Climate and Vectorborne Diseases

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Abstract: Climate change could significantly affect vectorborne disease in humans. Temperature, precipitation, humidity, and other climatic factors are known to affect the reproduction, development, behavior, and population dynamics of the arthropod vectors of these diseases. Climate also can affect the development of pathogens in vectors, as well as the population dynamics and ranges of the nonhuman vertebrate reservoirs of many vectorborne diseases. Whether climate changes increase or decrease the incidence of vectorborne diseases in humans will depend not only on the actual climatic conditions but also on local nonclimatic epidemiologic and ecologic factors. Predicting the relative impact of sustained climate change on vectorborne diseases is difficult and will require long-term studies that look not only at the effects of climate change but also at the contributions of other agents of global change such as increased trade and travel, demographic shifts, civil unrest, changes in land use, water availability, and other issues. Adapting to the effects of climate change will require the development of adequate response plans, enhancement of surveillance systems, and development of effective and locally appropriate strategies to control and prevent vectorborne diseases.

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Introduction

Global climate change poses the threat of serious social upheaval, population displacement, economic hardships, and environmental degradation. Human health also could be influenced by increased variability and sustained changes in temperature, rainfall patterns, storm severity, frequency of flooding or droughts, and rising sea levels.[1–13] Climate change and increased climatic variability are particularly likely to affect vectorborne diseases (Table 1). Much of the impact of climate on vectorborne diseases can be explained by the fact that the arthropod vectors of these diseases are ectothermic (cold-blooded) and, therefore, subject to the effects of fluctuating temperatures on their development, reproduction, behavior and population dynamics.[3,7,99–106] Temperature also can affect pathogen development within vectors and interact with humidity to influence vector survival and, hence, vectorial capacity. The seasonality and amounts of precipitation in an area also can strongly influence the availability of breeding sites for mosquitoes and other species that have aquatic immature stages. For those diseases that are both vectorborne and zoonotic (i.e., have vertebrate reservoirs other than humans), climatic variables can affect the distribution and abundance of vertebrate host species, which can, in turn, affect vector population dynamics and disease transmission.[106]

The purpose of this article is to review the influence of climate on the transmission and spread of vectorborne diseases and identify the most important gaps in our knowledge, including the degree to which studies on the impact of climatic variability on vectorborne diseases can help us understand the likely alterations of vector–host–pathogen relationships under conditions of sustained climate change. We also discuss how human behaviors, land use, and demographic factors can interact with climate to determine the actual burden of vectorborne disease among humans. Finally, we suggest approaches for adapting to the potential effects of climate change on the occurrence of vectorborne diseases in humans.

The article is organized into three main sections that provide examples of the effects of climatic variability on diseases transmitted by mosquitoes, other flying arthropods, and ticks and fleas, and discuss the potential effects of climate change on the distribution and incidence of the diseases. The article is divided in this manner because the vectors in each group exhibit distinct differences in their mobilities and host-seeking behaviors, their abilities to disperse over long distances, and the degree to which their distributions are tied to specific hosts or habitats.

Some mosquito species, for example, are highly mobile and can fly many kilometers or be transported

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Table 1. Selected examples of climatic factors influencing the transmission and distribution of vectorborne diseases

Disease (causative agent)	Vector	Relevant climatic factors	Effects of climatic variability or climate change	References
Parasitic vectorborne diseases				
Malaria (*Plasmodium vivax*, *P. falciparum*)	Mosquitoes	Temperature, rainfall, humidity, El Niño–related effects, sea surface temperatures	Disease distribution; pathogen development in vector; development, reproduction, activity, distribution, and abundance of vectors; transmission patterns and intensity; outbreak occurrence	14–27
Leishmaniasis (*Leishmania* spp.)	Sand flies	Temperature, precipitation, El Niño–related effects	Disease incidence and outbreak occurrence; abundance, behavior, and distribution of vectors	28–37
Chagas disease (*Trypanosoma cruzi*)	Triatomine bugs	Temperature, precipitation, humidity, severe weather event	Vector distribution, increased infestation of houses by vector	38–40
Onchocerciasis (*Onchocerca volvulus*)	Black flies	Temperature	Transmission intensity	41
Arboviral diseases				
Dengue fever (Dengue virus)	Mosquitoes	Temperature, precipitation	Outbreaks, mosquito breeding ,abundance, transmission intensity (extrinsic incubation period)	42–45
Yellow fever (Yellow fever virus)	Mosquitoes	Temperature, precipitation	Outbreaks, incidence; distribution, abundance, and breeding of mosquitoes, transmission intensity (extrinsic incubation period)	43,44,46
Chikungunya Fever (Chikungunya virus)	Mosquitoes	Temperature, precipitation	Outbreaks; mosquito breeding and abundance, transmission intensity (extrinsic incubation period)	43,44,47
West Nile virus disease (West Nile virus)	Mosquitoes	Temperature, precipitation	Transmission rates, pathogen development in vector, distribution of disease and vector	48–50
Rift Valley Fever (Rift Valley Fever virus)	Mosquitoes	Precipitation, sea surface temperatures	Outbreaks; vector breeding and abundance, transmission intensity (extrinsic incubation period)	43,44,51,52
Ross River virus disease (Ross River virus)	Mosquitoes	Temperature, precipitation, sea surface temperatures	Outbreaks, vector breeding and abundance, transmission intensity (extrinsic incubation period)	53
Tickborne encephalitis (Tickborne Encephalitis virus)	Ticks	Temperature, precipitation, humidity	Vector distribution, phenology of host-seeking by vector	54–62
Bacterial and rickettsial diseases				
Lyme borreliosis (*Borrelia burgdorferi, B. garinii, B. afzelii*, or other related *Borrelia*)	Ticks	Temperature, precipitation, humidity	Frequency of cases, phenology of host-seeking by vector, vector distribution	56–60,63–72
Tularemia (*Francisella tularensis*)	Ticks	Temperature, precipitation	Case frequency and onset	73
Human granulocytic anaplasmosis (*Anaplasma phagocytophilum*)	Ticks	Temperature, precipitation	Vector distribution, phenology of host-seeking by vector	63,65,66,68,69,71,74,75
Human monocytic ehrlichiosis (*Ehrlichia chafeensis*)	Ticks	Temperature, precipitation	Phenology of host-seeking by vector	68,76,77
Plague (*Yersinia pestis*)	Fleas	Temperature, precipitation, humidity, El Niño–related events	Development and maintenance of pathogen in vector; survival and reproduction of vectors and hosts; occurrences of historical pandemics and regional outbreaks, distribution of disease	78–98

