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Cholera Epidemic in Haiti, 2010: Using a Transmission Model to Explain Spatial Spread of Disease and Identify Optimal Control Interventions

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Background: Haiti is in the midst of a cholera epidemic. Surveillance data for formulating models of the epidemic are limited, but such models can aid understanding of epidemic processes and help define control strategies.

Objective: To predict, by using a mathematical model, the sequence and timing of regional cholera epidemics in Haiti and explore the potential effects of disease-control strategies.

Design: Compartmental mathematical model allowing person-to-person and waterborne transmission of cholera. Within- and between-region epidemic spread was modeled, with the latter dependent on population sizes and distance between regional centroids (a "gravity" model).

Setting: Haiti, 2010 to 2011.

Data Sources: Haitian hospitalization data, 2009 census data, literature-derived parameter values, and model calibration.

Measurements: Dates of epidemic onset and hospitalizations.

Results: The plausible range for cholera's basic reproductive number (R_0, defined as the number of secondary cases per primary case in a susceptible population without intervention) was 2.06 to 2.78. The order and timing of regional cholera outbreaks predicted by the gravity model were closely correlated with empirical observations. Analysis of changes in disease dynamics over time suggests that public health interventions have substantially affected this epidemic. A limited vaccine supply provided late in the epidemic was projected to have a modest effect.

Limitations: Assumptions were simplified, which was necessary for modeling. Projections are based on the initial dynamics of the epidemic, which may change.

Conclusion: Despite limited surveillance data from the cholera epidemic in Haiti, a model simulating between-region disease transmission according to population and distance closely reproduces reported disease patterns. This model is a tool that planners, policymakers, and medical personnel seeking to manage the epidemic could use immediately.

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Haiti, the poorest country in the Western Hemisphere (1), is in the midst of a cholera epidemic that has reportedly killed more than 4000 people and infected about 217 000 (as of 30 January 2011). Approximately one half of those infected have been hospitalized, and case-fatality rates in both community and hospital settings have been approximately 2% (2). The first laboratory-confirmed case was reported in the department of Artibonite (3–5), but cases have now been reported in all 10 administrative departments in the country. Control measures for the epidemic seem to be slowing transmission of the disease (2). The Pan American Health Organization has suggested that a vaccine campaign may be initiated (6–8), and low-cost approaches to the provision of cleaner water supplies have been advocated (3, 9).

Although epidemiologic surveillance constitutes an important component of the public health response to such an epidemic, publicly available surveillance data from Haiti have been relatively limited to date, whereas time series on hospitalizations and deaths by region are available (2). Epidemic data, combined with geographic and demographic information of a country's administrative regions, can be used to formulate and calibrate models of epidemics. These models can provide valuable insights into the nature of disease spread, help project the time course of the epidemic, and provide guidance on optimal control strategies (10–12).

Viboud and colleagues (13) and others (14) have demonstrated that spatial patterns of epidemic spread can be represented by using "gravity" models that characterize the interaction between geographic regions, with respect to epidemic spread as a function of population mass (13) and distance (13, 14). We used a gravity model to accurately predict the sequence and timing of regional cholera epidemics in Haiti by using publicly available data. We used a model based on the best available data and calibrated to

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Context

Haiti is in the midst of a cholera epidemic. Surveillance data to inform public health decision making are limited.

Contribution

The authors constructed a mathematical model of epidemic dynamics that is based on both population and distance. The model's results closely match the contour of the epidemic to date. The model was used to project the probable effect of different approaches to allocation of vaccines and clean water on the course of the epidemic.

Caution

The model does not include the effect of antibiotic treatment on transmission of cholera.

Implication

A publicly available tool to assist in managing the cholera epidemic in Haiti has been developed and can be further modified and refined.

—The Editors

reproduce the initial reported epidemic curve for Haiti and then evaluate the probable time course of Haiti's cholera epidemic in the absence of effective intervention and explore the potential effects of competing and complementary control strategies, including vaccine distribution and provision of clean water.

