CHAPTER 6

Climate change and infectious diseases

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Introduction

The previous chapter considered how short-term variations in climatic conditions and extreme weather events can exert direct effects on human death rates, physical injury, mental health and other health outcomes. Changes in mean climatic conditions and climate variability also can affect human health via indirect pathways, particularly via changes in biological and ecological processes that influence infectious disease transmission and food yields. This chapter examines the influences of climatic factors on infectious diseases.

For centuries humans have known that climatic conditions affect epidemic infections—since well before the basic notion of infectious agents was understood late in the nineteenth century. The Roman aristocracy took refuge in their hill resorts each summer to avoid malaria. South Asians learnt early that in high summer, strongly curried foods were less prone to induce diarrhoeal diseases. In the southern United States one of the most severe summertime outbreaks of yellow fever (viral disease transmitted by the *Aedes aegypti* mosquito) occurred in 1878, during one of the strongest El Niño episodes on record. The economic and human cost was enormous, with an estimated death toll of around 20 000 people. In developed countries today it is well known that recurrent influenza epidemics occur in mid-winter.

Infectious disease transmission should be viewed within an ecological framework. Infectious agents obtain the necessary nutrients and energy by parasitization of higher organisms. Most such infections are benign, and some are even beneficial to both host and microbe. Only a minority of infections that adversely affect the host's biology are termed "infectious disease".

During the long processes of human cultural evolution; population dispersal around the world; and subsequent inter-population contact and conflict; several distinct transitions in human ecology and inter-population interactions have changed profoundly the patterns of infectious disease in human populations. Since the early emergence of agriculture and livestock herding around 10 000 years ago, three great transitions in human/microbe relationships are readily recognizable (*1*):

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1. Early human settlements enabled enzootic infective species to enter *H. sapiens*.
2. Early Eurasian civilizations came into military and commercial contact around 2000 years ago, swapping dominant infections.
3. European expansionism over past five centuries caused transoceanic spread of often lethal infectious diseases.

This may be the fourth great transitional period. The spread and increased lability of various infectious diseases, new and old, reflects the impacts of demographic, environmental, technological and other rapid changes in human ecology. Climate change, one of the global environmental changes now under way, is anticipated to have a wide range of impacts upon the occurrence of infectious disease in human populations.

Disease classification

Broadly, infectious diseases may be classified into two categories based on the mode of transmission: those spread directly from person to person (through direct contact or droplet exposure) and those spread indirectly through an intervening vector organism (mosquito or tick) or a non-biological physical vehicle (soil or water). Infectious diseases also may be classified by their natural reservoir as anthroponoses (human reservoir) or zoonoses (animal reservoir).

Climate sensitivities of infectious diseases

Both the infectious agent (protozoa, bacteria, viruses, etc) and the associated vector organism (mosquitoes, ticks, sandflies, etc.) are very small and devoid of thermostatic mechanisms. Their temperature and fluid levels are therefore determined directly by the local climate. Hence, there is a limited range of climatic conditions—the climate envelope—within which each infective or vector species can survive and reproduce. It is particularly notable that the incubation time of a vector-borne infective agent within its vector organism is typically very sensitive to changes in temperature, usually displaying an exponential relationship. Other climatic sensitivities for the agent, vector and host include level of precipitation, sea level elevation, wind and duration of sunlight.

Documented and predictive climate/infectious disease linkages

The seasonal patterns and climatic sensitivities of many infectious diseases are well known; the important contemporary concern is the extent to which changes in disease patterns will occur under the conditions of global climate change. Over the past decade or so this question has stimulated research into three concentrations. First, can the recent past reveal more about how climatic variations or trends affect the occurrence of infectious diseases? Second, is there any evidence that infectious diseases have changed their prevalence in ways that are reasonably attributable to climate change? Third, can existing knowledge and theory be used to construct predictive models capable of estimating how future scenarios of different climatic conditions will affect the transmissibility of particular infectious diseases?

Modifying influences

Climate is one of several important factors influencing the incidence of infectious diseases. Other important considerations include sociodemographic influences such as human migration and transportation; and drug resistance and nutrition; as well as environmental influences such as deforestation; agricultural develop-

ment; water projects; and urbanization. In this era of global development and land-use changes, it is highly unlikely that climatic changes exert an isolated effect on disease; rather the effect is likely dependent on the extent to which humans cope with or counter the trends of other disease modifying influences. While recognizing the important independent role of these non-climatic factors, the focus of this section is to examine the extent to which they may compound the effects of climatic conditions on disease outcomes.

Disease classifications relevant to climate/health relationships

Several different schemes allow specialists to classify infectious diseases. For clinicians who are concerned with treatment of infected patients, the clinical manifestation of the disease is of primary importance. Alternatively, microbiologists tend to classify infectious diseases by the defining characteristics of the microorganisms, such as viral or bacterial. For epidemiologists the two characteristics of foremost importance are the method of transmission of the pathogen and its natural reservoir, since they are concerned primarily with controlling the spread of disease and preventing future outbreaks (*2*).

Climate variability's effect on infectious diseases is determined largely by the unique transmission cycle of each pathogen. Transmission cycles that require a vector or non-human host are more susceptible to external environmental influences than those diseases which include only the pathogen and human. Important environmental factors include temperature, precipitation and humidity (discussed in more detail in the following section). Several possible transmission components include pathogen (viral, bacterial, etc.), vector (mosquito, snail, etc.), non-biological physical vehicle (water, soil, etc.), non-human reservoir (mice, deer, etc.) and human host. Epidemiologists classify infectious diseases broadly as anthroponoses or zoonoses, depending on the natural reservoir of the pathogen; and direct or indirect, depending on the mode of transmission of the pathogen. Figure 6.1 illustrates these four main types of transmission cycles for infectious diseases. The following is a description of each category of disease, discussed in order of probable increasing susceptibility to climatic factors (*3*).

Directly transmitted diseases

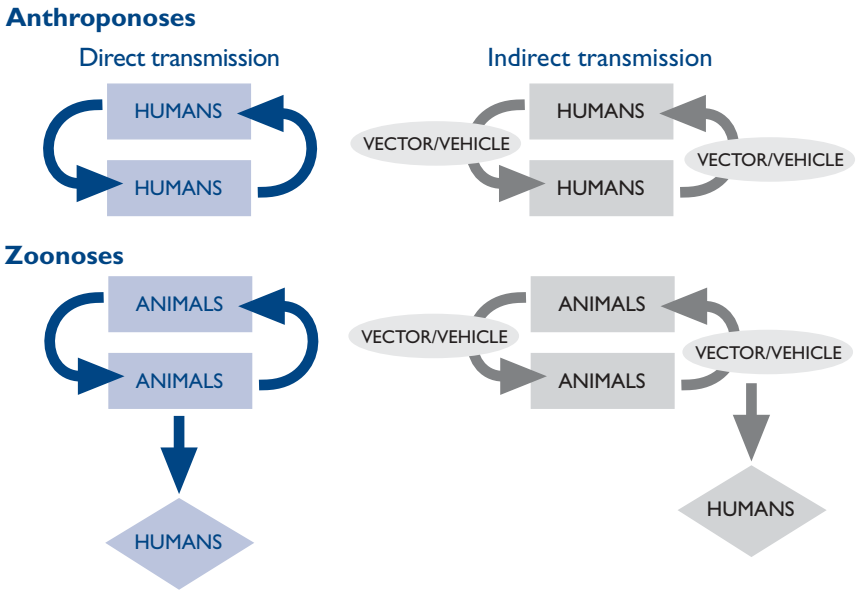
Anthroponoses

Directly transmitted anthroponoses include diseases in which the pathogen normally is transmitted directly between two human hosts through physical contact or droplet exposure. The transmission cycle of these diseases comprises two elements: pathogen and human host. Generally, these diseases are least likely to be influenced by climatic factors since the agent spends little to no time outside the human host. These diseases are susceptible to changes in human behaviour, such as crowding and inadequate sanitation that may result from altered land-use caused by climatic changes. Examples of directly transmitted anthroponoses include measles, TB, and sexually transmitted infections such as HIV, herpes and syphilis (*3*).

