# Prediction of the spatial evolution and effects of control measures for the unfolding Haiti cholera outbreak

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[1] Here we propose spatially explicit predictions of the residual progression of the current Haiti cholera outbreak accounting for the dynamics of susceptible and infected individuals within different local human communities, and for the redistribution among them of *Vibrio cholerae*, the causative agent of the disease. Spreading mechanisms include the diffusion of pathogens in the aquatic environment and their dissemination due to the movement of human carriers. The model reproduces the spatiotemporal features of the outbreak to date, thus suggesting the robustness of predicted future developments of the epidemic. We estimate that, under unchanged conditions, the number of new cases in the whole country should start to decrease in January. During this month the epidemic should mainly involve the Ouest department (Port-au-Prince) while fading out in northern regions. Our spatially explicit model allows also the analysis of the effectiveness of alternative intervention strategies. To that end our results show that mass vaccinations would have a negligible impact at this stage of the epidemic. We also show that targeted sanitation strategies, providing clean drinking water supply and/or staging educational campaigns aimed at reducing exposure, may weaken the strength of the residual evolution of the infection. **Citation:** Bertuzzo, E., L. Mari, L. Righetto, M. Gatto, R. Casagrandi, M. Blokesch, I. Rodriguez-Iturbe, and A. Rinaldo (2011), Prediction of the spatial evolution and effects of control measures for the unfolding Haiti cholera outbreak, *Geophys. Res. Lett.*, *38*, L06403, doi:10.1029/2011GL046823.

## 1. Introduction

[2] As a major cholera epidemic spreads through Haiti [*Butler*, 2010; *Zarocostas*, 2010; *Enserink*, 2010; *Walton and Ivers*, 2011] and the figures of the infection, up to the end of 2010, climb to 170,000 reported cases and 3,600 deaths (PAHO, Haiti cholera outbreak data, 2010, available at http://new.paho.org/hq/images/atlas_ihr/cholerahispaniola/atlas.html), the development of models to track, predict and possibly control the evolution of the outbreak, as well as to guide the allocation of medical staff and supplies, is gaining notable urgency. The disease started from the Artibonite river and progressively involved all the surrounding departments, exhibiting spatial patterns that call for a suitable modeling framework [*Codeço*, 2001; *Bertuzzo et al.*, 2008, 2010; *Righetto et al.*, 2011]. A complex set of processes is known to drive the dispersion of vibrios and the consequent spreading of the disease among communities [*Colwell*, 1996; *Pascual et al.*, 2002; *Lipp et al.*, 2002]. A primary mechanism of propagation is related to the dispersion through surface water. *V. cholerae* can in fact survive outside the human host in the aquatic environment and it may also live [*Islam et al.*, 1990, 1994] and evolve [*Meibom et al.*, 2005; *Blokesch and Schoolnik*, 2007] in symbiosis with phytoplankton and zooplankton. As a result, the bacteria, and therefore the disease, can spread through hydrologic pathways among human communities. This baseline dispersal mechanism, however, can be significantly enhanced by human mobility. In fact, susceptibles who travel or commute for food and water supply, educational, or business reasons may be exposed to cholera at destination sites and bring the infection back to the communities where they regularly live. In the same way, asymptomatic carriers can be responsible for long-range dissemination of the bacteria to distant communities, and their number may be much larger than those of reported cases [*King et al.*, 2008]. In fact, although most people infected by cholera do not show any acute symptoms, bacteria are present in their feces and can enter the environment thus spreading the disease [*World Health Organization*, 2010]. Human activity is also the most accredited explanation for the introduction of cholera into Haiti from a distant geographic source [*Chin et al.*, 2011]. Human mobility is expected to favor the emergence of the disease far from epidemic hotbeds, thus playing a crucial role in shaping the spatiotemporal patterns of cholera epidemics [*Colwell*, 1996]. This represents a key issue in the dynamics of any infectious disease [*Viboud et al.*, 2006], yet it has received relatively scarce attention with specific reference to cholera epidemics [*Righetto et al.*, 2011].