over long distances aboard planes, ships, or other vehicles.[107] Their distributions also are often associated more closely with the availability of suitable breeding habitats and climatic conditions than the presence of a narrow range of hosts or host habitats. Although capable of flight, certain other arthropod vectors, such as sand flies or triatomine bugs, typically disperse over more limited distances and can be largely restricted in distribution to certain host habitats that provide both suitable breeding areas and homes or resting sites for their hosts.[108,109] Similarly, fleas and ticks are wingless and, because of their limited mobility, often rely on the movements of their hosts for dispersal. Many of these species also spend considerable time in host nests or burrows, awaiting the return of specific hosts to these sites. Those tick and flea species that quest for hosts in more exposed environments, such as grassy fields or forest floors, also are likely to be exposed to the life-threatening effects of high temperatures or low humidity, or be forced to limit their questing to brief periods when conditions are less extreme.[54,98]

Although the mobility of ticks and fleas, as well as certain winged insects such as sand flies and triatomine bugs, is generally much more limited than that of mosquitoes, it should be noted that they can be transported over long distances by human-related activities such as the shipment of infested animals or the transport of luggage or other goods. This last factor poses the risk that even low mobility vectors, as well as the disease agents they transmit, could become established in new areas, including those that might become suitable habitats as a result of climate change. However, as noted below, successful introduction and establishment of local vectorborne disease cycles relies on not just the dispersal of the vectors but also many other ecologic and human-related factors.

Mosquito-Borne Diseases

The potential impacts of climate change on the transmission of vectorborne parasitic diseases, including malaria, must be considered against the backdrop of rapidly changing social, epidemiologic, and economic conditions. Support for implementation of evidence-based, proven interventions, particularly for malaria, has never been greater. As a consequence, surveillance and health information systems are better able to detect infections, and enhanced control measures are effectively reducing the number of malaria cases in many countries. Among these measures are insecticide-treated mosquito nets, indoor residual spraying, improved diagnosis by microscopy and rapid diagnostic tests, effective treatment of cases, and implementation of intermittent presumptive treatment of pregnant women. In addition, changing land use, drug and insecticide resistance, movement of significant populations to urban areas, and relocations of displaced groups of people are all having profound impacts on the distribution and incidence of malaria.

Although no single factor can explain levels of human malaria risk, climatic factors clearly can affect the transmission and geographic range of this disease. Temperature influences both the speed of development of the malaria parasite in the mosquito vector and the rate of development of the mosquito (and hence the number of potential mosquito generations per season and, therefore, vector abundance). *Plasmodium falciparum* transmission is limited by temperatures below 16°–19°C (61°–66°F), whereas *P. vivax* development can occur at temperatures as low as 14.5°–15°C (58°–59°F). Malaria parasite development also cannot occur above temperatures of 33°–39°C (91°–102° F) for *P. falciparum* and *P. vivax*,[7] indicating that increasing temperatures may restrict malaria transmission in some geographic regions. Vector density is important because it is directly proportional to the inoculation rate or the rate of malaria transmission from mosquitoes to people as well as the rate at which vectors will acquire infectious gametocytes from human hosts.

Precipitation affects vector populations at the larval and adult stages. Since many anopheline vectors of malaria breed in small natural pools of clean water, droughts usually result in decreases in vector populations and transmission by limiting the number and quality of vector breeding sites. However, the impact of changes in precipitation patterns on malaria transmission is dependent on the ecology of the vector species. In Africa, changes in rainfall will more rapidly affect the densities of *Anopheles gambiae*, a species that breeds in smaller water sources than those utilized by *An. funestus*, which can breed on the edges of larger bodies of water. The Sahel marks the northern limit of *P. falciparum* in Africa due to inadequate rainfall.[110] Similarly, long-term reductions in rainfall in Senegal and Niger have been associated with decreases in malaria,[111,112] presumably through reductions in breeding sites for *An. Gambiae*, and the reductions in rainfall predicted for Central America are expected to lead to reductions in malaria transmission.[113] However, reductions in transmission intensity in endemic areas following periods of reduced rainfall may actually increase the potential for subsequent epidemics due to an increase in the non-immune proportion of the populations living in those areas. In Irian Jaya, Indonesia, the drought caused by the 1997 El Niño was associated with a severe epidemic in the highlands in which >550 people died.[114] *An. punctulatus* is a major vector in Irian Jaya and it may be that the drought created breeding sites for this vector along the edges of the normally fast flowing rivers. Precipitation patterns also affect humidity which, in turn, affects adult mosquito survivorship. Under most climatic conditions, a vector must live for at least 10 days in order for an ingested malaria parasite to survive long enough to develop and yield infectious

sporozoites that will invade the salivary gland, which is the site from which the parasite can be transmitted to a susceptible human during blood feeding.