Zoonoses

Directly transmitted zoonoses are similar to directly transmitted anthroponoses in that the pathogen is transmitted though physical contact or droplet exposure

FIGURE 6.1 Four main types of transmission cycle for infectious diseases.
Source: reproduced from reference 3.



between reservoirs. However, these agents are spread naturally among animal reservoirs and the infection of humans is considered to be a result of an accidental human encounter. The persistence of these pathogens in nature is largely dependent on the interaction of the animal reservoir and external environment which can impact the rate of transmission, host immunity, rate of reproduction, and species death, rendering these diseases more susceptible to effects of climate variability. Hantavirus is a directly transmitted zoonosis that is naturally maintained in rodent reservoirs and can be transmitted to humans at times of increased local abundance of the reservoir (*4*). Rabies is another directly transmitted zoonosis that naturally infects small mammals, although with very little opportunity for widespread transmission, being highly pathogenic to its vertebrate host (*3*). Several of today's anthropogenic diseases, e.g. TB and HIV, originally emerged from animals.

Indirectly transmitted diseases (anthroponoses & zoonoses)

Indirectly transmitted anthroponoses are a class of diseases defined by pathogen transmission between two human hosts by either a physical vehicle (soil) or a biological vector (tick). These diseases require three components for a complete transmission cycle: the pathogen, the physical vehicle or biological vector, and the human host. Most vectors require a blood meal from the vertebrate host in order to sustain life and reproduce. Indirectly transmitted anthroponoses include malaria and dengue fever, whereby the respective malaria parasite and the dengue virus are transmitted between human hosts by mosquito vectors (vector-borne disease). Indirectly transmitted water-borne anthroponoses are susceptible to climatic factors because the pathogens exist in the external environment during part of their life cycles. Flooding may result in the contamination of water supplies or the reproduction rate of the pathogen may be

influenced by ambient air temperatures (*3*). Cholera is an indirectly transmitted water-borne anthroponose that is transmitted by a water vehicle: the bacteria (*Vibrio cholerae*) reside in marine ecosystems by attaching to zooplankton. Survival of these small crustaceans in turn depends on the abundance of their food supply, phytoplankton. Phytoplankton populations tend to increase (bloom) when ocean temperatures are warm. As a result of these ecological relationships, cholera outbreaks occur when ocean surface temperatures rise (*5*).

Indirectly transmitted zoonoses are similar to indirectly transmitted anthroponoses except that the natural cycle of transmission occurs between non-human vertebrates: humans are infected due to accidental encounters with an infected vehicle or vector. This class of disease involves four components in the transmission cycle: the pathogen, biological vector or physical vehicle, animal reservoir, and human host. These diseases are highly susceptible to a combination of ecological and climatic factors because of the numerous components in the transmission cycle, and the interaction of each of these with the external environment (*3*).

Complex cycles of disease transmission also exist for several diseases which cannot be classified simply by method of transmission or natural reservoir. Such a disease is Rift Valley fever where the virus is primarily a zoonotic disease, spread among vertebrate hosts by the mosquito species *Aedes*. Primarily under flood conditions, *Culex* mosquitoes may feed upon infected ungulate hosts. This vector is referred to as a bridge species because it feeds on humans also, resulting in spread of the virus outside its normal zoonotic cycle (*3*).

Climate sensitivity of infectious disease

Seasonality of infectious disease

Chapter 5 discussed patterns of winter mortality and infectious disease using the example of cyclic influenza outbreaks occurring in the late fall, winter and early spring in North America. This disease pattern may result from increased likelihood of transmission due to indirect social or behavioural adaptations to the cold weather such as crowding indoors. Another possibility is that it may be attributed directly to pathogen sensitivities to climatic factors such as humidity. In addition to influenza, several other infectious diseases exhibit cyclic seasonal patterns, which may be explained by climate.

In diverse regions around the world, enteric diseases show evidence of significant seasonal fluctuations. In Scotland, campylobacter infections are characterized by short peaks in the spring (*6*). In Bangladesh, cholera outbreaks occur during the monsoon season (*5*). In Peru, cyclospora infections peak in the summer and subside in the winter (*7*). Similarly, some vector-borne diseases (e.g. malaria and dengue fever) also show significant seasonal patterns whereby transmission is highest in the months of heavy rainfall and humidity. Epidemics of other infections (e.g. meningococcal meningitis) tend to erupt during the hot and dry season and subside soon after the beginning of the rainy season in sub-Saharan Africa (*8*).

Seasonal fluctuations of infectious disease occurrence imply an association with climatic factors. However, to prove a causal link to climate, non-climatic factors must be considered. Furthermore, in order to assess long-term climate influences on disease trends, data must span numerous seasons and utilize proper statistics to account for seasonal fluctuations.

Vector-borne diseases

Important properties in the transmission of vector-borne diseases include:

- survival and reproduction rate of the vector
- time of year and level of vector activity, specifically the biting rate
- rate of development and reproduction of the pathogen within the vector (*9*).

Vectors, pathogens, and hosts each survive and reproduce within certain optimal climatic conditions and changes in these conditions can modify greatly these properties of disease transmission. The most influential climatic factors for vector-borne diseases include temperature and precipitation but sea level elevation, wind, and daylight duration are additional important considerations. Table 6.1 gives an overview of the impact of climatic change on each biological component of both vector and rodent-borne diseases. The following paragraphs discuss several of these effects in greater detail.

Temperature sensitivity

Extreme temperatures often are lethal to the survival of disease-causing pathogens but incremental changes in temperature may exert varying effects. Where a vector lives in an environment where the mean temperature approaches the limit of physiological tolerance for the pathogen, a small increase in temperature may be lethal to the pathogen. Alternatively, where a vector lives in an environment of low mean temperature, a small increase in temperature may result in increased development, incubation and replication of the pathogen (*10*, *11*). Temperature may modify the growth of disease carrying vectors by altering their biting rates, as well as affect vector population dynamics and alter the rate at which they come into contact with humans. Finally, a shift in temperature regime can alter the length of the transmission season (*12*).

Disease carrying vectors may adapt to changes in temperature by changing geographical distribution. An emergence of malaria in the cooler climates of the African highlands may be a result of the mosquito vector shifting habitats to cope with increased ambient air temperatures (*13*). Another possibility is that vectors undergo an evolutionary response to adapt to increasing temperatures. There is recent evidence to suggest that the pitcher-plant mosquito (*Wyeomia smithii*) can adapt genetically to survive the longer growing seasons associated with climate change. Bradshaw and Holzapfel demonstrated this by documenting a change in the photoperiodic response between two different time periods in two populations of pitcher-plant mosquitoes. The change in response was correlated to a marked genetic shift within the mosquito species. A greater degree of micro-evolutionary response was associated with mosquito populations inhabiting higher latitudes; the hypothesis is that because these populations have greater selection pressure they have also a greater ability to evolve genetically. Although this study was limited to one specific species of mosquito, it suggests that other mosquitoes, perhaps disease carrying vectors, may undergo an analogous micro-evolution which would allow adaptation to altered seasonal patterns associated with global climate change (*14*).

Precipitation sensitivity

Variability in precipitation may have direct consequences on infectious disease outbreaks. Increased precipitation may increase the presence of disease vectors by expanding the size of existent larval habitat and creating new breeding

TABLE 6.1 Effects of weather and climate on vector and rodent-borne diseases[a].

Vector-borne pathogens spend part of their life-cycle in cold-blooded arthropods that are subject to many environmental factors. Changes in weather and climate that can affect transmission of vector-borne diseases include temperature, rainfall, wind, extreme flooding or drought, and sea level rise. Rodent-borne pathogens can be affected indirectly by ecological determinants of food sources affecting rodent population size, floods can displace and lead them to seek food and refuge.

Temperature effects on selected vectors and vector-borne pathogens

Vector
- survival can decrease or increase depending on species;
- some vectors have higher survival at higher latitudes and altitudes with higher temperatures;
- changes in the susceptibility of vectors to some pathogens e.g. higher temperatures reduce size of some vectors but reduce activity of others;
- changes in the rate of vector population growth;
- changes in feeding rate and host contact (may alter survival rate);
- changes in seasonality of populations.

Pathogen
- decreased extrinsic incubation period of pathogen in vector at higher temperatures
- changes in transmission season
- changes in distribution
- decreased viral replication.

Effects of changes in precipitation on selected vector-borne pathogens

Vector
- increased rain may increase larval habitat and vector population size by creating new habitat
- excess rain or snowpack can eliminate habitat by flooding, decreasing vector population
- low rainfall can create habitat by causing rivers to dry into pools (dry season malaria)
- decreased rain can increase container-breeding mosquitoes by forcing increased water storage
- epic rainfall events can synchronize vector host-seeking and virus transmission
- increased humidity increases vector survival; decreased humidity decreases vector survival.