## 2. Methods

[3] In our metacommunity framework, Haiti is divided into more than 500 local communities (representing the fourth administrative level, see Figure 1). For each community we model the dynamics of the number of susceptibles to the disease (initially coinciding with the total population, which had never been exposed to cholera and thus was lacking any immunity [*Butler*, 2010; *Chin et al.*, 2011]), infected individuals and *V. cholerae* abundance in the aquatic envi-

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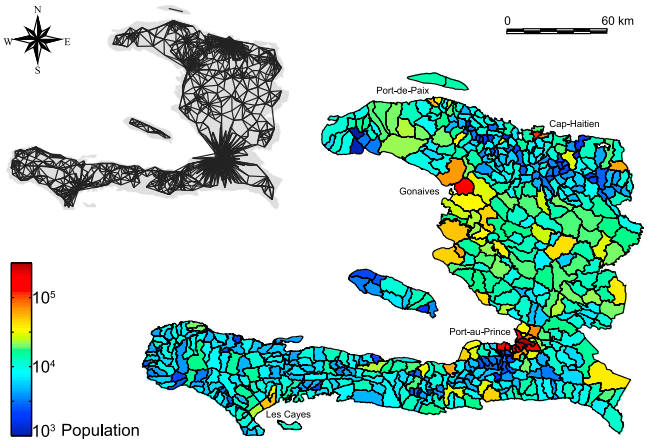


**Figure 1.** Maps of Haiti. Administrative subdivision (fourth level) color coded accordingly to population size. Each district represents a human local community in the model. The inset shows the network used to model the dispersion of pathogens among communities. For each node only the four most important outbound connections, as computed from the gravity model, are shown.

ronment. The key assumptions are that the rate at which susceptibles become infected depends on the concentration of pathogens in the available water and, in turn, that new free-living bacteria are produced by infected individuals through fecal contamination.

[4] As for pathogen transport, the epidemic information of the Haitian outbreak available at this stage (i.e., reported cholera cases aggregated at the department level (http://new.paho.org/hq/images/atlas_ihr/cholerahispaniola/atlas.html, see Figure 2) does not allow the assessment of the relative role of transport mechanisms discussed above. Moreover, the complete absence of any historical reference for a cholera epidemic in this region [*Chin et al.*, 2011] further complicates the modelling endeavor. For these reasons, we preliminarily resort to a simplified *V. cholerae* dispersion scheme according to which the flux of pathogens between two communities decays with the distance separating them and is proportional to the product of the pathogen concentration in the source community times population size of the destination community. The last assumption borrows concepts from the so called gravity models of transportation theory [*Erlander and Stewart*, 1990]. Gravity-like models have already been applied in the epidemiological literature to describe the impact of human mobility on the emergence of a suite of diseases, including influenza [*Eggo et al.*, 2010], HIV [*Thomas*, 1999] and measles [*Ferrari et al.*, 2008]. We argue that the dispersion model adopted here is able to capture the features of the two main transport mechanisms analyzed: a short-range water contamination and a long-range anisotropic transport induced by human mobility.

[5] Epidemiological dynamics and pathogen transport are therefore described by the following set of ordinary differential equations [*Bertuzzo et al.*, 2008, 2010]:

$$\begin{aligned}\frac{dS_i}{dt} &= \mu(H_i - S_i) - \beta\frac{B_i}{K+B_i}S_i \\ \frac{dI_i}{dt} &= \beta\frac{B_i}{K+B_i}S_i - (\gamma+\mu+\alpha)I_i \\ \frac{dB_i}{dt} &= \frac{p}{W_i}I_i - \mu_B B_i - l\left(B_i - \sum_{j=1}^{N} P_{ji}\frac{W_j}{W_i}B_j\right),\end{aligned} \tag{1}$$

where $S_i$ $(t)$, $I_i$ $(t)$ and $B_i$ $(t)$ are respectively susceptibles, infected individuals and pathogen concentration in each node $i$ of the spatial network at time $t$. For a detailed description of the model see the auxiliary material.[1] The host population is assumed to be at a demographic equilibrium, where $\mu$ is the human natality/mortality rate and $H_i$ is the size of the local community. The parameter $\beta$ represents the rate of exposure to contaminated water, and $B_i/(K + B_i)$ is the probability of becoming infected due to the exposure to a concentration $B_i$ of vibrios, $K$ being the half-saturation constant [*Codeço*, 2001]. Infected individuals recover at a rate $\gamma$, or die for natural or cholera-induced mortality at a rate $\mu$ or $\alpha$, respectively. Infected individuals contribute to the concentration of free-living vibrios at a rate $p/W_i$, where $p$ is the rate at which bacteria excreted by one infected individual reach and contaminate the local

[1] Auxiliary materials are available in the HTML. doi:10.1029/2011GL046823.

