Toward a General Theory for How Climate Change Will Affect Infectious Disease

Symposium 16 was organized by Jason R. Rohr, Pieter T. J. Johnson, Thomas R. Raffel, and Sara H. Paull, and held during the 2010 ESA Annual Meeting in Pittsburgh, Pennsylvania on 5 August 2010. The report was written by Thomas R. Raffel, University of South Florida, Tampa, Florida; Jason R. Rohr, University of South Florida, Tampa, Florida; Sara H. Paull, University of Colorado, Boulder, Colorado; and Pieter T. J. Johnson, University of Colorado, Boulder, Colorado.

Presenters:

Jason R. Rohr, University of South Florida; Pieter T. J. Johnson, University of Colorado at Boulder; "Introduction."

Diego Hernan Ruiz Moreno, Cornell University; C. Drew Harvell, Cornell University; Bette Willis, James Cook University; Cathie Page, James Cook University; Ernesto Weil, University of Puerto Rico; Aldo Croquer, University of Newcastle; Bernardo Angel, NOAA; Guillermo Jordan, Instituto de Ciencias del Mar y Limnología; Eric Jordan, Instituto de Ciencias del Mar y Limnología; Laurie Raymundo, University of Guam; "Global patterns of coral disease and relationships with climate and local ecological factors."

Matthew B. Thomas, Penn State University; Krijn P. Paaijmans, Penn State University; Andrew F. Read, Penn State University; "Evaluating the link between environmental temperature and transmission of malaria."

Sara H. Paull, University of Colorado at Boulder; Pieter T. J. Johnson, University of Colorado at Boulder; "Temperature-driven shifts in host-parasite interactions: Consequences for parasite transmission and amphibian pathology."

Andy P. Dobson, Princeton University, Susan J. Kutz, University of Calgary; "Climate change and the pathogens of Arctic vertebrates: Strong signal, strong effects, important deep implications for more diverse temperate and tropical systems."

A. Marm Kilpatrick, University of California at Santa Cruz; "Climate and vector-borne disease: From pattern to mechanistic analysis."

Mercedes Pascual, University of Michigan and Howard Hughes Medical Institute; Yael Artzy-Randrup, University of Michigan and Howard Hughes Medical Institute; Karina F. Laneri, University of Michigan; David Alonso, University of Groningen; Menno J. Bouma, University of London; "Climate change and epidemic malaria: a population dynamics perspective."

Thomas R. Raffel, University of South Florida; John M. Romansic, University of South Florida; Neal Halstead, University of South Florida; Taegan McMahon, University of South Florida; Jason R. Rohr, University of South Florida; "Climate variation mediates a host-parasite interaction: Field and laboratory evidence at multiple temporal scales."

Introduction

In keeping with the theme of the 2010 ESA Annual Meeting ("Global warming: the legacy of our past, the challenge for our future"), this symposium focused on how climate affects the ecology of infectious disease. The conventional wisdom that global climate change will increase diseases has placed climate change–disease interactions at the center of scientific, political, and public agendas. However, predicting climate change impacts is difficult, particularly for species interactions such as parasite–host relationships (Gilman et al. 2010), and whether climate change will increase or decrease infectious diseases has become a contentious question (Lafferty 2009).

This debate was highlighted in a recent forum discussion of climate change impacts on infectious disease (Wilson 2009). Researchers in this forum generally agreed that climate change is altering the distributions of some diseases and identified important problems for future research (as summarized by Wilson 2009). The goals of this symposium were to offer resolution, synthesis, and consensus on what we know about the relationship between climate change and disease, evaluate how to best apply predictive theory to this topic, and suggest future directions for the field to advance our understanding.

The general consensus at the end of this symposium was that many questions still remain about how climate will influence infectious disease, and that our ability to predict climate impacts is limited by several important challenges:

1. Creating better models to connect field data with experiments.

2. Understanding and accounting for effects of climatic variability in addition to broad means.

3. Identifying general patterns and principles in the thermal physiology of disease.

4. Determining where and in what systems we should expect climate to influence disease.

Modeling climate effects on disease

Model predictions are frequently used to set and justify disease control measures (Brochier et al. 1991, Tildesley et al. 2006), so it is important to develop models that correctly predict the disease distribution and incidence. Several presenters addressed this subject directly by presenting new models for predicting climate impacts on disease, particularly malaria, and much of the post-session discussion focused on challenges faced by disease modelers.

One challenge is how to account for intrinsic dynamics and other extrinsic drivers (e.g., human intervention) when assessing climate impacts on disease (Cobey and Koelle 2008, Pascual and Bouma 2009). This is especially problematic when intrinsic dynamics correlate with climatic fluctuations, or when climate variability is temporally or spatially confounded, making it difficult to assess which predictors are responsible for the observed pattern in disease (Rohr et al. 2008). Mercedes Pascual highlighted this problem, presenting a model assessing relative impacts of drug resistance and climate changes on malaria in the East African highlands. She found a strong climate signal, but concluded that neither climate nor drug resistance could entirely account for recent increases in malaria incidence. This discrepancy might be due in part to intrinsic dynamics, such as cycles of acquired immunity in the human population.