Pathogen
Few direct effects but some data on humidity effects on malarial parasite development in the anopheline mosquito host.

Vertebrate host
- increased rain can increase vegetation, food availability, and population size
- increased rain can cause flooding: decreases population size but increases human contact.

Increased sea level effects on selected vector-borne pathogens
Alters estuary flow and changes existing salt marshes and associated mosquito species, decreasing or eliminating selected mosquito breeding-sites (e.g. reduced habitat for *Culiseta melanura*)

[a] The relationship between ambient weather conditions and vector ecology is complicated by the natural tendency for insect vectors to seek out the most suitable microclimates for their survival (e.g. resting under vegetation or pit latrines during dry or hot conditions or in culverts during cold conditions).
Source: reproduced from reference 12.

grounds. In addition, increased precipitation may support a growth in food supplies which in turn support a greater population of vertebrate reservoirs. Unseasonable heavy rainfalls may cause flooding and decrease vector populations by eliminating larval habitats and creating unsuitable environments for vertebrate reservoirs. Alternatively, flooding may force insect or rodent vectors to seek refuge in houses and increase the likelihood of vector-human contact. Epidemics of leptospirosis, a rodent-borne disease, have been documented following severe

flooding in Brazil (*15*). In the wet tropics unseasonable drought can cause rivers to slow, creating more stagnant pools that are ideal vector breeding habitats.

Humidity sensitivity

Humidity can greatly influence transmission of vector-borne diseases, particularly for insect vectors. Mosquitoes and ticks can desiccate easily and survival decreases under dry conditions. Saturation deficit (similar to relative humidity) has been found to be one of the most critical determinants in climate/disease models, for example, dengue fever (*16*, *17*) and Lyme disease models (*18*).

Sea level sensitivity

The projected rise in sea level associated with climate change is likely to decrease or eliminate breeding habitats for salt-marsh mosquitoes. Bird and mammalian hosts that occupy this ecological niche may be threatened by extinction, which would also aid the elimination of viruses endemic to this habitat (*19*). Alternatively, inland intrusion of salt water may turn former fresh water habitats into salt-marsh areas which could support vector and host species displaced from former salt-marsh habitats (*19*).

Water-borne diseases

Human exposure to water-borne infections can occur as a result of contact with contaminated drinking water, recreational water, coastal water, or food. Exposure may be a consequence of human processes (improper disposal of sewage wastes) or weather events. Rainfall patterns can influence the transport and dissemination of infectious agents while temperature can affect their growth and survival (*20*). Table 6.2 outlines some of the direct and indirect weather effects on enteric viruses, bacteria and protozoa.

TABLE 6.2 Water and food-borne agents: connection to climate.

Pathogen groups	Pathogenic agent	Food-borne agents	Water-borne agents	Indirect weather effect	Direct weather effect
Viruses	Enteric viruses (e.g. hepatitis A virus, Coxsackie B virus)	Shellfish	Groundwater	Storms can increase transport from faecal and waste water sources	Survival increases at reduced temperatures and sunlight (ultraviolet)[a]
Bacteria Cyanobacteria Dinoflagellates	Vibrio (e.g. *V. vulnificus*, *V. Parahaemolyticus*, *V. cholerae* non-01; Anabaena spp., Gymnodinium Pseydibutzschia spp.)	Shellfish	Recreational, Wound infections	Enhanced zooplankton blooms	Salinity and temperature associated with growth in marine environment
Protozoa	Enteric protozoa (e.g. Cyclospora, Crytosporidium)	Fruit and vegetables	Recreational and drinking water	Storms can increase transport from faecal and waste water sources.	Temperature associated with maturation and infectivity of Cyclospora

[a] Also applies to bacteria and protozoa.
Source: Reproduced from reference 20.

Temperature sensitivity

Increasing temperatures may lengthen the seasonality or alter the geographical distribution of water-borne diseases. In the marine environment, warm temperatures create favourable conditions for red tides (blooms of toxic algae) which can increase the incidence of shellfish poisoning (*21*). Increasing sea surface temperatures can indirectly influence the viability of enteric pathogens such as *Vibrio cholerae* by increasing their reservoir's food supply (*5*). Ambient air temperatures also have been linked to hospital admissions of Peruvian children with diarrhoeal disease (*22*).

Precipitation sensitivity

Heavy rains can contaminate watersheds by transporting human and animal faecal products and other wastes in the groundwater. Evidence of water contamination following heavy rains has been documented for cryptosporidium, giardia, and *E.coli* (*4, 23*). This type of event may be increased in conditions of high soil saturation due to more efficient microbial transport (*20*). At the other extreme, water shortages in developing countries have been associated with increases in diarrhoeal disease outbreaks that are likely attributed to improper hygiene (*24*).

Documented and predicted climate/infectious disease links

Research investigating possible links between temporal and spatial variation of climate and the transmission of infectious diseases can be categorized into one of three conceptual areas:

1. evidence for associations between short-term climate variability and infectious disease occurrence in the recent past.
2. evidence for long-term trends of climate change and infectious disease prevalence.
3. evidence from climate and infectious disease linkages used to create predictive models for estimating the future burden of infectious disease under projected climatic conditions.

Historical evidence of climate/infectious disease links

The study of several infectious diseases has resulted in evidence for associations between climatic variations or trends and disease occurrence. These include encephalitis, malaria and various water-borne diseases.

Encephalitis

Evidence suggests that epidemics of certain arboviruses, such as Saint Louis encephalitis virus (SLEV), may be associated with climatic factors. Shaman and colleagues conducted a study on SLEV in south Florida. In this region the transmission cycle can be divided into:

- maintenance: January–March
- amplification: April–June
- early transmission: July–September
- late transmission: October–December.

Mosquito vectors interact with avian hosts during the period of amplification.

The objective of this study was to assess the relationship between precipitation level and SLEV transmission, using a hydrology model to simulate water table depth (WTD) and SLEV incidence in sentinel chickens to estimate human transmission risk.

Three episodes of SLEV transmission were observed in the duration of this study. Each episode occurred during a wet period directly followed by drought (defined by high and low WTD, respectively). These results suggest the following sequence of events predisposing springtime SLEV transmission: spring drought forces the mosquito vector, *Cx. nigripalpus*, to converge with immature and adult wild birds in restrictive, densely vegetated, hammock habitats. This forced interaction of mosquito vectors and avian hosts creates an ideal setting for rapid transmission and amplification of SLEV. Once the drought ends and water sources are restored, the infected vectors and hosts disperse and transmit SLEV to a much broader geographical area. This study suggests that similar drought induced amplification might occur in other arboviruses (*25*).

A similar effect of climate has been suggested for West Nile virus (WNV), introduced into the Americas in 1999. Amplification of the virus is thought to occur under the climatic conditions of warm winters followed by hot dry summers. Similar to SLEV, WNV is a vector-borne zoonotic disease, normally transmitted between birds by the *Culex pipiens* mosquito. The vector tends to breed in foul standing water. In drought conditions, standing water pools become even more concentrated with organic material and mosquito predators, such as frogs and dragonflies, lessen in number. Birds may circulate around small water-holes and thus increase interactions with mosquitoes. In 1999 such climatic conditions existed in the mid-Atlantic States. Together with urban and suburban environments suitable for avian species they are possible explanations for the epidemic (*26*).

Malaria

Scientific evidence suggests that malaria varies seasonally in highly endemic areas. Malaria is probably the vector-borne disease most sensitive to long-term climate change (*27*). Malaria thus provides several illustrative examples (based on historical studies) of the link between infectious disease and climate change, many of which have been described in the previous chapter.

Githeko et al. (*28*) compared monthly climate and malaria data in highland Kakamega and found a close association between malaria transmission and monthly maximum temperature anomalies over three years (1997–2000).

Patz and colleagues studied the effect of soil moisture to determine the effects of weather on malaria transmission. Compared to raw weather data, hydrological modelling has several potential advantages for determining mosquito-breeding sites. High soil moisture conditions and vector breeding habitats can remain long after precipitation events, depending on factors such as watershed, run-off and evapotranspiration. For *An. gambiae*, the soil moisture model predicted up to 45% and 56% of the variability of human biting rate and entomological inoculation rate, respectively (*29*).

