The role of climatic variability on cholera spreading in Bangladesh

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Abstract

Cholera is a disease transmitted through exposure to water contaminated by the bacterium \textit{Vibrio cholerae}. The disease is clearly linked to the variability of climatic factors, as infections are enhanced by intense seasonal precipitation (e.g. monsoon season). Here we propose a spatially explicit model for cholera and apply it to Bangladesh, where the disease is endemic, integrating the role of precipitation and temperature annual cycles. River networks represent one of the major pathways of disease spreading. The data structure designed for the application of the model is thus based on the hydrological connectivity network, as well as on the spatial distribution of the population and on the connections that regulate human mobility among communities. In this region, cholera incidence exhibits two annual peaks, although the main environmental drivers peak once per year during the monsoon season (from June to September). The proposed model attempts to explain these particular dynamics taking into account the annual fluctuations of water availability and considering hydro-climatological forcings as inputs for the model. For this purpose, a compartmental SIRB (Susceptible-Infected-Recovered-Bacteria) epidemiological model is integrated with a hydrological model. Results show that the introduction of two terms of transport (hydrological transport and human mobility) allows to generate spatial patterns of cholera prevalence that reproduce the bimodal pattern typically observed in this region.

Keywords: Epidemiology; Spatially explicit models; Climatic factors; Hydro-climatological forcings.
Cholera is an acute water-borne disease caused by the bacterium *Vibrio cholerae*, which colonizes the human intestine and produces an enterotoxin responsible for a watery diarrhea. Since cholera outbreaks are generally associated with the ingestion of contaminated food or water, it represents one of the most serious public health problems especially among populations in developing countries, which lack access to safe water and appropriate sanitation. According to the World Health Organization (WHO), almost 590,000 cases were recorded worldwide in 2011 and the number of cases is increasing [22].

The Bay of Bengal, with its extensive estuary formed by the delta of the Ganges-Brahmaputra-Meghna (GBM) system, is considered the native habitat of *Vibrio cholerae* [19]. This region is characterized by seasonal outbreaks that occur throughout the year with a bimodal annual distribution [1], while single annual peaks can be seen elsewhere (e.g. parts of Africa, South-east Asia and Latin America [10]). This seasonality suggests a clear key role of climatic factors in the dynamic of the disease. The annual cycle of epidemics in this particular endemic context has been historically linked to a range of environmental and climatic variables including precipitation [10], river discharge [1], sea surface temperature [6], and El Niño-Southern Oscillation [18].

Our aim is to develop a spatially explicit model of cholera transmission that integrates the role of the precipitation and temperature annual cycles on the dynamics of the disease. The model has been applied to the case of Bangladesh and includes two terms of pathogen transport: hydrological transport and human mobility.

The territory of Bangladesh is divided into more than 800 hydrological entities (Figure 1), identified on the basis of a Digital Elevation Model (DEM). Specifically, we traced the river network combining flow directions and flow accumulations maps, results of DEM manipulation, in order to identify the watersheds.
Fig. 1: Subdivision of Bangladesh in hydrological entities: the territory is divided into 880 watersheds, that are defined through elaboration of the DEM of the area.

The dispersion of bacteria depends on a complex set of processes. The network used to implement these mechanisms is described by a series of nodes, representing hydrological entities (where human communities live), and edges, representing pathways for the spread of the disease. We placed nodes at the centroid of each hydrological entity weighed on population and we considered two terms of transport that identify different edges:

- a first mechanism of propagation related to the dispersion through the river network;
- a second mechanism of propagation related to human mobility, described by fluxes of individuals on a completely connected graph.

For each node we model the dynamics of the number of susceptibles to the disease (initially coinciding with the total population), infected individuals, recovered and immune individuals, \textit{V. cholerae} abundance in the aquatic environment, and water availability.

Epidemiological dynamics and pathogen transport in a generic node \( i \) of the network are therefore described via a compartmental SIRB-like model similar to [5] represented by the following system of nonlinear differential equations:
\[
\frac{dS_i}{dt} = \mu(H_i - S_i) - \beta_i(J)(1-m)\frac{B_i}{K+B_i} S_i - m\left(\sum_{j=1}^{n} Q_{ij} \beta_j(J) \frac{B_j}{K+B_j}\right)S_i + \rho R_i
\]

\[
\frac{dI_i}{dt} = \beta_i(J)(1-m)\frac{B_i}{K+B_i} S_i + m\left(\sum_{j=1}^{n} Q_{ij} \beta_j(J) \frac{B_j}{K+B_j}\right)S_i - (\gamma + \alpha + \mu) I_i
\]

\[
\frac{dR_i}{dt} = \alpha_i - (\rho + \mu) R_i
\]

\[
\frac{dB_i}{dt} = -\mu_b(T)B_i + (1-m)p_i(J)I_i + mp_i(J)\sum_{j=1}^{n} Q_{ij} I_j - \lambda f_i B_i + \lambda \sum_{j=1}^{m} p_j \frac{W_j}{W_i} B_j
\]

\[
\frac{dW_i}{dt} = J_i(t)A_i - ET_i(t)A_i - \lambda W_i + \lambda \sum_{j=1}^{m} W_j
\]

where \(S_n\), \(I_n\), \(R_n\), \(B_i\), and \(W_i\) are respectively susceptibles, infected, and recovered individuals, pathogen concentration and water availability in each node of the spatial network at time \(t\). Figure 2 shows a schematic diagram of the model.