The role of climate in causing seasonal patterns of malaria is well established. Variations in numbers of malaria cases were related to weather patterns preceding the transmission seasons in Kenya, Madagascar, and Ethiopia. Increased incidence of malaria in the Kenyan highlands was significantly associated with rainfall and high maximum temperatures 3–4 months earlier.[115] In the highlands of Madagascar, much of the annual variability in malaria incidence was associated with minimum temperatures at the beginning of the transmission season.[14] In Ethiopia, malaria epidemics in 50 sites from the 1980s to the early 1990s were associated with high minimum temperatures in the preceding months.[116] Seasonal changes in malaria were also associated with climate variables in southern Africa.[15] The impacts of El Niño on the risk of malaria epidemics are well established in parts of southern Asia, Africa, and South America. Significant relationships have been shown between sea surface temperatures associated with the El Niño Southern Oscillation (ENSO) and malaria cases (or related mortality) in South America[16–18] and the El Niño Southern Oscillation Index (SOI) for southern Africa.[117]

Although the relationships between weather variables and malaria transmission over a short time frame are incontrovertible, documentation of the impacts of long-term climate change on malaria transmission are still debated, most notably in the geographic fringe areas of transmission where epidemics occur. Some studies using time–series data in East Africa concluded that recent increases in malaria incidence occurred in the absence of climate trends.[19–21] These studies posited that the rising number of malaria cases is explained by the development of drug resistance to the parasite coupled with a decrease in vector control activities. These conclusions were challenged by Patz,[22] who used updated temperature data to identify a significant warming trend that began at the end of the 1970s and was concurrent with the rise in malaria cases. Pascual and others[23] later reanalyzed data from these East Africa sites and concluded that a significant warming trend had indeed occurred since 1950. Additional modeling indicated that these small temperature changes would have a significant amplifying effect on mosquito population dynamics. However, long-term associations with climate and malaria were not found in southern Africa by Craig and colleagues.[15]

Regardless of whether climate change explains long-term patterns in malaria transmission, models are being developed that should help us better understand and predict how climatic factors might change transmission. Confalonieri and others[24] summarized a number of the models and their associated predictions for malaria. Although these models predict expanded transmission southward in Australia[118] and an increased number of days suitable for transmission in Portugal, it is likely that the capacity of these developed countries to respond with effective prevention programs will limit the potential risk. In Africa, the areas suitable for *P. falciparum* transmission are predicted to expand in some areas but contract in others.[25,26,113,119] In India, the malaria distribution is projected to expand to higher latitudes and altitudes.

In Africa, malaria epidemics are frequently triggered by climate anomalies that follow periods of drought.[27] In Botswana, rainfall totals for December to February can explain more than two thirds of the malaria incidence variability.[120] The finding that sea surface temperatures are related to both rainfall and annual malaria incidence suggested that a model could be developed to predict anomalies in the number of malaria cases based on sea surface temperatures in Botswana.[120] Therefore, a seasonal timescale "multimodel ensemble system" based on an ocean–atmospheric climate model was developed, and can provide 4 months more lead time in predicting malaria anomalies in Botswana compared with warning systems based solely on observed precipitation.[121] A forecasting model using the Normalized Difference Vegetation Index (NDVI), mean maximum temperature, rainfall, and number of malaria cases in the previous month had a 93% forecasting accuracy in Burundi.[122]

Presumably, climate change would affect malaria most noticeably by shifting its geographic range. Less noticeable would be a change in seasonal profile, occurring within an already-exposed population. This geographic shift will likely be noticed as the occurrence of epidemics among non-immune populations at the periphery of the present endemic areas. Hence, adaptation needs to include increased surveillance as part of an early warning system that uses climate data as one variable to predict outbreaks and is tailored to the specific ecologic requirements of the likely vectors. Healthcare providers also should be trained to recognize malaria and implement effective treatment after diagnostic confirmation, most likely with rapid diagnostic tests. As all age groups are equally susceptible to infection in epidemic-prone areas, mosquito control would be needed to protect the entire population by either indoor residual spraying or community-wide coverage with long-lasting insecticide-treated mosquito nets.

Elucidating the impact of climate on lymphatic filariais is difficult owing to the chronic nature of this disease, which is inefficiently transmitted and characterized by long incubation periods and an absence of epidemics that would signal its expansion into new geographic areas. The asymptomatic nature of most filarial infections also makes recognition of cases in previously non-endemic areas difficult. Lymphatic filariasis is spread by a multitude of vector species in the

genera *Culex, Anopheles, Aedes,* and *Mansonia*, a fact that will require development of regional models for predicting how climate changes will affect the different vector species. Further, mass drug administration campaigns to globally eliminate the disease have been launched in >50 countries. Even if the campaigns should falter, they should have sufficient impacts to make further geographic expansion of lymphatic filariasis unlikely.

The effects of climate change on the epidemiology of mosquito-borne viral diseases are not easily predictable. Although cursory consideration might conclude that increases in temperature and rainfall will produce increased incidence of arboviral diseases, in fact the ecologic determinants of these diseases interact in complex ways. The incidence of dengue, yellow fever, and Chikungunya fever, all transmitted by *Aedes aegypti* mosquitoes, sometimes increases during dry seasons because of increased peri-domestic water storage.[42,46,47] Extremely high temperatures can increase mosquito mortality, which could decrease arboviral disease transmission.[43] Heavy rainfall can wash out mosquito breeding sites.[44] Humans may seek refuge in air-conditioned buildings during heatwaves that might otherwise expose them to mosquito bites.[45] Thus a facile conclusion that higher temperatures and increased rainfall will lead to increased transmission of arboviral diseases must be tempered by more careful and thoughtful analysis of the interaction of ecologic variables with human behavior.[105]

Mosquito activity is often seasonal and the mosquito vectors of arboviral diseases can hatch and develop into active adults only when water is sufficiently abundant and the temperature is warm enough.[48] Furthermore, the distribution of most mosquito-borne arboviral diseases affecting humans is limited to temperate and tropical regions of the world. However, some diseases that are thought of as tropical, such as dengue and yellow fever, have historically occurred in temperate areas as far north as Philadelphia, New York, and Boston.[44] West Nile virus has recently caused seasonal epidemics in Russia and Canada[49,50] and a Chikungunya outbreak recently occurred in Italy.[123] The northward reach of dengue, yellow fever, West Nile virus disease, and Chikungunya is not attributable to global changes in climate but rather to importation of the etiologic viruses into receptive ecosystems during times when local climate is favorable for their transmission.[44,48–50] Thus, climate clearly influences the dynamics of arboviral disease transmission but it does so through complex interactions that may be difficult to predict.[53,105]

Increasing temperatures can increase the transmission of arboviruses by decreasing the development time of mosquito vectors (as was discussed earlier for malaria), by decreasing the extrinsic incubation period, and by increasing the viral titer in mosquitoes.[48,105] Reisen et al.[48] noted that areas of higher West Nile virus transmission in the northern U.S. from 2002 to 2004 experienced above-normal temperatures but areas of high transmission in the southern regions of the country did not. These investigators also showed that the effect of temperature on virus development in mosquitoes can vary depending on the species and strain of virus.