The link between malaria and extreme climatic events has long been the subject of study in the Indian subcontinent. Early in the twentieth century, the Punjab region experienced periodic epidemics of malaria. Irrigated by five rivers, this geographical plains region borders the Thar Desert. Excessive monsoon rainfall and resultant high humidity were clearly identified as major factors in the occurrence of epidemics through enhancement of both the breeding and life-

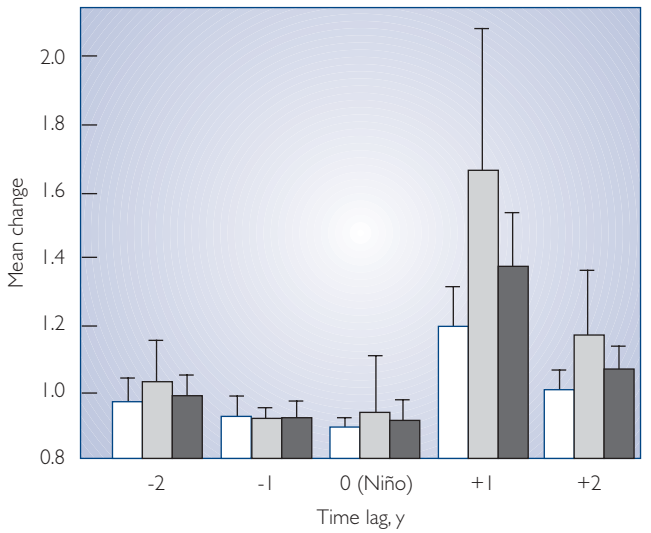


FIGURE 6.2 Relationship between reported malaria cases and El Niño in Venezuela. Average relative change in malaria incidence two years before (–1 and –2 years), during (year 0) and two years after El Niño event (+1 and +2) years). Data are for malaria deaths at the coast 1910–1935 (open bars), malaria cases for the whole country 1975–1995 (grey bars), and the average of both (black bars), with lines indicating the SEs. *Source: reproduced from reference 34.*

span of mosquitoes (*30*). More recently, historical analyses have shown that the risk of a malaria epidemic increased approximately five-fold during the year following an El Niño in this region (*31*, *32*). Further, the risk of an epidemic is greater in a year in which excess rain occurs in critical months. A strong correlation is found between both annual rainfall and the number of rainy days and the incidence of malaria in most districts of Rajasthan and in some districts in Gujarat (*33*).

The relationship between interannual climatic variation associated with the ENSO cycle and malaria has been examined in various other countries. For example, Venezuela experiences reduced rainfall during an El Niño year (*34*). Figure 6.2 illustrates that, consistently throughout the twentieth century, malaria rates increased on average by over one-third in the year immediately following an El Niño year. The likely reasons for this include the combination of mosquito-favouring, high rainfall in the post-Niño year with temporarily reduced immunity levels in the local population following the previous low-incidence year.

Water-borne disease

Most observed associations between climate and water-borne diseases are based on indirect evidence of seasonal variations. However, several studies provide quantitative evidence of water-borne diseases' links to climatic factors such as precipitation and ambient air temperature.

The previous chapter introduced one study of childhood diarrhoeal disease in Peru, a good example of historical evidence of a climate-health linkage. Checkley and colleagues used time series regression techniques to analyse the health effects of the 1997–98 EL Niño event on hospital admissions for diarrhoea. This study revealed several important findings. The El Niño event increased hospital admissions up to two-fold in winter, compared to expected rates determined from the previous four years. For each 1 °C increase in temperature, hospital admission increased by 8%. An additional 6225 cases of diarrhoeal disease were attributed to El Niño (*22*).

In another study, Curriero and colleagues examined the association between extreme precipitation and water-borne disease outbreaks in the United States

between 1948 and 1994. Their findings show a statistically significant association between heavy precipitation and water-borne disease outbreaks, over 50% of outbreaks being preceded by very wet months within the upper tenth percentile of a 50-year monthly rainfall record (*35*).

Early indicators for long-term trends in global warming

Many physical and biological indicators of long-term climate change effects have been documented. These include: thawing of permafrost; later freezing and earlier break-up of ice on rivers and lakes; pole-ward and altitudinal shifts in the ranges of a variety of plants and animals; earlier flowering of trees, emergence of insects and egg-laying of birds (*36*). However, human health outcomes are dependent on many upstream physical and biological systems. Disease analyses are complicated by the potential for numerous human population response options to reduce risk. Even if disease does occur, variability in detection and/or reporting remain major obstacles to determining valid trends in human disease incidence. Despite the difficulty that precludes a quantitative analysis of long-term trends in climate change and incidence of infectious diseases, several studies have reported such associations.

Rodo and colleagues found a robust relationship between progressively stronger El Niño events and cholera prevalence in Bangladesh, spanning a 70-year period. The investigators used innovative statistical methods to conduct a time series analysis of historical cholera data dating back to 1893, to examine the effect of non-stationary interannual variability possibly associated with climate change. In the last two decades, the El Niño Southern Oscillation (ENSO) has differed from previous decades. Since the 1980s there has been a marked intensification of the ENSO, beyond that expected from the known shift in the Pacific Basin temperature regime that began in the mid 1970s. The authors found the association of cholera incidence in the earlier half of the century (1893–1940) to be weak and uncorrelated with ENSO, while late in the century (1980–2001) the relationship is strong and consistent with ENSO. Past climate change, therefore, already may have affected cholera trends in the region via intensified ENSO events (*37*).

For vector-borne disease, linkages with climate may be questioned by the role of other factors such as socioeconomic, demographic and environmental influences. Kovats and colleagues offer a strategy for critically assessing the evidence for an association between vector-borne diseases and observed climate change. Important criteria for accepting a causal relationship between climate change and disease include:

- evidence for biological sensitivity to climate, requiring both field and laboratory research on important vectors and pathogens;
- meteorological evidence of climate change, requiring sufficient measurements for specific study regions;
- evidence for epidemiological or entomological change with climate change, accounting for potential confounding factors.

Kovats and colleagues stress the importance of frequent and long-term sampling to monitor the full range of specific vector species (*9*).

Evidence suggests a long-term association between climate change and tick-borne disease, such as encephalitis. In Sweden, Lindgren and colleagues conducted a study to determine whether the increasing incidence of tick-borne

encephalitis (TBE) could be linked to changes in the climate during the period 1960–1998. Regression analysis on incident TBE cases was conducted accounting for climatic factors for the two previous years, to account for the long lifespan of the ticks. Results indicate that the increase in TBE was associated with several climatic variables including: two mild consecutive winter seasons; temperatures favouring spring development; extended autumn activity in the year preceding the case; and temperatures favouring tick activity in the early spring of the incident year. One conclusion of this study is that the increased incidence of TBE can be explained by climate changing towards milder winters and early spring arrival. In 1994 Sweden reported the highest rates of TBE: a three-fold increase from the annual average. The year was preceded by five consecutive mild winters and seven early spring arrivals (*38*).

The investigators suggest a possible role of non-climatic factors in the increase incidence of TBE, including increased summer habitation in the area, availability of TBE vaccine and mammalian host populations respectively (*38*). Another opinion finds no causal link in the relationship between increased TBE and climate change in Sweden: elsewhere in Europe TBE shows variable patterns with season, suggesting the role of an alternative factor. Other explanations may be sociopolitical circumstances or changing agricultural patterns (*39*).

Predictive modelling

Models are important tools for analysing complex infectious disease transmission pathways. They allow investigators to link future geographically gridded projections of climate change (especially temperature and precipitation) generated by global or regional climate models to a model of the relationship between those climate variables and the occurrence of the disease of interest. Models will likely be important in directing future studies as well as predicting disease risk. The complex modelling required for the study of infectious diseases is a challenge but several successful attempts have been made. Modelling approaches can be classified into several categories including statistical, process and landscape based models (*40*).

Statistical based models

Empirical models incorporating a range of meteorological variables have been developed to describe the climatic constraints (the bioclimate envelope) for various vector-borne diseases. The CLIMEX model developed by Sutherst and colleagues (*41*, *42*) maps the geographical distribution of vector species in relation to climate variables. The assessment is based on an ecoclimatic index governed largely by the temperature and moisture requirements of the vector. CLIMEX analyses conducted in Australia indicate that the indigenous vector of malaria would be able to expand its range 330 km south under one typical scenario of climate change. However, such methods cannot include all factors that affect species distributions. Local geographical barriers and interaction/competition between species are important factors which determine whether species colonise the full extent of suitable habitat (*43*). Assessments may also include additional dynamic population (process-based) models (e.g. DYMEX).