Another challenge is choosing exactly what types of models to use for predicting climatic effects on disease systems. A common approach is to use information from laboratory experiments to determine the ideal conditions for pathogen transmission, and then use climatic models to project where and when these conditions will occur (Rosenthal 2009). However, models can become progressively more complex as researchers discover new and more subtle ways that environmental variables influence disease transmission, and there is a danger of creating over-fitted models with poor predictive power. Furthermore, laboratory experiments often fail to accurately represent the genetic variation present in natural populations of hosts and parasites, and the scale and realism of ecological experiments can further influence results (Tripet et al. 2008). Dr. Pascual suggested that these problems might be overcome by obtaining better concurrent data sets for disease and hypothesized drivers (climate and other factors), allowing model fitting to assess which factors best predict disease outcomes.

One major problem identified during the symposium was the common use of pseudoreplicated temperature treatments in experiments. Despite repeated calls by ecologists for better treatment replication (Hurlbert 1982, 2004), many researchers still use a single incubator for each temperature treatment in experiments, with multiple "replicates" within each incubator. This makes it difficult to determine whether effects are truly caused by temperature and not some other difference among incubators. Thomas Raffel presented one potential solution to this problem, building an array of 80 inexpensive incubators to truly replicate temperature treatments. Another potential solution is using a small number of incubators repeatedly in multiple temporal blocks. Regardless of the solution, researchers should be explicit about the limitations of their experimental designs, and use the appropriate nesting structure in statistics when possible.

Climate variability as a driver of disease

A common theme in the symposium was the need to account for effects of climatic variability in predictive models, in addition to broad means for temperature and precipitation (Benedetti-Cecchi 2003). Indeed, effects of temperature variability were brought up by every speaker in the symposium, including seasonality as a driver of host–parasite relationships, and heat wave frequency as a driver of epidemics in marine corals. Three presenters focused particularly on this topic, pointing out that models based on broad mean temperatures can provide poor predictions of disease outcomes, either (1) because they fail to account for nonlinear responses to temperature, or (2) because they fail to account for specific host and parasite adaptations to temperature variability (i.e., acclimation responses).

Marm Kilpatrick stressed the first mechanism, showing that some parameters underlying malaria transmission have nonlinear responses to temperature and precipitation. These nonlinear responses led to different model predictions, depending on the levels of stochasticity in temperature and precipitation. Measuring and accounting for these nonlinear responses to climate was identified as an important question for disease research during the postsession discussion.

Matthew Thomas discussed recent work showing that diurnal temperature fluctuations influence malaria development in ways not predictable from broad mean temperatures alone (Paaijmans et al. 2009, 2010). Diurnal temperature fluctuations around a low mean increased developmental rates, whereas fluctuations around a high mean decreased development, an effect predictable from nonlinear effects of temperature on biological parameters (Paaijmans et al. 2010). Although this effect was qualitatively predicted based on nonlinear responses to temperature (Paaijmans et al. 2009), Dr. Thomas said that

models based on nonlinear responses were unable to fully account for the observed effects of diurnal temperature in their laboratory experiments. Such a discrepancy could be caused by adaptations of host or parasite to predictable diurnal temperature shifts.

Adaptations to temperature variability were discussed broadly by Thomas Raffel, who categorized them as (1) acclimation responses following unpredictable temperature shifts (on short or long timescales), or (2) adaptations to predictable temperature shifts (such as diurnal or seasonal changes). Dr. Raffel showed that both types of adaptations influence susceptibility of amphibians to the pathogenic chytrid fungus *Batrachochytrium dendrobatidis*. These results suggest that climatic models based on constant temperature experiments will be insufficient to accurately predict climate effects on disease in variable-temperature environments. Of even more concern, the magnitude and direction of these acclimation effects depended on the amphibian species tested, suggesting that general patterns of acclimation responses might be difficult to identify. Acclimation responses to temperature fluctuations pose an especially serious challenge to developing accurate disease models, because measuring them requires complex experimental designs to account for the timescale and predictability of temperature variability in the system (Angilletta 2009). Therefore, an important question for researchers dealing with temperature variability is whether it will be more efficient to (1) parameterize relatively simple mean-temperature models using experiments that incorporate realistic temperature variability, or (2) to conduct experiments explicitly designed to measure acclimation responses and then incorporate these into more complex thermal models of disease.