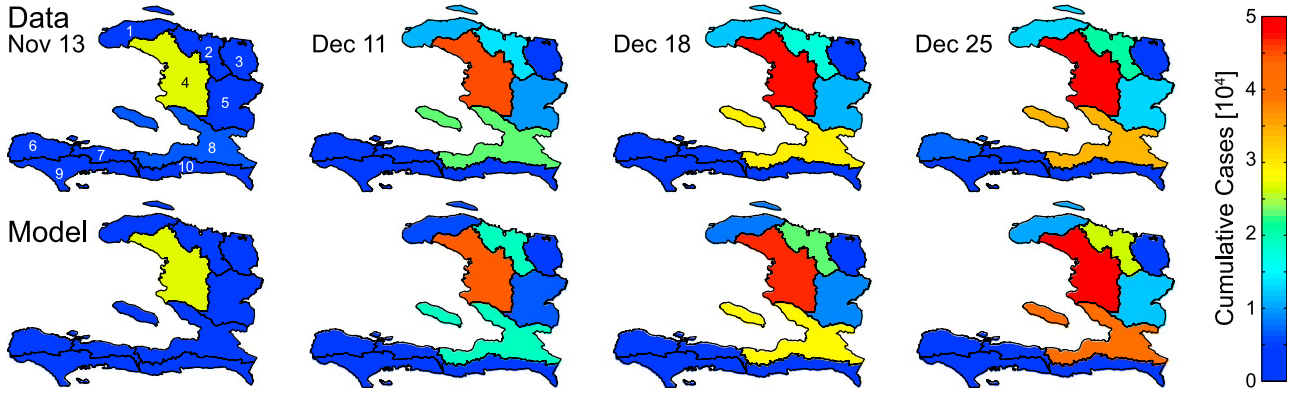


**Figure 2.** Spatial spreading of the Haiti cholera epidemic. Comparison between data and model results in the ten departments: 1) Nord-Ouest, 2) Nord, 3) Nord-Est, 4) Artibonite, 5) Centre, 6) Grand Anse, 7) Nippes, 8) Ouest, 9) Sud, 10) Sud-Est.

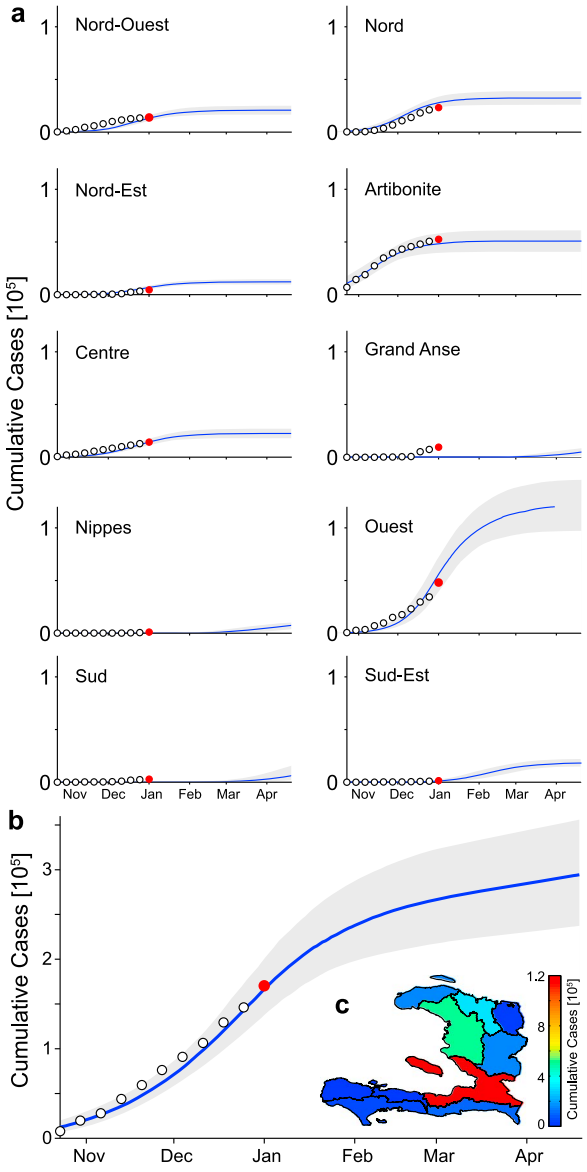


**Figure 3.** Predicted evolution of the Haiti epidemic. Predicted (solid line) and reported (circles) cumulative cases for (a) the ten administrative departments and (b) the whole country. Data reported in red circles were not used for model calibration as they became available upon submission. Grey shaded areas show the 5-95 percentile of the model prediction (see auxiliary material). (c) Spatial distribution of the predicted cumulative reported cases up to May 1, 2011.