Similarly, Martin and Lefebvre developed a Malaria-Potential-Occurrence-Zone model. This model was combined with 5 general circulation models (GCMs) of global climate to estimate the changes in malaria risk based on moisture and the minimum and maximum temperatures required for parasite development.

This model corresponded fairly well with the distribution of malaria in the nineteenth century and the 1990s, allowing for areas where malaria had been eradicated. An important conclusion of this exercise was that all simulation runs showed an increase in seasonal (unstable) malaria transmission (*44*).

Rogers and Randolph presented data contradicting the prevailing predictions of global malaria expansion. They used a two-step statistical approach that used present day distributions of *falciparum* malaria to identify important climatic factors and applied this information, along with projected climatic conditions, to predict future *falciparum* distributions. The model showed future *falciparum* habitat distributions similar to the present day. One of their conclusions is that the organism's biological reaction to temperature extremes will likely be balanced by other factors, such as precipitation (*45*).

Another approach, used by Reeves and colleagues, incorporates experimental and observational data to examine the effect of temperature on survival of mosquito species *Culex tarsalis*, the primary vector for St. Louis encephalitis (SLE) and western equine encephalitis (WEE). Observational data were obtained for two regions of California that differ consistently by an average of 5 °C. In the northern region vector populations peak in midsummer, southern populations peak in the spring. The experimental data was obtained by use of a programmable environmental chamber that allowed investigators to study the effect of temperature on a variety of factors including vector competence and survival. Investigators predict that an increase of 5 °C across California would result in a loss of WEE prevalence and an expansion of SLE in the warmer region (*19*).

Process-based (mathematical) models

A process-based approach is important in climate change studies as some anticipated climate conditions have never occurred before and cannot be empirically based.

Martens and colleagues have developed a modelling method (*46*, *47*, *48*, *49*). Their MIASMA model links GCM-based climate change scenarios with the formula for the basic reproduction rate (R_o) to calculate the 'transmission potential' of a region where malaria mosquitoes are present. The basic reproduction rate is defined as the number of new cases of a disease that will arise from one current case introduced into a non-immune host population during a single transmission cycle (*50*). This harks back to classical epidemiological models of infectious disease. Model variables within R_o that are sensitive to temperature include mosquito density, feeding frequency, survival and extrinsic incubation period (i.e. time required for parasite to develop the in the mosquito). The MIASMA approach models temperature effects on the last three of these processes, making an assumption (conservative in many habitats) that mosquito density remains unaffected by temperature increases. The model shows that the effects of small temperature increases on the extrinsic incubation period have large affects on transmission potential. This is consistent with the observation that the minimum temperature for parasite development is the limiting factor for malaria transmission in many areas.

In an effort to examine the apparent trend of increasing endemic malaria in the African highlands, Lindsay and Martens used the MIASMA model based on climate variables to identify epidemic prone regions in the African highlands and make predictions for future epidemic regions with projected changes in the climate. The model was used to calculate the effect of climate on factors such as mosquito development, feeding frequency, longevity and parasite incubation

time. Baseline transmission potential was compared to several futuristic scenarios including:

- 2 °C increase in ambient air temperature
- 2 °C increase in ambient air temperature and 20% increase in precipitation
- 2 °C increase in ambient air temperature and 20% decrease in precipitation.

Increasing temperature resulted in an increase in transmission potential at high elevations (>900 m). Also, transmission potential was found to decrease with decreasing precipitation. A combination of decreasing precipitation and increasing temperature is unfavourable for disease transmission (*51*).

Hartman et al. (*52*) used 16 GCM future scenarios to study their effect on climate suitability for malaria in Zimbabwe. Using the MARA/ARMA model (see Box 1) of climatic limits on *Anopheles* mosquitoes and *Plasmodium* parasites, the authors mapped the change in geographical distribution of endemic malaria. For all scenarios the highlands become more suitable for malaria transmission while the lowlands show varying degrees of change.

Process-based models also have been applied to dengue fever. Focks and colleagues developed a pair of probabilistic models to examine the transmission of dengue fever in urban environments. The container-inhabiting mosquito simulation model (CIMSiM) is an entomological model which uses information from weather to model outcomes such as mosquito abundance, age, development, weight, fecundity, gonotrophic status and adult survival. The dengue simulation model (DENSiM) uses the entomological output from the CIMSiM to determine the biting mosquito population. Survival and emergence factors are important predictors of population size within the DENSiM and gonotrophic development and weight are major influences on biting rates. These combined models provide a comprehensive account of the factors influencing dengue transmission. The on-going validation of these models will help to create a useful tool for future dengue control (*16*).

Landscape based models

Climate influences infectious disease transmission by not only affecting directly the rate of biological processes of pathogens and vectors but also influencing their habitats. Clearly there is potential in combining the climate-based models described above with the rapidly developing field of study which uses spatial analytical methods to study the effects of meteorological and other environmental factors (e.g. different vegetation types), measured by ground-based or remote sensors.

Satellite data can be used to identify the environmental limitations defining a vector/host/pathogen range. They can be analysed with weather data to determine the factors most important in describing current disease distribution, and the effect of projected changes in climate on this distribution (*53*). Other indices, such as the Normalised Difference Vegetation Index (NDVI), which correlates with the photosynthetic activity of plants, rainfall and saturation deficit also may be useful (*54*).

Remote sensing has been used in several studies of malaria. Mosquito distribution and malaria incubation time are dependent on climatic factors such as moisture and temperature. This allows the potential for satellite imagery of climate to predict mosquito distribution and transmission patterns. These extrinsic data, along with intrinsic variables such as immunity and nutritional status of the population, can help to create models appropriate at the local level for

present climatic scenarios. In turn these can be used as future warning tools for predicted climate scenarios (*55*). An illustrative example of this type of modelling is the MARA project which used satellite data to stratify malaria risk in the African highlands (Box 1).

Thomson et al. conducted satellite based spatial analysis in the Gambia to measure the impact of bed net use on malaria prevalence rates in children. Satellite data (NDVI) are used to measure changes in vegetative growth and senescence as proxy ecological variables representing changes in rainfall and humidity to predict length and intensity of malaria transmission. After accounting for spatial correlation of the villages used in the study, investigators found a significant association between malaria prevalence and both NDVI and use of bed nets (treated or untreated), by use of multiple regression analysis. This study suggests that NDVI data can be a useful predictor of malaria prevalence in children, having accounted for behavioural factors (*56*).

A three-phase study of malaria provides another example of satellite based predictive modelling. The first phase of this study tested the use of remote sensing data and ground surveillance data as predictive tools for the temporal and spatial distribution of larval populations of mosquito vector *Anopheles freeborni*, in California. The satellite measurements predicted 90% of peak densities of larvae as a function of rice field distance from livestock pastures. The second phase investigated the ecology of the primary malaria vector species *Anopheles albimanus* in the Mexican state of Chiapas: specifically, the association of mosquito larval populations with aquatic plant species, discerned though digitally processed satellite data. Results showed that transitional swamps and unmanaged pastures were the most important landscape factors associated with vector abundance (*57*). Phase three combined digitized map, remotely sensed and field data to define the association between vegetation and individual villages in Belize with high or low mosquito densities. These three studies show the usefulness of remotely sensed data for malaria surveillance (*58*).

Other vector-borne diseases have been studied using remote data. Rogers et al. mapped the changes of three important disease vectors (ticks, tsetse flies and mosquitoes) in southern Africa under three climate change scenarios (*59*). The results indicate significant potential changes in areas suitable for each vector species, with a net increase for malaria mosquitoes (*Anopheles gambiae*) (*53*). Thomson et al. used satellite data to map the geographical distribution of the sandfly vector, *Phlebotomus orientalis*, for visceral leishmaniasis in the Sudan (*60*).

In a Maryland study of *Ixodes scapularis* (the tick vector that transmits Lyme disease in the eastern United States) Glass and colleagues used GIS to extract information on a total of 41 environmental variables pertinent to the abundance of tick populations on white-tailed deer, the zoonotic host. They found tick abundance to be positively correlated with well-drained sandy soils and negatively correlated with urban land-use patterns, wetlands, privately owned land, saturated soils and limited drainage (*61*).