Some arboviruses, such as dengue and yellow fever viruses, are transmitted from humans to mosquitoes and back to other humans in direct mosquito–human cycles. Others, such as West Nile virus and eastern equine encephalitis virus, are transmitted from birds or other nonhuman vertebrates to mosquitoes, and incidentally from infected birds to humans, which are usually dead-end viral hosts. In the latter situation (transmission from birds or other nonhuman vertebrates to mosquitoes), a determination of the effects of climate change on disease transmission requires consideration of the impact of climate on the distribution and abundance of nonhuman vertebrate hosts, in addition to the impact on mosquitoes and on human behavior. For both mosquito–human–mosquito transmission and bird–mosquito–human transmission, changes in human behavior, such as water storage, land use and irrigation, patterns of dwelling construction, use of air-conditioning, and intensity of mosquito control efforts all can interact with climate to alter the incidence of human disease. Changes in human population density can influence patterns of behavior as well as influencing socioeconomic determinants of arboviral disease risk.

The effects of socioeconomic conditions and human behavior on the risk of arboviral disease transmission were illustrated through a study of dengue transmission on the U.S.–Mexico border. The seroprevalence of antibody against dengue virus was substantially higher on the Mexican side of the border despite higher infestations of the vector *Ae. aegypti* on the U.S. side that could clearly support epidemic transmission of dengue.[45] Since the communities that were studied had identical climate, climatic factors could not explain the difference in transmission. However the presence of air-conditioning in homes was substantially higher on the U.S. side of the border, and was found to be protective against dengue virus infection. Although climatic conditions were clearly favorable for dengue transmission on both sides of the border, better socioeconomic conditions limited transmission on the U.S. side.

The exploration of climatic determinants of arboviral disease transmission has led to efforts to predict outbreaks by examining climate trends.[51] One elegant example of this is the forecasting of outbreaks of Rift Valley fever in East Africa using satellite data to identify areas of high green vegetation development, and combining this with data on sea surface temperatures in the

Pacific and Indian Oceans.[52] The risk of Rift Valley fever increases when heavy rainfall fills local land depressions called "dambos," where the vector mosquitoes breed. The combination of data on greening vegetation and sea surface temperatures could have predicted all of three Rift Valley fever outbreaks that occurred between 1982 and 1998 without falsely predicting any outbreaks during that period.[52] However, Gatton and colleagues[53] in Australia illustrated the complexity of using climatic factors to predict Ross River virus disease in Queensland. They were not able to find any set of climate variables that could predict Ross River virus disease outbreaks across the state. The climate variables that could predict outbreaks varied across different regions of Queensland and across different seasons. Thus, increased risk of outbreaks during summer in the southern regions was correlated with increased temperatures in the spring and early rainfall in summer, but in the northern regions increased spring temperatures decreased the risk of outbreaks.[53] During autumn, the risk of outbreaks in the southern areas was decreased by high temperatures, but in the central coastal region, high temperature increased the risk of outbreaks.[53] This study well illustrates the pitfalls of assuming a simple and uniform relationship between climatic factors and risk of arboviral disease across different time periods and geographic areas.

Severe weather patterns that could come with global climate change have been implicated in causing increased incidence of arboviral disease.[124,125] However, natural disasters have only rarely been shown to cause increases in arboviral disease in the U.S.[126] There was no apparent increase in dengue transmission following Hurricane Georges in Puerto Rico in 1998, and Hurricane Katrina did not appear to cause any increase in reports of West Nile virus disease or St. Louis encephalitis in Louisiana or Mississippi in 2005.[127,128] Any true relationships between arboviral disease incidence and severe weather patterns are also not likely to be explained by simple and uniform models.

The complexities of the ecologic determinants of arboviral diseases should not impede public health preparedness for changes in distribution of the diseases that might occur with or without changes in climate. The introduction of West Nile virus into North America and its spread across the continent exemplify the importance of effective public health surveillance systems to detect changes in arboviral disease incidence and transmission patterns, and to guide and monitor strategies for disease prevention.[129,130] Data from such surveillance systems can be used to explore the impact of climatic factors on disease transmission.[48] Further research into the effects of climate on arboviral disease transmission could help develop, target, and increase the effectiveness of prevention strategies. The effective application of models to predict the effects of climate change on these diseases will likely require careful consideration of local ecologic conditions and microclimates. Effective prevention of arboviral diseases in an era of rapid global change will require well-developed public health systems along with socioeconomic development, mosquito control programs, and deployment of effective mosquito repellents and preventive vaccines.

Diseases Transmitted by Other Flying Arthropods

Predicting the effects of climate change for other parasitic diseases like leishmaniasis is complicated by the presence of vertebrate reservoirs in the transmission cycle that also would be affected by climatic events. Like malaria, leishmaniasis has a number of different vectors and the responses of these vectors to climate changes will vary. Although leishmaniasis is often associated with drier conditions, sand fly vectors need high humidity, as well as cooler temperatures and specific soil types in order to thrive. Their limited flight range also requires that they be in close proximity to humans for transmission to occur.[30]

In Bahia State of Brazil, the number of leishmaniasis cases increased after a 2-year lag following droughts associated with El Niño.[31] It was hypothesized that the droughts resulted immediately in low vector densities and transmission intensities, which also led to both waning herd immunity and an associated increase in susceptible human and reservoir populations in endemic areas. Subsequent rainy seasons led to increases in both vector densities and subsequent infection rates in high-risk populations. The 2–6-month incubation period plus the time from onset of symptoms to diagnosis was responsible for the 2-year lag in reported cases after El Niño. The spatial analysis of Thompson and others[32] hypothesized that increases in leishmaniasis cases in Ceara, Brazil were associated with a drought that stimulated human migration to urban areas and clustering of people around water supplies, a factor that increased risks for humans as the limited water sources and high humidity associated with them also resulted in concentration of vector populations (*Lutzomia longipalpis*) around these same sites.