METHODS

Data Sources

Information on the timing and magnitude of the cholera epidemic in Haiti was obtained from 3 complementary sources: the HealthMap system (http://healthmap.org/en/), the Ministère de la Santé Publique et de la Population (MSPP) of the Republic of Haiti (2), and a summary report by the U.S. Centers for Disease Control and Prevention (15). The HealthMap system is an automated surveillance platform that continually identifies, characterizes, and maps events of public health and medical importance, including outbreaks and epidemics, on the basis of Internet-based information sources (16). Data inputs for HealthMap include media sources, discussion groups, and government Web sites. As such, HealthMap may be more sensitive than traditional surveillance systems but may also be limited by unfavorable signal–noise ratios (16).

Because regional MSPP data had inconsistencies (for example, cumulative case counts reported at a given date often disagreed with cumulative case counts that were manual tabulated from serial reports), we calibrated a geographically explicit "meta-population" model (17) based on both national estimates of cumulative hospitalized case counts and dates of first reported case in each region.

Model

We built a "susceptible–infectious–recovered" compartmental transmission model that characterized the population as susceptible to infection, infected and infectious to others, or recovered or otherwise "removed" from risk for further infection. We also added a water compartment to the model. The water compartment could be contaminated by infected and infectious persons and could in turn infect susceptible persons. **Appendix Figure 1** (available at www.annals.org) is a schematic representation of the model. This modeling approach was described by Tien and Earn (18) for the simulation of diseases that can be transmitted through both person-to-person contact and contaminated water, such as cholera.

We constructed the models for the population of each of Haiti's 10 administrative departments. These populations were combined to form a meta-population model, in which disease could spread both within a given department (or "patch") or between patches (implicitly reflecting the movement of people from one region to another) (19). The model was constructed by using the Berkeley Madonna software package (developed by Robert Macey and George Oster at the University of California at Berkeley, Berkeley, California). Complete model details and additional information on model parameterization are provided in the **Appendix** (available at www.annals.org).

Model Parameterization

The basic reproductive number (R_0) is an important index of epidemic potential for a communicable disease (10–12, 20). Existing estimates of R_0 for cholera vary widely (21–23). We obtained seed estimates from the published biomedical literature of the duration of infectiousness in patients with cholera and durability of *Vibrio cholerae* in source water (18). We assumed that cholera could be transmitted through either contaminated water or close contact but that waterborne transmission (or consumption of food items contaminated with infective water) was a far more important method of transmission (24–26). Most documented cases of person-to-person transmission occur in households, usually because of infection in persons involved in food preparation (27, 28).

Plausible ranges for the environmental survival of *V. cholerae* were derived from studies of bacterial survival in sediments (29). Population sizes were obtained from 2009 Haitian census data (30). We used centroids for each department's capital city to calculate straight-line distances between patches (**Appendix Figure 2**, available at www.annals.org). To account for the shape of the country, we assumed that Haiti was divided into 2 zones when calculating distances: the lower zone included Grand'Anse, Sud, Nippes, and Sud-Est, and the upper zone included Nord-Ouest, Nord, Nord-Est, Artibonite, and Centre. Ouest was treated as a conduit between the 2 zones, such that the distance between 2 departments in different zones was calculated as the sum of the distance between the department

in zone 1 and Ouest and between Ouest and the department in zone 2. For example, the distance between Grand'Anse and Centre was the sum of the distance between the capital of Grand'Anse and the capital of Ouest plus the distance between the capital of Ouest and the capital of Centre.

Model Calibration

Because cumulative data on case counts for each department were inconsistent, we calibrated our model by modifying the dependence of transmission rate on distance (d^{-n}) to best reproduce the ordering of case appearance by department (**Appendix Table 1**, available at www.annals.org). We considered values of n that ranged from 0.8 to 3.0. Goodness of ordering was evaluated by calculating Spearman correlation coefficients for observed versus expected order of first case appearance in the 9 non-Artibonite departments. Ordering was optimized for n ranging from 2.0 to 2.4 (and was identical for n in this range). For simplicity, we used an n of 2.0. We subsequently optimized model fit through iterative adjustment of components of R_0, as well as κ (the "gravitational constant") and ξ (the pathogen decay rate in water) to minimize the least-squares distance between overall model hospitalization estimates and those reported by MSPP, by using the optimize function of the Berkeley Madonna software package. We estimated credible intervals for model parameters by iteratively refitting our multipatch susceptible–infectious–water–recovered model, assuming that errors in case counts were Poisson-distributed (20).