water resource reservoir $W_i$. Bacteria die at a constant rate $\mu_B$ and undergo dispersal at rate $l$. The probability $P_{ij}$ of pathogen movement from node $i$ to node $j$ of the network is defined as

$$P_{ij} = \frac{H_j \exp(-d_{ij}/D)}{\sum_{k \neq i}^{N} H_k \exp(-d_{ik}/D)}, \qquad (2)$$

where $d_{ij}$ is the distance between nodes $i$ and $j$, $D$ is the mean dispersal distance and $N$ is the number of nodes in the network. While several parameters can be estimated from the literature, four model parameters, namely the dispersal rate, the average dispersal distance, the initial time of the epidemic and the basic reproductive number, are obtained through a calibration procedure contrasting the weekly reported cases in each Haitian department (Figure 3a) as recorded in the epidemiological dataset and simulated by the model (see auxiliary material for a complete description of parameters estimation and calibration).

## 3. Results and Discussion

[6] As shown in Figures 2 and 3, the model is able to reproduce the timing and the magnitude of the epidemic in the ten Haitian departments, in particular in Artibonite and Ouest, the most populated – and most scourged by the disease – regions. On the other hand, the onset of the epidemic in southwestern regions (Grand Anse) is not well captured. While the model predicts the outbreak in late spring, the latest data suggest that the infection has already reached this area. This could be due to a shortcut in the transmission of the disease that is not well reproduced by the transport model, or to particularly poor sanitation conditions in this area, which are not accounted for in the model. As more detailed epidemic data become available, they could readily be integrated into the model in order to understand this particularly fast transmission pathway. However, we argue that the model ability to reproduce the basic timescales of pathogen transport and local disease evolution grants robustness to the foreseen evolution of the epidemic. This is also supported by the latest data, not used in the model calibration, which agree with the predictions (Figure 3).

[7] The mechanistic description of the major processes governing the transmission of the disease allows us to directly quantify the effects of possible intervention strategies, such as vaccination campaigns [*Calain et al.*, 2003; *Chaignat et al.*, 2008; *Chaignat*, 2008; *Cyranoski*, 2011]. Figure 4a shows the estimated deviation from the expected residual evolution of the epidemic if 150,000 individuals are vaccinated with the administration of two doses in the capital Port-au-Prince starting January 1, 2011 during a week (see auxiliary material for the implementation of the vaccination model). As expected, given the relative low figure of doses considered (300,000 doses, which however correspond to the supply that should be available within the next few months (http://new.paho.org/hq/images/atlas_ihr/cholerahispaniola/atlas.html)), benefits are negligible. Different spatial allocations provide similar results. The small effectiveness of this intervention is also due to the fact that full immunity could take up to three weeks to build up [*Jertborn et al.*, 1993]. Moreover, at this stage of the epidemic, it is likely that vaccines are misused to immunize people who have already been infected without showing symptoms and are therefore already immune. We estimate that to be effective, a vaccination campaign should have envisaged a twenty times larger supply of doses and an early administration. This would have halved the final toll of cases (Figure 4a). Needless to say, these results refer to ideal vaccination strategies. Unavoidable delays and difficulties in mounting such campaigns [*Butler*, 2010] would further weaken their effects. The organization of vaccine administration under complex emergencies is, in fact, particularly challenging as it can divert public health workers from the