Computer models are predicting the geographic and seasonal distribution of *P. papatasi* and the potential for leishmaniasis transmission using weather data (temperature and humidity) and remotely sensed data (such as NDVI) in southwest Asia.[28] Similarly the probable distribution of *P. orientalis* in Sudan was modeled using climatic and environmental variables (rainfall, temperature, altitude, soil type, and satellite-derived environmental proxies [NDVI and land surface temperature]).[33] The analyses suggested that *P. orientalis* occupies a "climate space" with 400–1200 mm (16–47 in) annual rainfall and an annual mean maximum

temperature between 34°C and 38°C (93°F and 100°F). Within this space, the vector was associated with soil type and the occurrence of Acacia-Balanites woodland. Ecologic niche modeling in Brazil is providing insights into the ecologic basis for differences in the distributions of three sand fly species.[34]

Recent changes in the distributions of cutaneous leishmaniasis are being reported. Cases are now being found further north in Europe.[35] In addition, changes in the pattern of distribution of the vectors in southern Europe are being reported.[36,37] Studies in Colombia suggest that under climate change scenarios, the increased frequency of droughts is likely to increase the incidence of leishmaniasis.[29] Ecologic niche models developed in southern Brazil for *L. whitmani* suggests that the leishmaniasis-endemic areas in southern Brazil, northern Argentina, and western Chile will expand with possible appearance of autochthonous cases of cutaneous leishmaniasis on the eastern slopes of the Peruvian Andes, where transmission of the disease has not been reported.[34] A temperature-based model predicts that global warming could greatly increase both the geographic and seasonal distribution of sand fly vectors in Southwest Asia.[30]

Onchocerciasis. Although relatively little is known about the impact of climate on onchocerciasis (River Blindness), differences in temperatures have been related to transmission. In Venezuela, geologic substrates, landscape types, and vegetation types influence transmission intensity, with different black fly vectors being associated with particular landscapes.[41] Presumably, climate change could alter local landscape usage and vegetation types, thereby affecting black fly distributions and transmission of the causative agent of this disease (*Onchocerca volvulus*).

Chagas disease. The distributions of triatominae vectors of Chagas disease or American trypanosomiasis are associated with high temperatures, low humidities,[38,39] and certain types of vegetation.[40] Together with rainfall, climatic variables have been used to create transmission risk maps that predict house infestations with *Triatoma dimidiata* and infection rates with *Trypanosoma cruzi* in Mexico.[131] In the aftermath of Hurricane Isidore, the risk of Chagas transmission in Mexico increased significantly due to the increase in the number of *T. dimidiata* infesting houses. This increase was hypothesized to be due to the death of feral animals that would normally serve as hosts for this vector.[132] A similar scenario could happen in other Chagas-endemic areas. In Brazil, the introduced vector species, *T. infestans*, is found only in domestic ecotopes, whereas others, such as *T. brasiliensis* (native species) are found in natural environments but can colonize and reinvade domiciliary environments after interventions.[133] Severe climatic events could potentially trigger significant increases in the number of *T. brasiliensis* colonizing houses. Unlike American trypanosomiasis, a clear link between African trypanosomiasis and climate change or even interannual variability is unclear[134] due to the association of the disease with cattle and the impacts of population movements, deforestation, and drug resistance.

Tickborne and Flea-Borne Diseases

Ticks represent a notable threat to public health because they maintain multiple and diverse disease agents (e.g., bacteria, viruses, and parasites) within zoonotic cycles and serve as bridging vectors between zoonotic reservoirs and humans.[76,135] Major tickborne diseases include: Lyme borreliosis (caused primarily by *Borrelia burgdorferi*, *B. afzelii*, and *B. garinii*); tularemia (*Francisella tularensis*); tickborne relapsing fever (multiple *Borrelia* spp. including *B. hermsii* and *B. duttonii*); human granulocytic anaplasmosis (*Anaplasma phagocytophilum*); human monocytic ehrlichiosis (*Ehrlichia chaffeensis*); Rocky Mountain spotted fever (*Rickettsia rickettsii*); tickborne encephalitis (TBE viruses); and babesiosis (*Babesia microti*, *B. divergens*). In Europe, the two major tickborne diseases, TBE and Lyme borreliosis, have increased in incidence and cases have shifted to higher elevations or latitudes. Presently, it is unclear whether these changes are attributable to a well-documented change in climate, or alterations in human land use or movement patterns.[55,61,62,136–139]

Tick life cycles and the transmission dynamics of tickborne disease agents have been summarized elsewhere.[54,68,76,77,135] For the purpose of this review, the salient points are:

1. Human exposure to tickborne pathogens is restricted to geographic locations where both vector tick populations and the tickborne pathogens are established.
2. The time of onset and frequency of tickborne diseases in humans is determined, in part, by seasonal patterns of activity by vector ticks.[64,69,70,140]
3. The incidence of tickborne diseases is a function of tick abundance, prevalence of infection in ticks, and contact rates between humans and infected ticks.[55,63,64,74,75,135,140–149]

Ticks are restricted to geographic locations where climatic conditions are suitable for completion of their life cycles[135,143–145,150–154] and changing climatic conditions (i.e., temperature and precipitation) may shift the geographic range and seasonal period of disease risk and alter transmission dynamics within endemic areas, thereby resulting in changes in spatial and temporal patterns of human disease. Brownstein and others[71] created a climate-based logistic regression model based on the distribution of *Ixodes scapularis* (a primary vector of the agents of Lyme borreliosis, babesiosis, and human granulocytic anaplasmosis in eastern North

America) and then extrapolated the model using predicted climate change scenarios. The resulting model indicated a future expansion of the tick's range into Canada, and a reduction of the vector in its southernmost distribution. Using a population modeling approach, Ogden et al.[65] also anticipated a northerly range expansion for *I. scapularis* in Canada. Reports of *I. scapularis* from all provinces east of Alberta, Canada support this scenario.[155–157]