We performed 1000 stochastic simulations, with parameters drawn from uniform distributions for plausible ranges of values to develop projections of time to epidemic peak in each of Haiti's 10 departments.

Optimization of Control Strategies

Recent reports suggested the availability of approximately 1 million doses of a 50% effective vaccine (31) that can be used to control Haiti's cholera epidemic (7, 8), but the timing of their availability is unclear. Because the most widely available vaccine preparation is administered on a 2-dose schedule, with doses administered at least 1 week apart (32), this would constitute vaccination for 500 000 people in Haiti. We introduced vaccination into the model by moving persons from the susceptible compartment to the recovered (immune) compartment at a time representing completion of vaccination. We explored the projected effect of vaccination on total case counts under different assumptions about time to completion of vaccination by using 3 strategies of vaccine distribution: equal distribution to all 10 of Haiti's departments, distribution in proportion to the population, and distribution according to a model-based projection of optimal allocation of vaccine. Optimal allocation was estimated by iteratively minimizing total case counts subject to the constraint of 500 000 available doses, again by using Berkeley Madonna's optimize function. We also explored the relative effect of replacing vaccination with provision of clean water (9, 33) to the same number of people who could be vaccinated and the number of people who would need to receive clean water to have the same effect on epidemic spread as that achievable through vaccination.

Changing Dynamics of Infection Over Time

We calibrated our base-case model to reproduce initial dynamics of cholera transmission in Haiti, in the absence of effective disease-control interventions. However, the rate of growth in case counts has slowed appreciably over time, which probably reflects the effects of disease-control efforts by governmental and nongovernmental agencies. We evaluated the probable effect of disease-control interventions by refitting our model to incorporate data from January 2011, with decreases in the effective reproductive number simulated by using a simple discount factor (f) (34), such that the reproductive number (R) at time t was taken to be $R_t = R_0/(1+f)^t$.

Role of the Funding Source

We received no funding for this study.

RESULTS

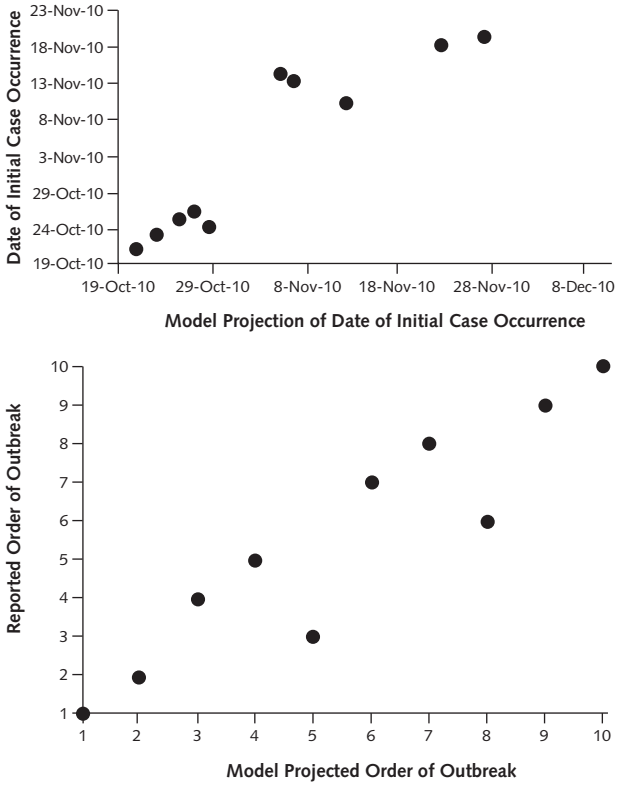
Model Parameterization and Calibration

Appendix Table 2 (available at www.annals.org) includes the best-fit parameter estimates based on 1000 stochastic simulations. The best-fit estimate for R_0 for cholera was approximately 2.78 (plausible range, 2.06 to 2.78), which is within the range generated by our group and others (21–23). Using an inverse square-distance term in our gravity model combined with best-fit parameters, we found close correlation between model projections of ordering initial cases and initial case dates by department and between those reported by the MSPP and the U.S. Centers for Disease Control and Prevention (15) (Spearman correlation coefficient for ordering, 0.97 [$P < 0.001$]; Spearman correlation coefficient for case dates, 0.92 [$P < 0.001$]) (**Figure 1**). Cumulative hospitalized case counts projected by the model agreed closely with those reported by the MSPP (**Appendix Figure 3**, available at www.annals.org).