Fig. 2: Schematic diagram of the model: red blocks represent the state variables of the epidemiological model, the blue block represents the state variable of the hydrological model, the arrows describe the fluxes. The dashed arrow that starts from the bacteria in the local water reservoir indicates that their abundance indirectly acts on the fluxes of individuals from susceptible to infected compartment.
The dynamics of the susceptible compartment is described by the balance among population demography, infections due to contact with \textit{V. cholerae} and immunity loss. The host population is assumed to be at a demographic equilibrium, where $\mu$ is the human mortality rate and $H_i$ is the size of the local community. The fraction $B_i/(K+B_i)$ is the logistic dose-response curve [8] representing the probability of becoming infected due to the exposure to a concentration $B_i$ of vibrios, $K$ being the half-saturation constant. The parameter $\beta_i(J)$ represents the rate of exposure to contaminated water, depending on precipitation $J$. Individuals can get infected in their original node $i$ or during a daily trip in a different node $j$, with $m$ and $Q_{ij}$ being the fraction of moving people and the probability of moving between any two nodes $i$ and $j$, respectively.

Infected individuals recover at a rate $\gamma$, or die for natural or cholera-induced mortality at a rate $\mu$ or $\alpha$, respectively. Recovered from the disease lose their immunity and become susceptibles again at a rate $\rho$.

To simulate the spread of the disease, we describe the propagation due to hydrological transport as a random walk process on an oriented graph [2], where edges are represented by segments of the river network in each hydrological entity. We assume that vibrios move between any two nodes of the network with a probability given by:

\[
P_{ij} = \begin{cases} 
\frac{P_{out}}{d_{out}(i)P_{out} + d_{in}(i)P_{in}} & \text{if } i \to j \\
\frac{P_{in}}{d_{out}(i)P_{out} + d_{in}(i)P_{in}} & \text{if } i \leftarrow j \\
0 & \text{elsewhere}
\end{cases}
\]

where $P_{out}$ and $P_{in}$ are the probabilities of moving along an outward or inward edge respectively, and $d_{out}$ and $d_{in}$ are the out-degree or in-degree of each node, defined through the elaboration of the DEM.
Bangladesh extends over most of the delta of the GBM basin, which covers a total area of over one million square kilometers. For a more realistic analysis, we also consider the volume of water that enters the system through the river flow from portions of the GBM network located outside the administrative boundaries of Bangladesh. The water volume is proportional to drainage area [14] and it has been estimated for the three nodes shown in the left panel of Figure 3.

Cholera spread is affected also by human mobility. Fluxes of individuals that move among the nodes of the river network are described as a function of local population size and distance between any two nodes, with a gravitational model:

$$Q_{ij} = \frac{H_i e^{-d_{ij}/D}}{\sum_{k=1}^{n} H_k e^{-d_{ij}/D}}$$

where $H_i$ is the population living in node $i$, $d_{ij}$ is the distance between two nodes $i$ and $j$, $D$ is the mean dispersal distance characterizing human movement and $n$ is the total number of nodes in the network.

The right panel of Figure 3 shows the most important connections in a small portion of the territory. For each node the three connections with the highest values of mobility fluxes are shown.

![Network connectivity](image)

**Fig. 3:** Network connectivity. (a) River network and basins of the Ganges, Brahmaputra and Meghna in the territory of Bangladesh. Red circles represent the points where the three rivers cross the administrative boundaries of Bangladesh. (b) Most important connections of the mobility graph for a small part of the territory.
In order to study the role of hydro-climatological forcings on cholera dynamics, we calculated for each node of the network the annual pattern of precipitation and temperature, as moving averages of the available time series [11, 12] (Figure 4). Both environmental variables are used as direct inputs in the model, forcing specific processes as detailed below.

Fig. 4: Average annual pattern of precipitation and temperature in the node representing Dhaka, the capital of Bangladesh. (a) Annual pattern elaborated from 13 years of daily data of precipitation. (b) Annual pattern elaborated from 64 years of monthly data of temperature.