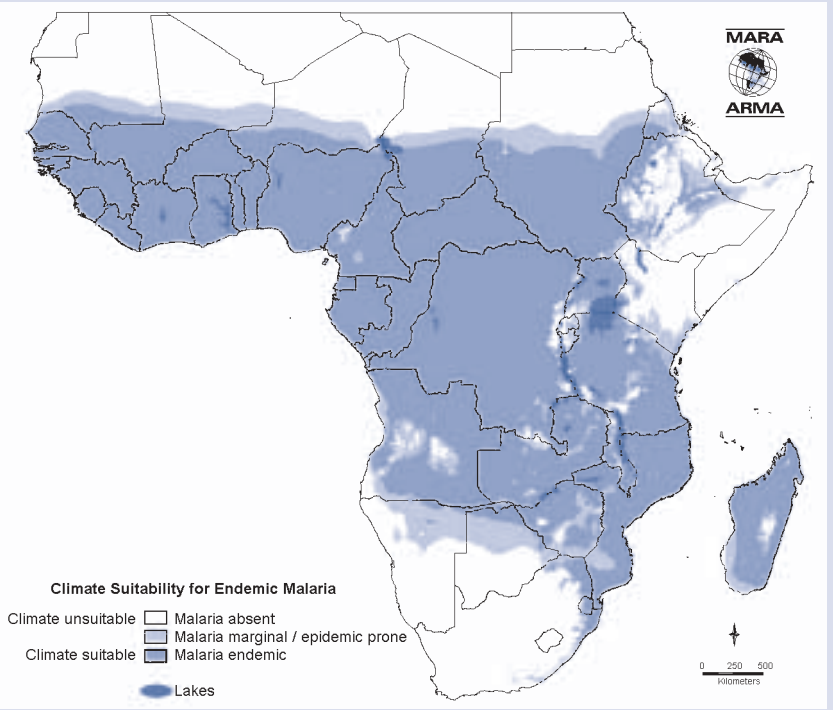
Recent work by Kitron's group shows similar results in the distribution and abundance of *Ixodes scapularis* in Wisconsin, northern Illinois, and portions of the upper peninsula of Michigan. Tick presence was positively associated with sandy or loam-sand soils overlying sedimentary rock (*62*). Deciduous or dry to mesic forests also were positive predictors. Absence was correlated with grasslands; conifer forests; wet to wet/mesic forests; acidic soils of low fertility and a clay soil texture; and Pre-Cambrian bedrock.

BOX 6.1 The Highland Malaria Project

WHO estimates that approximately 300–500 million cases of malaria occur worldwide each year. A global increase in malaria may be associated with deforestation, water development projects, and agricultural practices in poor countries. High altitude regions have been protected from malaria endemicity because parasite sporogony and vector development are inefficient in low temperatures. However, there appears to be an emergence of malaria in the African highlands. This may be attributable to a true change in disease pattern caused by increasing temperatures associated with climate change. As global temperatures continue to rise, it is important to have a system that allows public health practitioners to forecast where and when malaria epidemics may occur.

The Highland Malaria Project (HIMAL) is part of the umbrella international collaboration "Mapping Malaria Risk in Africa" (MARA). The project consists of two phases. The main objective of phase one was to create a stratified model of malaria risk for several select regions in the African highlands using GIS based modelling, and to compare these special models to the known historical distribution of malaria epidemics. This phase of the project prepared for a future phase two with the goal of predicting where and when malaria epidemics may occur.

FIGURE 6.3 Fuzzy climate suitability for transmission of malaria across Africa, according to the MARA (Mapping Malaria Risk in Africa) climate suitability model. Areas of climate unsuitability include both deserts (limited by low rainfall), and highland areas (limited by cold temperatures), for example on the border between Uganda and Rwanda. *Source: Produced by Marlies Craig/MARA project (63).*



The HIMAL model used fuzzy suitability fractions to predict the likelihood of conditions suitable for malaria transmission for any given location. Suitability fractions between zero and one were calculated for each location by overlaying the average monthly temperature by the mean rainfall over several years(*64*). More conceptual definitions of the regions defined by the suitability scale include:

Continued

- perennial: conditions always suitable for transmission;
- seasonal: conditions suitable for short season every year;
- epidemic: long-term variations in climate render conditions suitable for transmission on irregular basis;
- malaria free: conditions always unsuitable for transmission.

The strength of this project was the technique used to validate the model using data from several East African countries, including Kenya, Uganda, Rwanda/Burundi, and the United Republic of Tanzania. The purpose of the validation was to compare the model estimates to real historical malaria transmission intensity data. This data came from a variety of sources including surveys, seasonal data, published and unpublished studies, and site visits. Information on climate, as well as parasite rates, spleen rates (enlarged spleen) and epidemic locations were obtained for a total of 1713 sample points.

One important consideration is that the parameters used to create the climate suitability scale (average continental monthly temperature and mean rainfall over several years) were static and gave an average expected risk. Temporal variation in transmission and annual fluctuation or long-term systematic changes in climate therefore may have been masked.

In the validation study the model predictions based on fuzzy climatic estimates closely approximated the known distribution of malaria, based on case data and historical maps across most of the continent (including the highlands). However, discrepancies along some large river valleys and other locations may be attributed to several possible limitations of the model.

One possible limitation was the use of rainfall estimates to predict vector habitats. Rainfall alone may not account for vector breeding grounds along lakes, riverbanks and flood plains. Lake Bunyonyi in Uganda provides a suitable breeding site for vectors, and may act as a spawning point for malaria epidemics in the surrounding areas. In addition, the model was unable to account for other possible confounders such as health services, malaria control programmes and drug resistance.

Using the historical malaria data this project was able to make several important observations. Highland epidemics generally tend to occur within defined altitudinal ranges and these epidemic areas generally are limited to small, discrete areas. Also the historical evidence showed that the most significant widespread epidemics occurred during or after abnormal weather events. Incorporating additional local factors into geographical models will enhance predictability of future malaria epidemics.

ENSO and predictive models for early warning systems

New insights gained from observations of extreme climate variability accompanying the El Niño phenomenon can be employed for ENSO-based disease predictions. Early warning systems (EWS) are feasible given that ENSO events can be anticipated months in advance. Several examples of these ENSO-based climate studies are presented in the previous chapter. The examples below describe studies that found strong ENSO/disease associations and either are already used for early warning (e.g. Glass et al) or have good potential for a weather-based disease early warning system.

By analysing hantavirus pulmonary syndrome (HPS) in the American southwest, Glass et al. (*65*) found human cases of disease to be preceded by ENSO-related heavy rainfall, with a subsequent increase in the rodent population. Landsat Thematic Mapper satellite imagery collected the year before the outbreak was used to estimate HPS risk by logistic regression analysis. Satellite and elevation data showed a strong association between environmental conditions and HPS risk the following year. Repeated analysis using satellite imagery from a non-ENSO year (1995) showed substantial decrease in medium to high-risk areas.

The United States' Indian Health Service uses this ENSO-based predictive model in a regional hantavirus early warning system.

Linthicum et al. (*66*) found a strong relationship between Rift Valley fever and ENSO-driven rainfall in East Africa. Rift Valley fever virus outbreaks in East Africa from 1950 to May 1998 followed periods of unusually high rainfall. By using Pacific and Indian Ocean sea surface temperature anomalies, coupled with satellite normalized difference vegetation index (NDVI) data, it was demonstrated that Rift Valley fever outbreaks could be predicted up to five months in advance of outbreaks in East Africa. Near-real-time monitoring with satellite images could pinpoint actual affected areas, with good prospects of becoming a useful disease EWS for targeting livestock vaccination to protect both animals and humans.

The World Health Organization regional office for south-east Asia has voiced a need for an operational early warning system that would provide sufficient lead time (one to three months) to permit mobilization of control operations. Focks and colleagues (unpublished data) have developed a prototype dengue EWS. Predictive variables include: sea surface temperature anomalies (five month running mean of spatially averaged SST anomalies over the tropical Pacific: 4 °S–4 °N, 150 °W–90 °W as measured by the Japanese Meteorological Association) and past monthly cases of dengue in several cities. With these variables, the probability of an epidemic year can be forecasted one to two months before peak transmission season. The two and one month forecasts had respective error rates of three and two per thirty-five years. This EWS is sufficiently accurate and will be put into use in Yogyakarta, Indonesia in 2002.

Pascual and colleagues (*37*, *67*) conducted analysis of ENSO-cholera relationships in Bangladesh. Results from non-linear time series analysis support ENSO's important role in predicting disease epidemics. Considering a possible threshold effect (*37*), it may be feasible to develop a cholera EWS for the region.