Estimated Time to Peak and Duration of Epidemic Under Initial Conditions

Figure 2 presents the projected timing of peaks in the epidemics, based on 1000 stochastic simulations with parameter values drawn from plausible ranges. Without effective intervention, the epidemic in the initially seeded region (Artibonite) was projected to peak at 100 to 150 days after initial seeding. Most other regional epidemics peaked at 200 to 250 days after initial seeding. Epidemics in the Sud, Grand'Anse, and Nippes departments were projected to peak last, nearly 1 year after the initial case in Artibonite. They continued at an incidence of more than 200 cases per 100 000 persons in December 2011 in these regions. An animated representation of the course of regional

Figure 1. **Correlation between model projections and MSPP reports on initial case dates (*top*) and ordering of outbreaks (*bottom*).**



Close correlation is observed between model projections and reported dates of epidemic onset by region. MSPP = Ministère de la Santé Publique et de la Population.

epidemics, by department, is available online (**Supplement**, available at www.annals.org).

Optimal Intervention Strategies

We evaluated the effect of 3 competing strategies for use of 1 million doses of vaccine (sufficient for vaccination of approximately 500 000 persons): equal allocation to each of Haiti's 10 departments; allocation in proportion to the population; and allocation based on optimization, such that the total cases were reduced maximally. Unsurprisingly, for each strategy earlier completion of vaccination was associated with a greater reduction in case counts than was later completion of vaccination, although even vaccination before the onset of the epidemic did not reduce total case counts by more than 3.2% because of the limited quantity of vaccine available. The relative advantage of using an optimized distribution strategy, compared with vaccination based on proportional or equal allocation, increased the later that vaccination occurred, although the relative benefit of vaccination in all strategies diminished with time (**Figure 3**, *top*). Nonetheless, the benefit associated with vaccination was far greater than that of allocation of clean water (**Figure 3**, *bottom*). We estimated that 1.7 to 2.0 times as many people would need to be given access to clean water to achieve an equal reduction in cholera cases that can be achieved through optimal allocation of vaccine (**Appendix Table 3**, available at www.annals.org). The combination of clean water and vaccination was projected to have a superadditive effect (projected reduction in cases resulting from both interventions was greater than the sum of the effects of individual interventions) (**Appendix Figure 4**, available at www.annals.org).

Optimal allocation of vaccine focused largely on Ouest department, because of the highly "connected" nature of this department with its large population (focused in Port-au-Prince) and central location, and on Centre department, which serves as a "crossroads" for cholera spread. However, because vaccination is increasingly delayed, larger shares of the vaccine were optimally reallocated to such regions as Nippes and Grand'Anse, which were projected to peak latest (**Appendix Figure 5**, available at www.annals.org).

Changing Dynamics of Infection Over Time

We calibrated our base-case model to reproduce initial dynamics of cholera transmission in Haiti in the absence of disease-control efforts interventions. Model fits obtained by using a longer time series, for hospitalizations to 14 January 2011, suggested a higher R_0 (2.90), with a decrease in R_0 by an average of 1.8% per day (**Figure 4**). By contrasting this epidemic with simulations using an R_0 of 2.78 (as in the base case) or 2.90, we estimate that disease-control interventions have probably prevented thousands of cases of cholera (as of February 2011).

Discussion

Although cholera is preventable through treatment of sewage and provision of clean drinking water (as are other highly virulent enteric diseases), it continues to take a terrible toll worldwide (35–37). The ongoing cholera epidemic in Haiti is a stark reminder of the degree to which this infrastructure, taken for granted in high-income countries, remains unavailable in most of the world. The *V. cholerae* strain responsible for the current epidemic was presumably introduced by a person or persons visiting Haiti from South Asia (38). Regardless of the route of introduction, the limited availability of clean drinking water and sewage treatment in Haiti have permitted the rapid emergence of a cholera epidemic that is now active in all regions of the country. As of February 2011, more than 4000 cholera-related deaths have been recorded (2).