In Europe, geographic shifts in the distribution of *I. ricinus*, the primary vector of the agents of Lyme borreliosis and TBE, have been attributed to climate change. Long-term field studies exploiting an altitudinal gradient in the Czech Republic provide evidence that the distribution of *I. ricinus* has shifted significantly upward in elevation as temperature has increased over the last few decades.[56–59] In addition, the northern distribution of *I. ricinus* is believed to have shifted toward higher latitudes in Sweden[60] in response to a reduction in the number of very cold winter days.[62]

Time of onset of human illness and frequency of infection are both associated with seasonal changes in the abundance of host-seeking vector ticks.[64,69,70,73] Because host-seeking phenology is strongly affected by temperature and precipitation,[63,66,68,72] it is likely that climate change will alter the timing and duration of peak risk of exposure to tickborne pathogens. In the far western U.S., the peak seasonal occurrence of Lyme borreliosis cases coincides with the peak questing period of nymphal *I. pacificus*.[69] Temporal trends in questing activity of *I. pacificus* nymphs revealed that the duration of peak questing activity (the number of days with nymphal density within 75% of the absolute peak value) was positively associated with rainfall and negatively associated with air temperatures in April–May.[72] The duration of peak questing was 82% longer in cooler, coniferous areas compared with warmer, drier oak woodland habitats.[66] This observation suggests that warmer temperatures and reduced rainfall could shorten the duration of peak tick activity and, thus, reduce overall risk. Conversely, increasing temperatures could prolong the questing season in some situations. For example, the active period of *I. ricinus* has historically spanned March to November in Germany but, during recent mild winters, questing nymphs and adults were collected from September through January.[67]

The above examples demonstrate the potential for climate change to induce shifts in the geographic distribution and timing of peak abundance of vector ticks. Although tick abundance is positively associated with human risk of exposure to tickborne pathogens, humans cannot become infected, regardless of tick population size, in areas where the pathogen is lacking. Therefore, it also is important to consider how climate change could affect enzootic pathogen transmission cycles and, ultimately, affect infection prevalence in host-seeking ticks. Many ticks of medical importance (e.g., *Ixodes* spp. and *Dermacentor* spp.) have broad host preferences and some (e.g., *I. pacificus*, *I. ricinus*, *I. scapularis*) commonly infest a plethora of different hosts including rodents, insectivores, lagomorphs, ungulates, birds, and lizards.[63,77,142,146,147,158] Among such a wide assortment of vertebrate hosts, reservoir competency for a given pathogen can range from very low to very high, and some hosts (e.g., certain species of lizards in the case of *B. burgdorferi*) may even be refractory to pathogen infection (zooprophylaxis).[159–162] In situations where the majority of ticks feed on highly competent reservoir hosts, prevalence of infection in ticks is expected to be high relative to situations in which most ticks feed on ineffective reservoir hosts.[142,146,147,149,158] Thus, infection prevalence is closely tied to vertebrate host community structure, which is regulated by many factors aside from climatic ones (e.g., predator–prey dynamics, habitat suitability, availability of food resources).

The complexity of these interactions makes it difficult to predict the effects of climate change on tickborne diseases. However, one intriguing speculation is that a warmer climate may result in increased ranges and abundances of *Borrelia*-refractory lizards, and that this may lead to reduced intensity of enzootic transmission of *Borrelia burgdorferi* in areas where lizards previously were rare. Because of these complexities we believe there is a critical need to begin long-term ecologic studies aimed at understanding the interaction between climatic factors and (1) geographic distributions of vector ticks,[163] (2) seasonal host-seeking activity, and (3) relative abundance of reservoir-competent and -incompetent hosts and prevalence of infection in ticks.

Fleas are best known as vectors of *Yersinia pestis*, the etiologic agent of plague, a disease that has caused millions of human deaths, especially during the Black Death of the Middle Ages. Each of the three major pandemics was probably influenced by climatic events. Tree ring and glacial ice core data indicate that an extreme and sudden drop in worldwide temperatures occurred within 5 years of the beginning of the first major plague pandemic (Justinian's Plague) in 1540 and that this cooling trend persisted for several years. Similarly, the Black Death of the mid-fourteenth century was preceded by unusually wet summers and warm springs in Central Asia, the region where this pandemic probably originated.[78] The last or so-called modern pandemic is generally believed to have begun in southwestern China in the mid-nineteenth century. Tree-ring data indicate that the early years (1855–1870) of this pandemic were wetter and warmer than normal.[78]

Although this pandemic began in China, the Indian subcontinent was the region most affected, suffering repeated outbreaks of plague from 1896 to the 1920s. The timing of outbreaks in much of this area was heavily influenced by seasonally varying climatic fac-

tors, primarily rainfall and temperature. In a given year outbreaks dwindled in intensity as precipitation peaked during the monsoon and increased as conditions became drier and warmer. Case numbers began to fall as temperatures exceeded 26.7°C (80°F) and epidemics came to a virtual stop at 29.4°–32.2°C (85°–90°F).[79] Brooks[80] also noted that the seasonal occurrences of human plague outbreaks were affected by both temperature and saturation deficits, the latter being a measure of atmospheric "dryness" that accounts for the effects of both temperature and humidity.[164] Specifically, it was noted that epidemics came to an end as temperatures exceeded approximately 27°C (81°F) and saturation deficits of 0.76 cm (0.3 in). Similar observations were made during plague outbreaks in Vietnam.[81] Temperature also appears to determine the northern limits of *Y. pestis* distribution, as nearly 95% of human cases occur in regions with mean annual temperatures in excess of 13°C (55°F) and the vast majority of large plague outbreaks occur within areas where these values range from 24° to 27°C (75° to 81°F).[82]

More recently, Parmenter and others[83] demonstrated that human cases of plague in New Mexico occurred more frequently following periods of above-average winter–spring precipitation. A later study[84] demonstrated that time-lagged late winter–early spring precipitation was positively correlated with the frequency of human plague in northeastern Arizona and northwestern New Mexico. The number of days above certain threshold temperatures (35°C [95°F] and 32°C [90°F] in the Arizona and New Mexico models, respectively) was inversely correlated with human case numbers and it was suggested that high temperatures might adversely affect flea survival or transmission of *Y. pestis* by fleas. Parmenter[83] proposed a trophic cascade model to explain the positive effect of precipitation on the frequency of human plague. According to this model, increased rainfall in this semi-arid region leads to enhanced availability of rodent food sources and heightened rodent reproduction, factors that are likely to increase risk of plague epizootics among rodents and the spread of the disease to humans. Enscore and colleagues[84] later suggested revising this model to account for the effects of threshold temperatures on plague transmission.

