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The impact of climate on the disease dynamics of cholera

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Abstract

The size of infectious disease outbreaks frequently depends on climate influences as well as on the level of immunity in the host population. This is particularly the case with vectorborne and waterborne diseases, for which pathogen transmissibility critically depends on ecological conditions. Here, a mathematical model that was applied to the bacterium *Vibrio cholerae* to understand its disease dynamics in Bangladesh is reviewed. When interfaced with empirical case data on cholera, the model shows that climate plays a pivotal role in modulating the size of outbreaks, with local, regional, and global indices of climate variability showing a link with pathogen transmissibility. Furthermore, the incidence of cholera may occasionally be surprisingly low at times when climate seems to favour cholera transmission.

Keywords: Bangladesh, cholera, climate, immunity, infectious disease
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Many infectious diseases are characterized by epidemic outbreaks that vary in size, both seasonally and interannually. For example, malaria incidence in the highlands of East Africa is known to peak every summer, with larger outbreaks occurring every 3 years [1]. Similarly, dengue outbreaks in Thailand occur annually between June and October [2], with larger outbreaks occurring every 2–4 years [1,3]. As with malaria and dengue, cholera dynamics in Bangladesh also show evidence of seasonal and interannual variability: more individuals become infected with the bacterium during the spring and during the autumn than during the summer monsoon season or the dry winter [4], and outbreaks are much larger in some years than in others [5](Fig. 1).

To ultimately predict when and where outbreaks of these infectious diseases will occur, it is necessary to understand the factors contributing to these seasonal and interannual patterns in disease incidence. In the case of vector-borne and waterborne diseases, one critical factor affecting the patterns in disease incidence is climate variability. For vector-borne diseases, temperature and rainfall levels are known to affect mosquito development times and viral amplification rates [6]. These rates in turn affect the transmission rate of vector-borne pathogens, such as those causing malaria and dengue. In the case of waterborne diseases, climate can affect standing water levels, as well as standing water properties, including salinity, temperature, ionic content, and resident biota. These factors can affect pathogen survival rates in their aquatic reservoir [7], and thereby also affect the pathogen's transmission rate.

Although it is clear that climate variability can affect disease dynamics, which climate variables are most relevant to the dynamics, and at which scales these climate variables act, are difficult to ascertain. This is primarily because we do not have information on how pathogen transmission rates vary in time. Instead, in the best case scenarios, we know only the magnitude of case outbreaks over time. These temporal fluctuations depend only partially on the transmission rate of the pathogen; they also depend on the non-linear interaction between infected individuals and the susceptible host population. For example, a period of low disease incidence may be a result of low transmission rates, or it may be a result of a low number of susceptible individuals in the population (because of previously occurring disease outbreaks). Owing to this confounding factor of immunity in the population, the role of climate cannot be easily isolated by correlations with disease incidence [8].

Instead of attempting to identify the role of climate through simple correlation with disease incidence, we must adopt more sophisticated approaches to identifying climatic drivers. These approaches include the development of mathematical models and statistical non-linear time-series analyses. Specifically, the mathematical models must explicitly allow for temporal fluctuations in herd immunity levels and provide a mechanism for including the effects of climate variability. In this article, I discuss the formulation of a previously published compartmental mathematical model [9] and its sta-

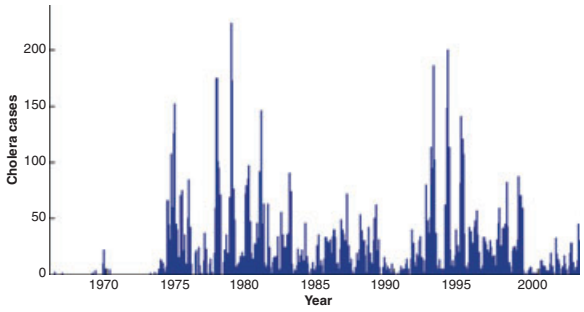

Fig. 1. Interannual variability in the size of cholera outbreaks in Matlab, Bangladesh. Only cholera cases of the El Tor strain are shown. Reproduced from [5].

tistical fit to cholera incidence data [5] (Fig. 1). The disease dynamics of cholera are modeled with a difference equation of the form:

$$I_{t+1} = \beta_t I_t \frac{S_t}{N_t},$$

where I_t is the number of infected individuals, S_t is the number of susceptible individuals, N_t is the population size, and β_t is the transmission rate of the pathogen, all at time *t*. The schematic of this mathematical model is shown in Fig. 2. According to this model, infected individuals (*I*) transmit the bacterium to susceptible individuals (*S*), at a rate β. (Division by the population size, *N*, simply rescales the transmission rate, β, and makes the model statistically more tractable.) Fluctuations in herd immunity are captured by variation in $\frac{S_t}{N_t}$ over time. The effect of climate variability on cholera dynamics is captured in fluctuations in the transmission rate, β, over time. This model is sufficiently general in form to be applied to other infectious diseases. In addition to this equation, which determines the number of infected individuals over time, the model requires another equation that tracks

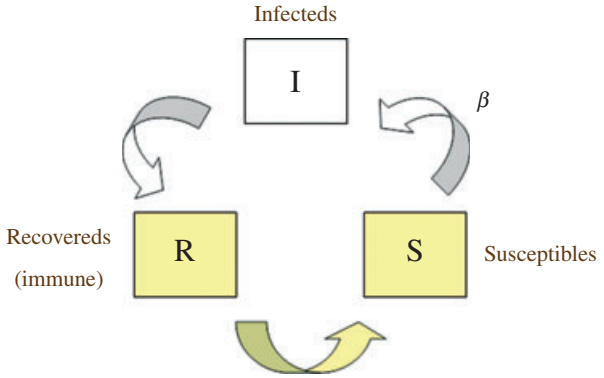

Fig. 2. A schematic of the mathematical model applied to cholera dynamics, described in detail in [9].

how the number of susceptible individuals changes over time. More specific details on the model formulation can be found in [9] and [5].