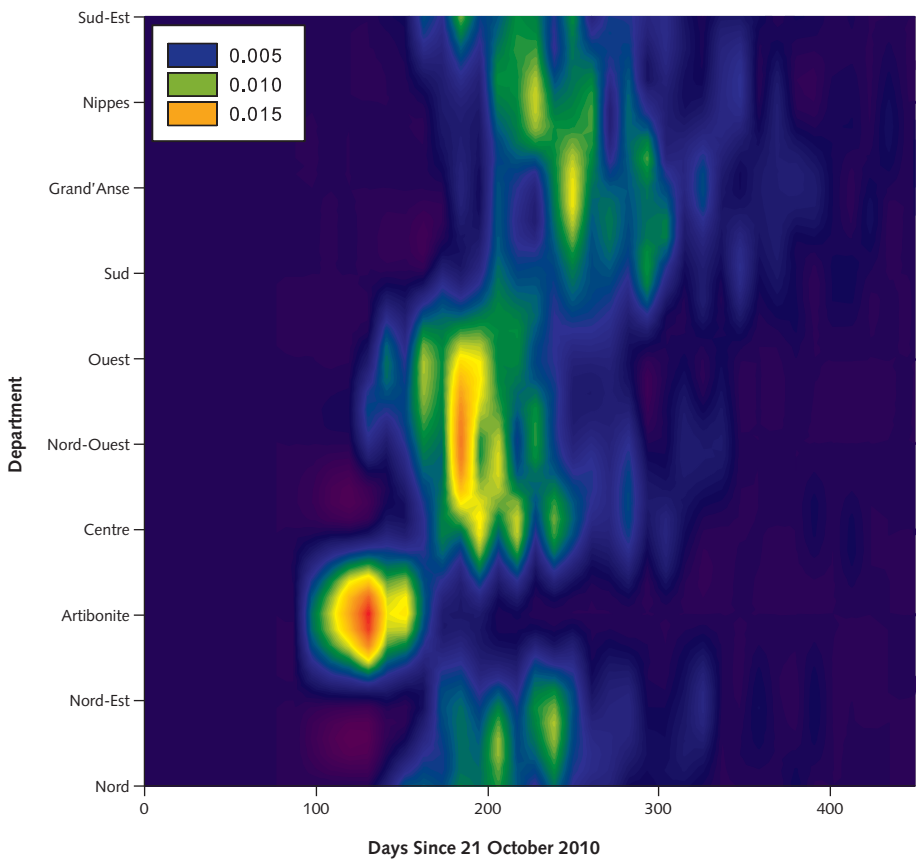
Mathematical models of infectious diseases, such as the one we describe here, represent an idealized or a simplified version of complex disease systems, but they may provide insights into the behavior of these systems and can serve as a tool for decision making under uncertainty (10–12). We constructed a relatively simple patch model representing Haiti, with each department influencing infec-

tion risk in persons who reside in other regions in a manner proportionate to the size of the departments in question and inversely proportional to the square-distance between them. We found that such a simple gravity model accurately reproduced both the initial magnitude of the cholera epidemic in Haiti and the timing of onset of regional epidemics. Gravity models have been used to project the movement of influenza in affluent countries, such as the United States and France, and have also been used to model the dynamics of measles and influenza in the United Kingdom in the prevaccination era (39, 40). To our knowledge, our study is the first application of a gravity model of epidemic spread in a low-income country.

On the basis of a model that is well-calibrated to the initial months of the cholera epidemic in Haiti, we can produce plausible projections on the future tempo of this epidemic in the absence of an effective intervention, but we can also quantify the effect of disease-control interventions in Haiti. Although any attempt to precisely predict the future with a mathematical model should be viewed with caution, we can qualitatively project with confidence that the cholera epidemic in Haiti is likely to continue for several months and, without effective intervention, has not yet peaked in the last-affected departments. However, deviation of the epidemic curve from initial model projections suggests that interventions on the ground are changing the dynamics of this disease and have probably already averted a substantial burden of morbidity and mortality.

