managing wildlife populations to increase resilience within a framework of flexible adaptive management practices.

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