The results of fitting this model to the time series shown in Fig. 1 clearly indicate that, once fluctuations in herd immunity are taken into account, a strong signal of climate forcing is seen in the dynamics of cholera outbreaks. Our results, described in [5], show that cholera dynamics are affected by climate variability at multiple different scales (local, regional, and global). First, we found that the seasonal variation in transmission levels was clearly associated with the timing of the monsoon that hits Bangladesh locally: transmission rates of the bacterium were low during the summer rains and the dry winter, and peaked in the spring and in the autumn (Fig. 3a). Second, we found that long-term variation in transmission rates had an inverse correlation with Brahmaputra river discharge anomalies and northeast India rainfall levels (Fig. 3b). These regional climate influences therefore play a modulating role at interannual time-scales. Third, we found that the short-term unexplained variation in cholera transmission rates (assumed to be statistical noise in the model) showed a significant 8–10-month lagged correlation with the global climate index ENSO, the El Niño Southern Oscillation (Fig. 3c). ENSO has previously been shown to affect cholera dynamics through the use of statistical methods, such as scale-dependent correlation [10], which identify strong local correlations between two time series (here, climate variability and disease incidence).

In addition to finding evidence for climatic effects on cholera dynamics in Bangladesh, this research identified an important interaction between herd immunity fluctuations ($\frac{S}{N}$) and climate forcing (affecting transmission, β). During certain times of moderate or even low cholera incidence, climate indices and reconstructed transmission rates indicated strongly favourable conditions for the spread of cholera. To understand the reasons for the occurrence of this phenomenon, we looked more closely at herd immunity levels during these periods. We found that cholera outbreaks could not occur, even in the presence of favourable climate conditions, if a larger outbreak had occurred within the previous several years. This is because, following a large outbreak, levels of herd immunity remain high, such that the system would be in a 'refractory period', unable to respond to any external climate forcing, owing to the lack of susceptible hosts in the population. A clear example of a refractory period occurred in 1986–1987, following the prolonged cholera outbreaks occurring between 1977 and 1982.

In sum, to understand the factors contributing to the seasonal and interannual variation in the size of infectious disease outbreaks, it is necessary to disentangle the role of

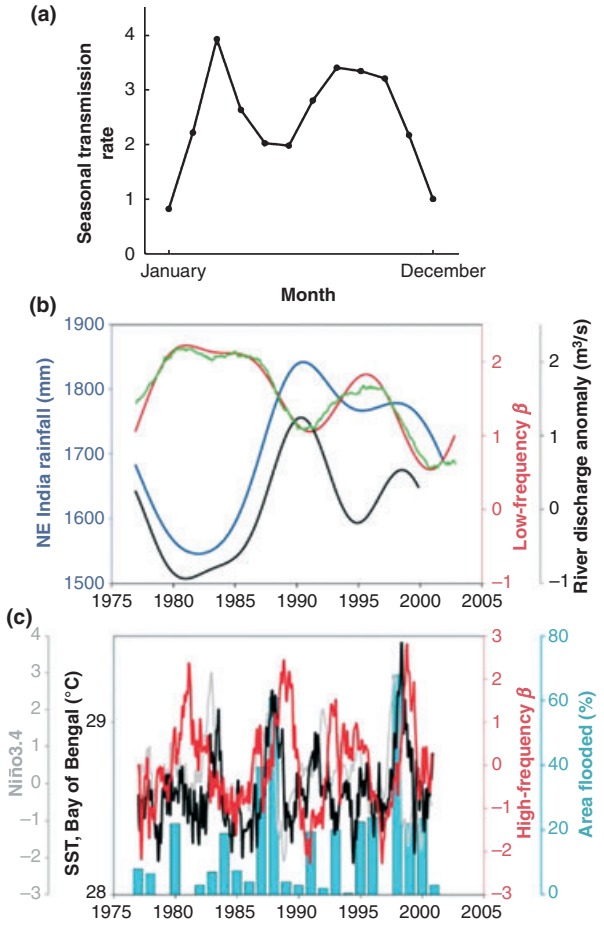

Fig. 3. The effect of climate on the transmission of cholera. (a) Statistical fit of cholera's seasonal transmission rates in Bangladesh. Peaks of transmission occur in the spring and in the autumn. Transmission troughs occur during the summer monsoon and during the dry winter. (b) Regional climate variables (northeast India rainfall (blue) and Brahmaputra river discharge levels (black)), and their inverse correlation with long-term cholera transmission rates (green and red). (c) Niño3.4 (grey), a global climate index for ENSO, and its positive lagged correlation with cholera transmission of high frequency (red). Cholera transmission lags Niño3.4 by 8–10 months. Also shown are the lagged correlation between Niño3.4 and sea surface temperature (SST) in the Bay of Bengal (black), and the percentage of Bangladesh flooded (turquoise bars). The effect of Niño3.4 on cholera dynamics may act through more local variables such as SST and flooding. Subplots a–c reproduced from [5].

climate from the role of herd immunity fluctuations. Understanding their separate effects, as well as their interaction, is critical for the development of effective early-warning systems for infectious disease outbreaks.

Transparency Declaration

The author declares no conflicts of interest.

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