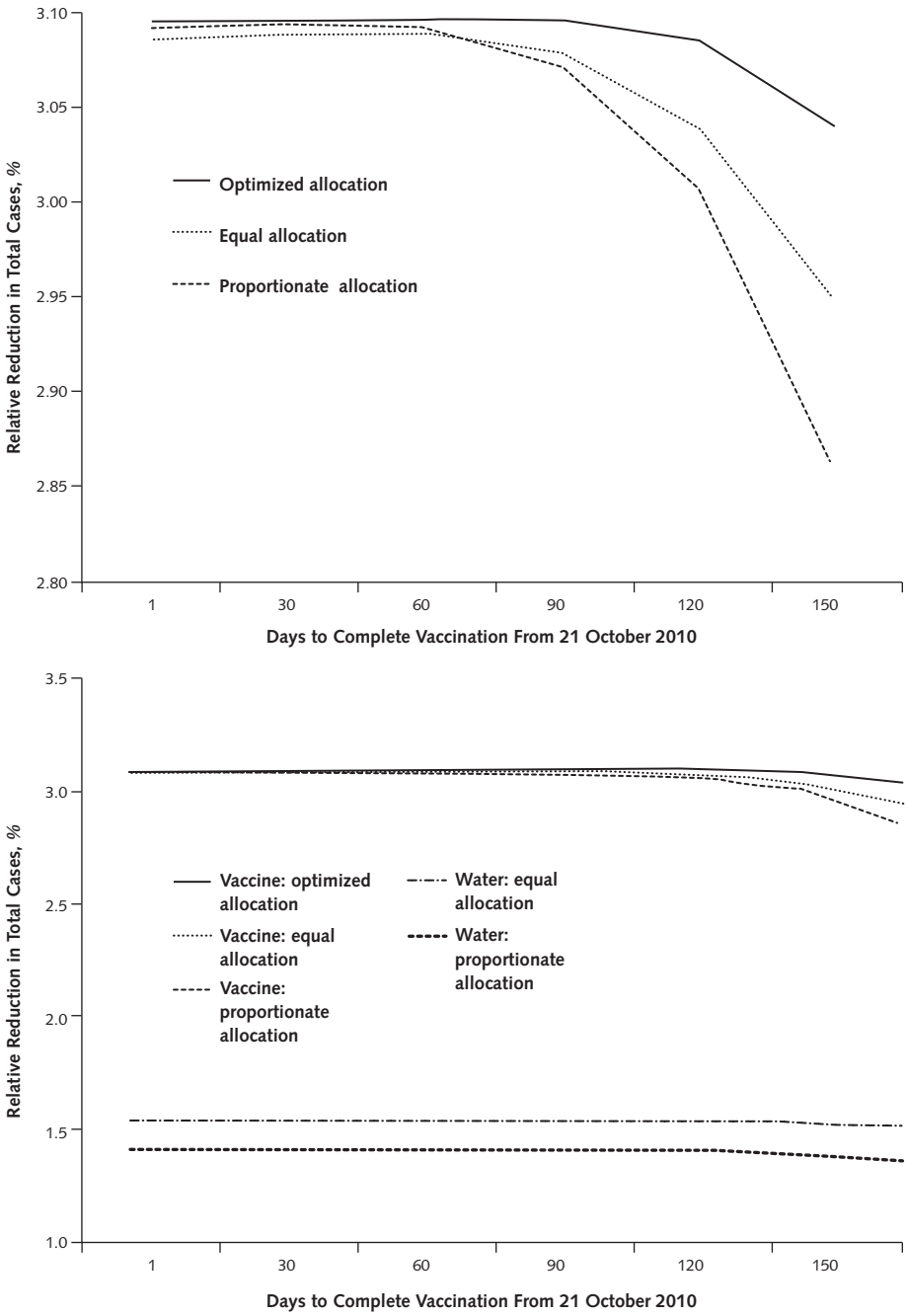
Both vaccination and provision of clean water should mitigate this epidemic; however, our projections suggest that the limited number of vaccine doses available, combined with the substantial time to distribute the vaccine in a country with limited transportation infrastructure and health care resources, will make the effect of vaccination fairly modest. However, given the potential for thousands of additional cholera cases in Haiti and the high (>1%) case-fatality rate associated with cholera in Haiti, a reduction in total case counts of even a few percent will translate into a substantial number of lives saved. Furthermore, the transmissibility of cholera in Haiti (as assessed by the reproductive number) has probably been reduced substantially by ongoing disease-control efforts. The relative effect