We consider that during and after the monsoon season, when rainfall is more abundant, a large part of the region is flooded and people crowd not affected areas; this is typically accompanied by a deterioration of sanitation systems, which results in an increase of environmental contamination and in a reduced access to treated water [5]. From a modeling point of view, this is reflected in the following formulation for the exposure and contamination rates $\beta(t,J)$ and $p(t,J)$:

$$\beta_J(t) = \beta_0(1 + \phi J(t))$$

$$p_J(t) = p_0(1 + \phi J(t))$$

where $\beta_0$ and $p_0$ are the baseline values for the exposure and contamination rates, and $\phi$ quantifies the effect of precipitation $J$ on these parameters at each time $t$. 
We also include the effect of temperature on the ability of cholera bacteria to survive and multiply in the environment. Since warmer temperatures are known to favor the growth of *V. cholerae* in the surface water [5], we assume that mortality of the bacteria depends on temperature as follows:

\[
\mu_B(T) = \bar{\mu}_B \left(1 - \varepsilon \frac{T - \bar{T}}{T_{\text{max}} - \bar{T}}\right)
\]

where \(\bar{\mu}_B\) is the average vibrio mortality, \(T_{\text{max}}\) and \(\bar{T}\) are the maximum and the mean temperature during the year, and \(\varepsilon\) quantifies the effect of temperature on *V. cholerae* mortality. Temperature also influences evapotranspiration as detailed above.

We are interested in the long-term behavior of the system, thus we simulate the process for 10 years (each year with the same hydro-climatological pattern) and we analyze the patterns of cholera prevalence in the final year of the simulation. Epidemiological parameters used to run the model can be found in the literature (Table 1), while the parameters related to pathogen transport have been set as follows:

- for hydrological transport, we assume that the probability of moving along an outward edge is \(P_{\text{out}} = 0.5\) and that the dispersal rate through the river network is \(\lambda = 0.01 \text{ d}^{-1}\); we consider the sea as a bacterial reservoir, so that \(f_i = 0.25\) in the outlet nodes, 1 elsewhere;
- for human mobility, we assume a mean dispersal distance \(D = 10 \text{ km}\) for daily trips and a value for the fraction \(m\) of moving population of 0.2.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Units</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>(\mu)</td>
<td>(1/(70.6 \cdot 365))</td>
<td>(\text{d}^{-1})</td>
<td>[7]</td>
</tr>
<tr>
<td>(\beta_0)</td>
<td>1</td>
<td>(\text{d}^{-1})</td>
<td>[3, 8, 15, 20]</td>
</tr>
<tr>
<td>(\rho)</td>
<td>(1/(3 \cdot 365))</td>
<td>(\text{d}^{-1})</td>
<td>[13]</td>
</tr>
<tr>
<td>(\gamma)</td>
<td>0.2</td>
<td>(\text{d}^{-1})</td>
<td>[3, 4, 8, 15]</td>
</tr>
<tr>
<td>(\alpha)</td>
<td>0</td>
<td>(\text{d}^{-1})</td>
<td>[20]</td>
</tr>
<tr>
<td>(\bar{\mu}_B)</td>
<td>0.2</td>
<td>(\text{d}^{-1})</td>
<td>[3, 4, 8, 15, 16, 20]</td>
</tr>
<tr>
<td>(\rho_0/K)</td>
<td>(10^6)</td>
<td>individual(^4) (\text{d}^{-1} \text{ m}^{-3})</td>
<td>[9, 21]</td>
</tr>
</tbody>
</table>

Tab. 1: Epidemiological parameter values used for simulation, with units and references.
Figure 5 shows two temporal patterns of global prevalence generated by our model. The annual prevalence is characterized by one or two peaks per year, depending on whether we want to consider the effect of precipitation or not.

Fig. 5: Global prevalence simulated with our model. (a) Global prevalence in absence of rainfall dependence ($\phi = 0$): the pattern exhibits a single peak in spring, due to low bacterial dilution. (b) Global prevalence considering the effect of precipitation on cholera spreading ($\phi = 0.8$): the pattern exhibits also a second outbreak in autumn, caused by increase in the rates of exposure and contamination.

The global patterns generated by the model suggest some considerations:

- low dilution of cholera bacteria in water is responsible for the spring peak;
- the effect of intense precipitation characterizing the monsoon season determines the increase in the rates of exposure and contamination, so that the fall peak occurs only including in the model the dependence on rainfall. However, the summer flood washes out the system and thus the second peak is less important than the first one.

At a local level, it can be noticed that prevalence patterns are qualitatively different according to the position of the nodes in the network (Figure 6). The spring outbreak occurs earlier in the communities near the coast, but its intensity is greater in upstream nodes. During the spring peak, people can get infected earlier in the coastal areas because of bacteria that colonize permanently the coastal region (i.e. the outlet nodes). Then, bacteria reach inland areas through the river network and movement of infected individuals. Prevalence is higher where bacterial concentration is higher (i.e. water volume is
lower), so that the most intense peaks occur far from the coast, in the upstream nodes of the river network. Coastal communities do not exhibit the fall outbreak because of bacterial dilution in the downstream nodes, where water volume is higher.

Fig. 6: Annual prevalence in different communities. The disease starts spreading near the coast and then reaches the inland areas, where there is also a second outbreak in autumn.

Overall the results presented in this work support the crucial role of hydro-climatological factors in controlling the spatiotemporal progression of the disease in Bangladesh, identifying both seasonal and spatial dynamics (from spring to fall and from coast to inland). The importance of climatic variability suggests the need of a more detailed study of the environmental forcings. Predictive models for the relevant hydro-climatological variables, coupled with spatially explicit eco-epidemiological models, will be key tools to better understand, forecast and possibly control cholera dynamics.

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