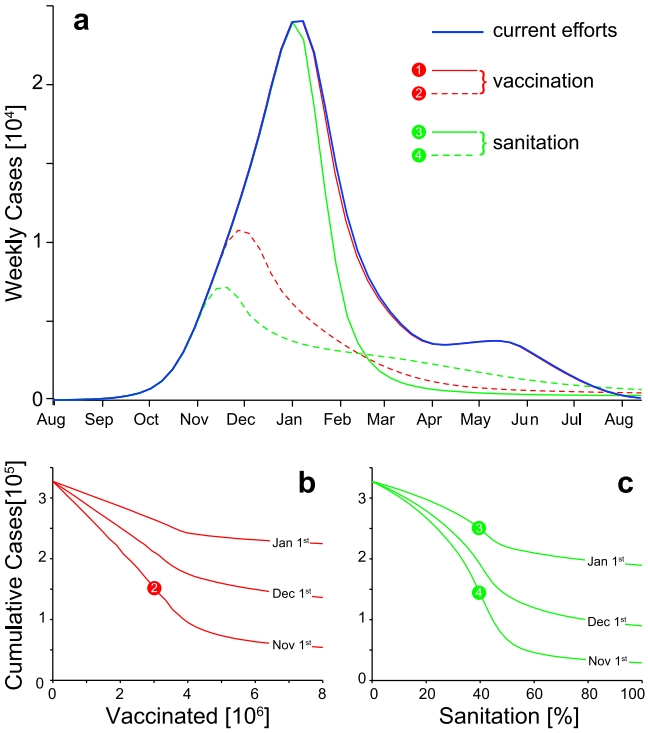


**Figure 4.** Evaluation of alternative intervention strategies. (a) Weekly cases computed under the assumptions of: current efforts (blue line); 1) 300,000 vaccination doses (corresponding to 150,000 people vaccinated) administered in Port-au-Prince within one week starting 01/01/2011 (solid red line); 2) 6,000,000 vaccinations doses (corresponding to 3,000,000 people vaccinated) administered uniformly through the Haitian population within one month starting 01/11/2010 (dashed red line); 3) a 40% reduction in one months for the probability of ingesting contaminated water starting 01/01/2011 (solid green line); 4) a 40% reduction in one months for the probability of ingesting contaminated water starting 01/11/2010 (dashed green line). Expected total number of cases as a function of (b) the population vaccinated and (c) the reduction of the probability of ingesting contaminated water. All the interventions are deployed in one month starting from the date reported in the curve labels. Points highlighted in Figures 4b and 4c refer to the cases presented in Figure 4a.

priority of patients care and sanitation, thus worsening the situation [*Chaignat et al.*, 2008].

[8] We have also examined the possible effects of prevention measures aimed to provide targeted clean water supply (through water purification systems or filters) and to educate people about hygiene and handling of water and food [*Chaignat et al.*, 2008; *Ivers et al.*, 2010; *Walton and Ivers*, 2011]. Obviously it is difficult to compare such interventions to vaccination campaigns in terms of logistic efforts, costs and benefits. In fact, while vaccinations act only against cholera, sanitation undoubtedly has other positive effects. However, our analysis can provide estimates of the system response to different sanitation targets. Results show that a set of measures leading to a 40% reduction of the probability to ingest contaminated water or food, enforced in a month timespan, could greatly reduce the residual progression of the disease (Figure 4a). This strategy, whose feasibility is debatable due to current civil unrest, could have been as beneficial as an early vaccination campaign if promptly deployed at the onset of the epidemic (Figure 4a). A summary of the effects of the two intervention strategies is presented in Figures 4b and 4c where the expected total cumulative cases are reported as a function of sanitation and vaccination efforts for different starting dates. These control measures exhibit a very small marginal benefit beyond a certain threshold. In fact efforts leading to exceed either a 50% reduction of the probability of ingesting contaminated water or the vaccination of 4 million individuals do not allow a significant decrease of the cumulated cases.

## 4. Conclusions

[9] The catastrophic outcomes of the ongoing Haiti cholera epidemic (http://new.paho.org/hq/images/atlas_ihr/cholerahispaniola/atlas.html) call for the development of quantitative tools to study and, possibly, control the residual evolution of the outbreak. A quick resolution of the current epidemic might also limit the further spread of the disease beyond country borders, with possible implications for the Caribbean ecosystem and whole Latin America [*Chin et al.*, 2011].

[10] The development of these modeling tools will certainly benefit from a deeper integration of epidemiological, socioeconomical and environmental data [*Clark et al.*, 2001]. To this end, the effort made by the Pan American and the World Health Organization in making real-time data available to the scientific community through a dedicated online platform (http://new.paho.org/hq/images/atlas_ihr/cholerahispaniola/atlas.html) represents a preliminary yet highly commendable step forward. We believe that pursuing this endeavor is instrumental to develop quantitative models that can be effectively used – in the very course of an outbreak – to allocate health care resources and evaluate alternative strategies of emergency management.

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