Figure 2. **Heat map showing the timing of epidemic peak in Haiti, by department.**



Timing is based on 1000 stochastic simulations, as described in the text. An increasing intensity of color denotes more simulations projecting that region's epidemic to peak at a given time. The epidemic in Artibonite, home of the initial outbreak, is projected to peak first; epidemics in Grand'Anse, Nippes, and Sud are projected to peak last.

Figure 3. **Projected relative benefit of competing vaccination strategies and of vaccination versus allocation of clean water.**



Top. Optimized allocation was always more effective than either equal or proportional allocation of vaccine, although the difference between strategies increased with delay in vaccination. **Bottom.** Compared with allocation of clean water, vaccination was projected to reduce far more cases of cholera.

of a given level of vaccine coverage will be higher if the reproductive number is lower (11, 12), and as such, the effect of vaccination may be greater than projected in our analysis.

Using our model as a platform to evaluate optimal strategies for distributing the vaccine, we project that, regardless of vaccination timing, optimized distribution is more effective than equal distribution to all departments or distribution based on population. Although an optimized strategy favors provision of most vaccine doses to the populous central regions of Haiti, as the epidemic progresses more vaccine should be reallocated to regions of the country that are "weakly connected" and consequently have late-onset epidemics that have not peaked.

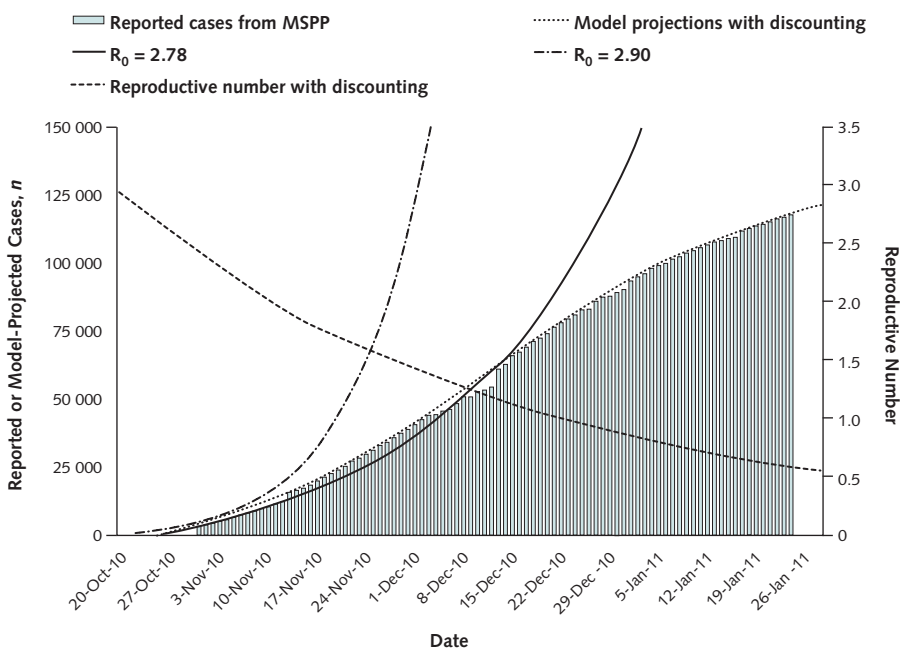
We also evaluated the relative effect of provision of clean, safe water to all people who might be reached by vaccination. Although universal access to clean water would probably have a major effect on cholera dynamics, clean water distributed to a relatively small subset of the population had a much smaller effect on case counts than did vaccination of the same number of people. Although this may seem counterintuitive, the result would be expected on the basis of the important role that susceptible persons play in perpetuating epidemics: People who have clean water are still vulnerable to infection through other routes, such as person-to-person transmission, whereas vaccinated persons are effectively removed both as potential cholera recipients and as sources of cholera for others.