Modifying influences

Climate is one of several factors that can influence the spread of infectious disease. Human activities and behaviours also are critical determinants of disease transmission. Sociodemographic factors include (but are not limited to): increasing trends in travel, trade, and migration; erratic disease control efforts; emerging drug or pesticide resistance; and inadequate nutrition. Environmental influences include: changes in land-use, such as the clearing of forested land, agricultural development and water projects, urban sprawl; as well as ecological influences. These sociodemographic and environmental influences may act in synergy or antagonistically with climatic factors, exacerbating or lessening the impact on infectious disease transmission of either factor acting independently.

Sociodemographic influences

Human travel trade and migration

Dramatic improvements in human ability and efficiency to travel have affected infectious disease transmission. Within the incubation time for diseases such as malaria, dengue and West Nile virus, an infected person can travel the distance from a rain forest in Africa to a United States suburb (*68*). The movement of food across borders also can result in the importation of infectious agents, as in the case of cyclospora transported into the United States on berries from South America (*69*). Humans who migrate from disease free areas to endemic regions

typically lack immunity, making them susceptible to infection and transmission of the disease. This is of relevance for new settlers living at the forest's edge on cleared farmland who are particularly susceptible to zoonotic parasites. In addition, migrants may act as reservoirs: carrying pathogens home to their native regions.

Disease control efforts

While biological and technical knowledge are needed to control the spread of infectious diseases, additional requirements include political will, financial resources and national stability. Successful moves towards eradication and control of communicable diseases, such as smallpox (eradication) and polio (control), largely are attributable to unwavering global commitment. In other scenarios, erratic disease control efforts have had detrimental consequences for human infection. In 1947 the Pan-American Health Organization (PAHO) initiated a programme to eradicate *Aedes aegypti*, the mosquito vector for both dengue and yellow fever. By 1972 this mosquito had been eradicated from 73% of the area originally infected: 19 countries of the Americas. However, nearly one decade later, lack of continuing public support and withdrawal of funding resulted in re-establishment of the mosquito in nearly the entire original habitat. Subsequently, major epidemics of dengue have erupted in several South and Central American countries as well as parts of Africa and Asia (*70*).

Drug resistance

Drug resistance results from an infectious agent genetically mutating to avoid harm from drugs. Resistance to important anti-malarial drugs has been rising in many parts of the world since the 1970s. Chloroquine's use as a treatment for malaria infections has led to the broad geographical spread of resistant *P. falciparum* in Africa (*71*). Similarly, the large scale use of antimicrobials in livestock and humans has lead to resistance among bacterial enteropathogens, an important problem in developing countries that lack medical supervision to dispense appropriate medication (*72*).

Nutrition

Malnutrition is an important determinant of infectious disease morbidity and mortality. Micronutrients play an important role in the ability to mount an effective immune response against infection. Malnutrition is a particularly important risk factor for diarrhoeal diseases in children in developing countries (*73*).

Environmental influences

Land-use influences

Land-use changes typically are undertaken with the intention to improve livelihoods, economic well-being and quality of life. This is achieved in many cases. However, as well as adverse environmental effects, adverse human health effects may be an unintended outcome (*74*, *75*, *76*). With increased land-use changes such as deforestation and increased agriculture and crop irrigation, climate variability's adverse effect on infectious diseases may be heightened. Several of these environmental factors are given in Table 6.3, a few are described in detail below.

Deforestation: The status of the world's forests is threatened by: conversion for crop production or pastures; road or dam building; timber extraction; and the

TABLE 6.3 Examples of environmental changes and possible effects on infectious diseases.

Environmental changes	Example diseases	Pathway of effect
Dams, canals, irrigation	Schistosomiasis	↑ Snail host habitat, human contact
	Malaria	↑ Breeding sites for mosquitoes
	Helminthiasies	↑ Larval contact due to moist soil
	River blindness	↓ Blackfly breeding, ↓ disease
Agricultural intensification	Malaria	Crop insecticides and ↑ vector resistance
	Venezuelan haemorraghic fever	↑ rodent abundance, contact
Urbanization, urban crowding	Cholera	↓ sanitation, hygiene; ↑ water contamination
	Dengue	Water-collecting trash, ↑ *Aedes aegypti* mosquito breeding sites
	Cutaneous leishmaniasis	↑ proximity, sandfly vectors
Deforestation and new habitation	Malaria	↑ Breeding sites and vectors, immigration of susceptible people
	Oropouche	↑ contact, breeding of vectors
	Visceral leishmaniasis	↑ contact with sandfly vectors
Reforestation	Lyme disease	↑ tick hosts, outdoor exposure
Ocean warming	Red tide	↑ Toxic algal blooms
Elevated precipitation	Rift valley fever	↑ Pools for mosquito breeding
	Hantavirus pulmonary syndrome	↑ Rodent food, habitat, abundance

Source: reproduced from reference 3.

encroachment of urban areas. Historically these activities have been associated with changes in infectious diseases in the local population. The diseases most frequently affected are those that exist naturally in wild ecosystems and circulate among animals, especially those with vertebrate reservoirs and invertebrate vectors. In general such changes result from factors affecting the populations of animal reservoirs, vectors, and pathogens, or from factors associated with human exposure. Deforestation and forest fragmentation in Latin America has resulted in an increase in the incidence of visceral leishmaniasis associated with an increase in the number of fox reservoirs and sandfly vectors that have adapted to the peri-domestic environment (*77*). Finally, removal of vegetation (and thereby transpiration of plants) can alter local weather patterns significantly.

Agricultural development and other water projects: Agricultural development can lead to an increase in diarrhoeal disease. In intensely stocked farmland, heavy rains can cause contamination of water resources by *Cryptosporidium parvum* oocysts. Infiltration of high quality water treatment and supply systems can occur: a 1993 occurrence in Milwaukee, USA, resulted in 400 000 cases of cryptosporidiosis (*78*). Intense cattle farming and livestock operations in combination with factors related to watershed management have been implicated in such outbreaks (*79*). A similar mechanism is involved in giardiasis where a variety of animals may serve as reservoirs of Giardia lamblia and contaminate surface water with their excreta. Predicted flooding accompanying climate change could increase the water contamination trends associated with agricultural development.

Agricultural development in many parts of the world has resulted in an increased requirement for crop irrigation, reducing water availability for other uses and increasing breeding sites of disease vectors. An increase in soil moisture associated with irrigation development in the Southern Nile Delta following the construction of the Aswan High Dam has caused a rapid rise in the mosquito *Culex pipiens* and consequential increase in the mosquito-borne disease,

Bancroftian filariasis (*80*, *81*). Onchocerciasis and trypanosomiasis are further examples of vector-borne parasitic diseases that are triggered by changing land-use and water management patterns. Projected droughts will necessitate expanded irrigation to counter water stress, which could create more breeding sites for vector-borne diseases.

Urbanization: Urbanization is associated with a range of health problems, including vector-borne diseases such as dengue and malaria (*82*), diarrhoeal (*83*) and respiratory diseases (*84*). Overcrowding and pollution resulting from inadequate infrastructure can trigger these conditions. At present, there are an estimated four billion cases of diarrhoeal disease each year, causing over two million deaths. Studies have shown that water sanitation and hygiene interventions can greatly reduce water-related diseases (*85*, *86*).

Ecological influences

In addition to land-use changes, there is a host of indirect links between infectious disease and environmental conditions that are mediated through changes in ecosystems resulting from human activities (*40*). Zoonoses and vector-transmitted anthroponoses, dependent on the ecology of non-human animals, will be especially sensitive to the effects of these ecological changes. An estimated 75% of emerging infectious diseases of humans have evolved from exposure to zoonotic pathogens (*87*), therefore any changes in the ecological conditions influencing wildlife diseases have the potential to impact directly on human health (*3*, *88*). Lyme disease in the north-east United States is an example of this (Box 2).

Climate change will likely modify the relationships between pathogens and hosts directly by: altering the timing of pathogen development and life histories; changing seasonal patterns of pathogen survival; changing hosts' susceptibility to pathogens (*12*, *93*). However, ecosystem processes can influence human infectious diseases indirectly (*3*, *40*, *94*).