The above model clearly suggests that precipitation or other climatic variables are likely to influence the frequency of human plague indirectly by affecting the spread of plague among the rodents and fleas that act as sources of infection for humans. Recent studies have supported this argument. Stapp and others[85] reported that patterns of plague-related die-offs of prairie dog colonies on the Pawnee National Grasslands in north central Colorado followed El Niño Events. Using methods similar to Enscore,[84] Collinge and others[86] also demonstrated that the frequency of plague epizootics among prairie dog colonies in Montana was positively associated with time-lagged precipitation and the number of warm days in a year but negatively correlated with hot temperatures. However, they were unable to demonstrate a similar relationship for plague epizootics among prairie dogs in Boulder County CO leading them to propose that the effects of climate on plague transmission in prairie dogs might be greatest in those areas, such as Philips County, Montana, where rainfall amounts show strong annual peaks rather than areas, such as Boulder County CO where the months and seasons with the greatest rainfall are likely to vary greatly from one year to another.

Favorable climatic conditions can lead to dramatic increases in rodent reproduction. Some have hypothesized that the likelihood of plague epizootics occurring among rodents increases greatly when densities of these animals exceed certain levels.[165] However, this was not convincingly demonstrated until recently, when Davis et al.[166] reported that continued persistence and spread of plague epizootics among great gerbils (*Rhombomys opimus*) in Kazakhstan was dependent on threshold population sizes for these hosts. In a later paper, Stenseth and colleagues[78] demonstrated that plague among gerbils was positively correlated with wetter summers and warmer springs and predicted that a 1°C (1.8°F) increase in these temperatures will lead to a >50% increase in plague prevalence among gerbils.

Enscore et al.[84] suggested that threshold temperatures might be important because excessively high temperatures adversely affect flea survival or the abilities of fleas to retain the foregut blockages thought by some to be required for efficient transmission of *Y. pestis*. Numerous studies have noted that, at temperatures above approximately 27°–28°C (81°–82°F), these blockages begin to break down.[87–89] Recently, it was reported that these blockages consist of a matrix of plague bacteria and a *Y. pestis*–produced biofilm which is synthesized at temperatures below 27°C (81°F) but breaks down at higher temperatures, resulting in the loss or considerable reduction of any blockage in the flea's foregut.[90] According to some, the adverse effect of high temperatures on the retention of blockages in fleas could explain why plague epidemics often come to a halt as local temperatures exceed approximately 27°C (81°F).[87] Although this is possible, it should be remembered that flea survival can be reduced by high temperatures and that reductions in flea population size could decrease epidemic activity. In addition to its effects on block formation and retention, temperature also can influence the ability of *Y. pestis* to establish and maintain itself in the flea's gut, as indicated by a study that found that only 1 of 101 infected fleas lost their infections at ≤23°C (≤73°F) but 9 of 74 became cleared of infection when held at 29.5°C (85°F).[88]

The effects of temperature on fleas are not limited to their abilities to retain and transmit *Y. pestis* at different temperatures. These insects have a life cycle that, in

some respects, resembles that of mosquitoes or biting flies in that only the adult stages are parasitic and consume blood meals from their hosts. The eggs of most plague vectors are laid in either the nests or burrows of their hosts, where they hatch into legless wormlike larvae that feed on detritus and occasionally blood-containing feces from actively feeding adult fleas in the same nest or burrow. Following a series of molts and a period of a few weeks to months, the fully developed larvae spin pupal cocoons in preparation for their transformation to adults. The survival and development of these immature stages is significantly influenced by temperature and relative humidity in the nest environments. In general, development rates will increase with temperatures, although excessive temperatures, particularly when accompanied by low relative humidity, can adversely affect survival of immature stages, especially larvae.[79,91–93] Conversely, extremely high relative humidity values (>90%) can adversely affect larval survival through promoting fungal growth that appears to be pathogenic for the larvae.[81,94]

Adult fleas that are allowed to feed often are relatively insensitive to the effects of high temperature and low humidity, presumably because the water provided by the host blood meal replaces that lost by the flea in these otherwise unfavorable environments.[91,95] Starving fleas, which are unable to replace water lost through desiccation, quickly succumb to hot, dry conditions,[93,95,96] as demonstrated by the fact that survival of rat fleas (*Xenopsylla cheopis*) is inversely proportional to the atmospheric saturation deficiency (reviewed in Pollitzer[95]). *X. cheopis* fleas held at 35 mm (1.4 in) saturation deficiency and constant temperature survived 15 times longer than fleas held at a deficiency of 5 mm (0.2 in). Conversely, under conditions of constant saturation deficiency, the longevity of adult fleas was found to decrease by one half to one third when these insects were exposed to a 10°C (18°F) rise in temperature.

High temperatures or low humidities may influence flea behavior by keeping these insects from questing for new hosts at burrow entrances or other sites where exposure to hot, dry conditions could adversely affect their survival. Although starving fleas must eventually find a host and take a blood meal or die, their survival is likely to be at least temporarily prolonged by remaining within the relatively cool, humid environments of the host's nest or burrow until environmental conditions improve in less protected but potential feeding environments, such as burrow entrances. That such a strategy is likely to be successful is suggested by numerous studies showing that certain species of fleas, some of which were infected with *Y. pestis*, were able to live unfed in burrows for many months to well over a year.[98] This last observation has led to the suggestion that survival of infected fleas within burrows is likely to represent a significant reservoir mechanism for *Y. pestis*.[98] If climate change alters the microclimates within rodent burrow systems, it could have a significant impact on the maintenance of *Y. pestis* in an area, but the ameliorating effect of the subterranean burrow is likely to decrease the impact of these microclimate changes compared with those observed in exposed surface sites and might temporarily provide lower temperature, higher humidity refuges for infected fleas.