Searching for general patterns of thermal physiology in disease systems

Unless we can identify general patterns of responses to climate, it will be difficult if not impossible to predict community-level impacts of climate and effects on nonmodel organisms. Determining whether there are similar responses for related parasite and host taxa to climate change will require broad phylogenetic surveys of parasite and host responses, probably using meta-analytical approaches. It might also be possible to derive general predictions for host–parasite systems from metabolic theory. For example, ectothermic organisms have fundamentally different responses to temperature than endothermic organisms (Angilletta 2009), leading to very different predictions for how they and their parasites should adapt to temperature variation (Raffel et al. 2006). Metabolic theory also predicts faster metabolisms in smaller organisms (West et al. 2002), suggesting that parasite acclimation responses might generally be faster than host responses. Such an effect might make ectothermic organisms more susceptible to infection when temperatures become more variable (Raffel et al. 2006, Rohr and Raffel 2010).

Parasites might also be expected to evolve faster than their hosts in response to climate change, due to their typically shorter generation times (Raffel et al. 2008). This has implications for predicting parasite range shifts in response to climate change, because it implies that parasites might be more capable of adapting to new climatic conditions than their hosts. Therefore, parasites might be more limited by dispersal, or by the ability of their hosts to adapt and/or disperse, than by their ability to adapt to new environmental conditions. For example, Andy Dobson showed that disease emergence in large arctic mammals is driven in part by new interactions among host species due to species range shifts (Kutz et al. 2009). However, emergence of some arctic parasites has been associated with increased survival of infectious stages in the environment, due to longer summer periods without ice (Kutz et al. 2009).

Parasites with complex life cycles might be particularly constrained in their responses to climate change, because their transmission cycles depend on continued overlap in the ranges of their definitive and intermediate hosts (Hechinger and Lafferty 2005). If, for example, the definitive host's range shifts northward in response to climate change but the intermediate host maintains its historic range, the range over which the parasite can persist will shrink or even disappear (Gilman et al. 2010). Sara Paull expanded on this idea to explore the potential for temporal shifts of parasite–host interactions in seasonal systems. In her trematode–tadpole system, increasing temperatures enhanced the infectivity of trematodes. However, tadpoles also developed faster at warmer temperatures, quickly reaching developmental stages at which they were less susceptible to infection. Therefore, the outcome of climate change for this parasite will depend on changes in the timing of snail abundance, parasite development, and tadpole development in response to temperature.

Discovering generalities in the thermal biology of disease will require greater collaboration between parasitologists and thermal biologists. For example, recent advancements in thermal biology have included models describing how thermal physiology mediates predator–prey interactions (Angilletta 2009, Mitchell and Angilletta 2009), and similar models might be applicable to parasite–host interactions.

Where should we expect climate change impacts on disease?

Ultimately, the future of climate change science will depend largely on how policymakers prioritize funding for research on different topics and systems. Andy Dobson pointed out that little attention has been given to arctic parasite–host systems, where climate change has been and is projected to be much more extreme than in tropical and temperate regions (IPCC 2007). As argued by Kutz et al (2009), rapid climate change and the relative simplicity of the ecosystem could make the Arctic an ideal model system for studying climate impacts on disease. However, this argument contrasts with studies suggesting that tropical animals will be more sensitive to climate change because they have narrower temperature tolerances (Calosi et al. 2008, Deutsch et al. 2008, Tewksbury et al. 2008). Marine organisms also tend to have narrow thermal ranges (Portner 2002), and Diego Moreno emphasized that even small increases in temperature can exacerbate disease outbreaks in coral (Sokolow 2009). It will be important to assess potential regional impacts of climate on disease, not based on the magnitude of climate change alone, but also on the thermal tolerances of particular organisms (Deutsch et al. 2008).

Notably, all of the pathogens and parasites discussed during this symposium had ectothermic hosts (e.g., amphibians, corals, mosquitoes) or transmission stages in the environment (e.g., nematodes of arctic mammals). These parasites might be more sensitive to environmental conditions than directly transmitted parasites of endotherms, which live in the relatively constant-temperature environment of their hosts (Raffel et al. 2006, Harvell et al. 2009). Perhaps as a result of this reasoning, much of the available research on climate and disease has focused on malaria, which has an ectothermic vector (Harvell et al. 2009). However, climate change will also influence the ecology and physiology of endothermic hosts, so it will also be important to assess climate change impacts on directly transmitted diseases, such as influenza and tuberculosis (Rosenthal 2009).

Recommendations for future research

- To improve model predictions of climate impacts on disease, we recommend (1) incorporating intrinsic dynamics, spatiotemporal confounders, and small-scale temperature variability into models, and (2) developing and using better concurrent data sets of disease and hypothesized drivers to

validate models.

- To improve empirical studies of climate effects on disease, we recommend (1) using combinations of laboratory, field, and mesocosm experiments to improve experimental realism, (2) avoiding pseudoreplicated experimental treatments (e.g., temperature), and (3) quantifying nonlinear responses to climate and biological adaptations (e.g., acclimation) to temperature variability.
- To move toward a general theory of climate and disease, we recommend (1) greater collaboration between disease researchers and thermal biologists, (2) the use of meta-analysis to seek general (e.g., phylogenetic) patterns of thermal adaptation, and (3) tests of metabolic theory predictions for host–parasite interactions.

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