Forecasts of infectious diseases' responses to climate change are complicated by the difficulties associated with predicting how ecosystems will respond to changes in climate (*40*, *94*). Geographical distributions and abundances of species that compose ecological communities depend, in part, on patterns of temperature and precipitation (*36*). The link between metabolic rates and temperature means that average temperatures also will have an influence on the growth rates and generation times of many organisms (*36*, *95*, *96*). Patterns of precipitation also will influence species abundance and distribution by determining plant/habitat range and/or vector breeding sites (*97*). Any changes in the aquatic community will affect organisms involved in human infectious disease: mosquitoes that transmit diseases such as malaria and dengue fever develop in aquatic habitats. Changes in precipitation amounts in turn will alter the availability of suitable habitats for larval mosquitoes.

One of ecology's current challenges is to predict how species will respond. An initial approach has been to couple data on climate tolerances for species and their current geographical distributions with projections from climate models in an attempt to determine where suitable conditions for the species might develop. In one study of 80 tree species, species varied in how closely their current distributions correlated with climate. There were also strong differences between species in the predicted impact of future climate change (*98*). Analogous patterns appear when examining expected changes in animal communities (*99*).

This variability in climate sensitivity is only one aspect of the expected differences in how species will respond to climate change. Species also will vary in

BOX 6.2 Ecological influences and Lyme disease

Variability in the prevalence of Lyme disease in the north-east United States provides an informative example of how changes in ecological conditions can produce changes in an infectious disease of humans.

As land-use patterns have shifted away from agriculture and second-growth forests have become more prevalent, the populations of ticks have changed (*36*). Human infection rates have risen over time with the increase in contact between humans and ticks (*89*). Spatial variation in risk to humans is influenced by the ecology of the mammalian hosts of the tick. White-tailed deer are the primary host for adult ticks and their population size is an important determinant of tick abundance in a particular region (*90*, *91*). However, while population size is an important factor determining the probability of a human being bitten, not all ticks will be infected with the Lyme disease bacterium. The proportion of infected ticks in an area appears to be linked to the relative abundance of highly competent small mammal reservoirs for the *B. burgdorferi* bacteria, specifically white-footed mice (*89*, *91*).

The probability of a human contracting Lyme disease in a given area is a function of the density of infected ticks, which in turn depends on the population size of deer and mice. Additional ecological relationships will influence the abundance of these mammalian hosts. A good example is the key role played by oak trees (*92*). The links between these trees and human disease start with the periodic production of acorns by masting oak trees. Acorns are a high quality food for wildlife, and deer tend to concentrate in their vicinity during the fall and winter. These concentrations of deer result in larger numbers of larval ticks. At the same time, white-footed mice also increase in abundance in areas with masting oaks. The interplay between these species dramatically increases both the concentration of ticks and the proportion of ticks infected with Lyme-causing spirochaetes (*89*, *91*).

Recent modelling studies suggest that complete understanding of the ecology of Lyme disease will need to include other ecological influences (*91*). Results suggest the probability of a tick becoming infected depends not simply on the density of white-footed mice, but on the density of mice relative to other hosts in the community. Under this scenario, the density effect of white-footed mice (efficient reservoirs for Lyme disease) can be diluted by increasing density of alternative hosts that are less efficient at transmitting the disease. These results lead to the conclusion that increasing host diversity (species richness) may decrease the risk of disease through a dilution-effect (*91*).

Habitat fragmentation (e.g. due to urban sprawl and road building) may exacerbate the loss of species biodiversity, thereby increasing the risk of Lyme disease. Wildlife biodiversity decreases when human development fractures forests into smaller and smaller pieces. Deforestation also can lead to closer contact between wildlife and humans and their domestic animals. Each of these ecosystem changes has implications for the distribution of micro-organisms and the health of human, domestic animal and wildlife populations.

their abilities to disperse to new geographical areas and compete with the species already in place. Some species have limited ability to disperse, others will be able to shift ranges rapidly (*100*). Once in a new area, species vary greatly in their ability to become established and increase in population size (*101*).

There is conflicting evidence about the speed at which species might evolve in response to climate change. The necessary genetic variability exists in many species but the pace of environmental change may outstrip their ability to evolve

(*102*). Given evolutionary change's importance in the emergence of new and newly virulent diseases, better understanding of its role in infectious disease ecology is a critical area of research concern (*102*).

While significant uncertainties exist about the exact nature of the ecological changes expected as climate changes, there is little doubt that ecosystems will change. Indeed, widespread changes are already seen in both the geographical range of species and the timing of annual events (phenology). Analyses of ecological data from recent decades have revealed widespread shifts in species' range, abundance and phenology, associated with the comparatively moderate climatic changes of the past century (*103*). It also appears that some species have undergone adaptive evolution in response to recent climate change (*104*): the pitcher-plant mosquito for example. Changes in ecological relationships will become more obvious as expected changes in climate continue over coming decades (*36*).

There is ample evidence that species will differ in their sensitivity to climate and respond to climate change at different rates (*36*, *103*). It is highly likely that this differential ability to respond will break up important ecological relationships: in western Europe there is a well studied ecological relationship between oak trees, winter moths that feed on the leaves, and insectivorous birds that feed on moth caterpillars. Analyses show that during recent warmer springs, these organisms have not responded equally to changes in climate, threatening to disrupt the ecological linkages in the community (*105*, *106*).

Severe epidemics of cholera strike regularly in many parts of the developing world (*107*, *108*). The timing of these epidemics is partly explained by environmental and ecological conditions that are influenced by climate. In particular a significant reservoir of the cholera-causing organism, *Vibrio cholerae*, appears to reside in marine ecosystems where it attaches to zooplankton (*5*, *107*). Populations of these small crustaceans in turn depend on the abundance of their food supply (phytoplankton). Phytoplankton populations tend to increase (bloom) when ocean temperatures are warm. The result is that cholera outbreaks are associated with warmer ocean surface temperature via a series of ecological relationships: phytoplankton blooms lead to higher numbers of zooplankton and their associated *Vibrio cholerae*, which in turn are more likely to infect exposed humans (*5*, *107*, *108*).

Climate also will impact on the diseases of plants and non-human animals. This impact provides a pathway for complex interactions where ecosystems change in response to climate and alter the conditions for infectious disease organisms and vectors. Resulting changes in the patterns of infectious disease may in turn lead to further ecological disruption through the changing distributions and populations of target plants and animals of those infectious agents (*93*). With growing awareness of the importance of disease in ecosystems and the link to human health, it may be possible to detect such complex pathways in current systems. For example, the interactions between emerging wildlife diseases such as mycoplasmal conjunctivitis in wild house finches in the eastern United States and the spread of West Nile virus in the same geographical area (*109*, *110*).

Conclusions and recommended future steps

The purpose of this chapter is to highlight the evidence linking climatic factors such as temperature, precipitation, and sea level rise, to the lifecycles of infectious diseases, including both direct and indirect associations via ecological

processes. Many studies demonstrate seasonal fluctuations in infectious diseases but few have documented long-term trends in climate-disease associations. A variety of models has been developed to simulate the climatic changes and predict future disease outbreaks although few have controlled successfully for important sociodemographic and environmental influences. Gaps in knowledge indicate that future initiatives are required in the following areas:

Increase in active global disease surveillance. The lack of precise knowledge of current disease incidence rates makes it difficult to comment about whether incidence is changing as a result of climatic conditions. Incidence data are needed to provide a baseline for epidemiological studies. These data also will be useful for validating predictive models. As these data are difficult to gather, particularly in remote regions, a centralized computer database should be created to facilitate sharing of these data among researchers (*40*).

Continuation of epidemiological research into associations between climatic factors and infectious diseases. In order to draw a causal relationship between climate change and patterns of infectious disease, research needs to prove consistent trends across diverse populations and geographical regions. This will best be accomplished by implementing rigorous study designs that adequately control for social and environmental confounders (*40*). International collaboration between researchers is important (*36*) as well as interdisciplinary collaboration between specialists such as epidemiologists, climatologists and ecologists, in order to expand the breadth of information. A comprehensive study of mosquito-borne diseases, for example, requires a combination of entomologists, epidemiologists and climatologists to work together to examine the associations of changing vector habitats, disease patterns and climatic factors. Epidemiological data can be shared with policy-makers to make preventive policies (*36*).

Further development of comprehensive models. Models can be useful in forecasting likely health outcomes in relation to projected climatic conditions. Integrating the effects of social and environmental influences is difficult but necessary (*40*).

Improvements in public health infrastructure. These include public health training, emergency response, and prevention and control programmes. Improved understanding is needed of the adaptive capacity of individuals affected by health outcomes of climate change, as well as the capacity for populations to prepare a response to projected health outcomes of climate change (*36*).

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