Recently, Nakazawa and others[97] evaluated spatial patterns and shifts of plague transmission in the U.S. since 1960, and assessed whether these shifts were consistent with what would be expected for any climate change that occurred over that period. Their results suggested that the pattern of human plague cases had indeed shifted northward as temperatures have warmed since the 1960s. The resulting ecologic niche models and estimates of projected climate change from two general circulation models were used to identify possible future shifts in the spatial pattern of human plague in the U.S. It was predicted that human plague should continue to occur at relatively high rates in the highly endemic areas of New Mexico and surrounding areas, but some northward expansion of the disease could occur into Wyoming and Idaho. Whether such shifts would result in significant increases in human cases will depend on many factors, including those related to human behavior, rodent sanitation practices, land use, and the influences of local factors on vector and host ecology.

Fleas also transmit murine typhus, a rickettsial disease that is widespread on all continents except Antarctica and occurs in a wide range of temperatures from hot, humid, tropical areas to cold montane and semiarid ones.[167] Murine typhus cases in the U.S. are most common (94% of total cases) in eight southern states where climates are warm and humid through most of the year. Transmission of this agent is seasonal, peaking in late spring and early autumn, corresponding with the periods of peak abundance for the primary vector, *X. cheopis*. As noted in the above discussion on plague, the survival and development of this flea is heavily influenced by temperature and humidity. This fact, along with the noted seasonality of the disease, suggests that climatic variability could influence transmission of murine typhus and that the warming temperatures suggested by most climate change scenarios could result in the disease moving northward, although incidence in humans is likely to be influenced by other factors, including levels of rat infestation and flea burdens on rats in peri-domestic areas.

Conclusion

Abundant evidence indicates that climatic variation can affect the reproduction, development, population dynamics and host-seeking behaviors of arthropod vectors, as well as their abilities to transmit disease agents.

The studies reviewed here suggest that the climatic variability and occurrence of extreme weather events (heatwaves, severe storms, floods, or drought) projected to occur under most climate change scenarios could affect the transmission of vectorborne diseases. Many millions of people potentially could suffer from the effects of climate change on vectorborne diseases, but the precise impacts of these effects are difficult to predict. In some areas, climate change could increase outbreaks and the spread of some vectorborne diseases while having quite the opposite effect on other vectorborne diseases.

The difficulties encountered in predicting the impacts that climate change will have on vectorborne diseases are due in part to the many factors other than climate that interact to determine the incidence of vectorborne disease in humans, including vector and host ecology, human culture and behavior, land use, and other locally variable conditions. The facile prediction that an increase in global temperatures and heightened precipitation will expand the range of a certain vector (or vectors) to higher latitudes and altitudes might indeed turn out to be true in some instances, but the mere establishment of suitable vectors for a particular agent does not necessarily mean that spread to humans will commonly occur, as indicated by the limited transmission of dengue and malaria in the southern U.S. In these instances, competent vectors (*Ae. aegypti* and *An. quadrimaculatus*, respectively) are present[45,99,168] and infected individuals or vectors occasionally enter this region, but local transmission has been limited by factors unrelated to the climatic suitability of the areas for the relevant vector species. In instances where a vectorborne disease is also zoonotic, the situation is even more complex, because not only must the vector and pathogen be present but a competent vertebrate reservoir host other than humans must also be present.

Thus, determining the effects of climate change on the incidence, spread, and geographic range of vectorborne diseases is challenging. Although past outbreaks have sometimes been associated with extreme climate events and climatic variability, confidence in using these studies for predicting future events is often low, or the results are contentious. This is partly because of the lack of adequate long-term data sets tracking relevant variables in most regions, including the distribution and abundance of vectors and the past incidence of vectorborne diseases. Furthermore, the lack of well-designed long-term studies makes it difficult to determine if observed changes in transmission and distribution of vectorborne diseases are related to climate or to one or more of the many other global changes concurrently transforming the world, including increased economic globalization, the high speed of international travel and transport of commercial goods, increased population growth, urbanization, civil unrest, displaced refugee populations, water availability and management, and deforestation and other land-use changes.

Regardless of any uncertainties about whether climate change will occur or how this process will affect human health, the public health community needs to be prepared to respond to such changes should they occur. In order to do this, the existing public health infrastructure will have to be enhanced, including the capacity to monitor vector populations and to conduct surveillance for vectorborne diseases. Special emphasis should be placed on monitoring the spread of these diseases and their vectors into areas that adjoin existing foci. Additional surveillance should be done in airports or seaports where vectors, hosts, or pathogens might invade a region after being transported over long distances. If a particular vector or vectorborne disease suddenly appears in an area, additional efforts should be undertaken to determine whether this range extension is temporary or represents an actual establishment of the vector or a focus of infection. In those instances where a vectorborne disease is also zoonotic, a search for potential vertebrate reservoirs should be done. Longitudinal surveillance within known foci of major vectorborne diseases could help determine whether climate change or increased climatic variability is affecting transmission rates and the incidence of human cases in these areas.

Whenever possible, efforts should be made to develop and evaluate appropriate mathematical models to describe the relationships between climatic factors and the spread or incidence of vectorborne diseases. Such models can be useful for planning purposes and help authorities anticipate how human risks of vectorborne disease might be affected by climate change. The effectiveness of prevention strategies, including the use of insecticides and other means of vector control, host control techniques, environmental management strategies, vaccines, and therapeutic agents should also be evaluated and monitored. Although these efforts to enhance our knowledge and response capabilities in anticipation of future climate change are likely to place heavy demands on already limited resources, they are clearly necessary and should have the added benefit of increasing overall public health capacity, including the development of improved vectorborne disease surveillance systems.

Additional information on responding to climate change and its potential impact on human health is available at the CDC website (www.cdc.gov/Features/ClimateChange/).

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