As with any mathematical model, ours is a simplified representation of reality and is limited by the nongranular nature of the data available for model parameterization in this particular outbreak. Nonetheless, we believe that model credibility is strengthened by excellent calibration, with respect to both epidemic timing and national cumulative hospitalizations. Our treatment of vaccination as a "step function" is probably at odds with the practical realities of vaccine distribution, but nonetheless should provide qualitative insights into the relative value of vaccination strategies and approaches to targeting these limited resources. Furthermore, we have not considered antimicrobial drug use as a component of cholera-control interventions; limited data suggest that such antimicrobials as azithromycin could be used to decrease the duration of infection in patients with cholera (41). Our model does, however, provide a platform for the exploration of such an approach.

Our projections are the results of a model calibrated to *initial* epidemic dynamics in the absence of an intervention; the animated representation of the course of regional epidemics (**Supplement**) ignores control measures, which are likely to reduce the severity of regional epidemics (and may already be doing so, thanks to the hard work and dedication of government health workers and local and international relief workers). Our subsequent refitted model suggests that these efforts have resulted in a substantial decrease in the transmissibility of cholera in Haiti.

In conclusion, a relatively simple patch dynamic transmission model of cholera that explicitly represents the "gravitational pull" of larger regions and shorter between-region distances in Haiti reproduces the dynamics of the current epidemic in Haiti. The model projects that the epidemic is likely to last well into 2011 and suggests that adaptive strategies for vaccination may provide a modest reduction in morbidity and mortality in the economically challenged country. Although the model's projections are not substitutes for empirical study of disease dynamics, we hope they may spur the international community to pro-

Figure 4. **Recalibration of the model to incorporate reduction in effective reproductive number over time.**



A best-fit model (*dotted line*) incorporating an R_0 of 2.90 and discounted at a rate of 1.8% per day reproduces reported cumulative hospitalizations well. Estimated values for the reproductive number by time are plotted. The reproductive number may have fallen below 1.0 in mid-December; <1.0 is no longer associated with exponential growth (11). The gap between case counts with the discounted model, and models in which the reproductive number (2.78 [base case] and 2.90) is reduced only through depletion of susceptible persons through infection provides an index of the effect of disease-control interventions in Haiti to date. MSPP = Ministère de la Santé Publique et de la Population; R_0 = basic reproductive number.

vide the additional logistic, economic, and political support that is needed to quell this epidemic.

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Reproducible Research Statement: *Study protocol:* Not applicable. *Statistical code:* Available from Ms. Tuite (e-mail, ashleigh.tuite@utoronto.ca) or Dr. Fisman (e-mail, david.fisman@utoronto.ca). *Data set:* Publically available from HealthMap (http://healthmap.org/en/), the MSPP of the Republic of Haiti (2), and the U.S. Centers for Disease Control and Prevention (15).

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Appendix

Model Details

We built a "susceptible–infectious–recovered" compartmental transmission model that characterized the population as susceptible to infection, infected and infectious to others, or recovered or otherwise "removed" from risk for further infection. We also added a water compartment to the model. The water compartment could be contaminated by infected and infectious persons and could in turn infect susceptible persons. **Appendix Figure 1** presents a schematic representation of the model. This model approach was described by Tien and Earn (18) for the simulation of diseases that can be transmitted through both person-to-person contact and contaminated water, such as cholera.

We constructed the models for the population of each of Haiti's 10 administrative departments. These populations were combined to form a meta-population model, in which disease could spread both within a given department (or patch) or between patches (reflecting the movement of people from one region to another) (19). The model was constructed by using ordinary differential equations, such that for the ith patch (with i from 1 to 10):

$$\frac{ds_i}{dt} = \mu - \lambda_i s_i - \mu s_i$$

$$\frac{dx_i}{dt} = -\gamma x_i + \lambda_i s_i - \mu x_i$$

$$\frac{dr_i}{dt} = \gamma r_i - \mu r_i$$

$$\frac{dw_i}{dt} = \xi(x_i - w_i)$$

Here, s_i, x_i, and r_i are the proportions of the population in the susceptible, infectious, and recovered (immune) or removed (through cholera-specific mortality) states, respectively, and w_i is the concentration of *V. cholerae* in local waters, rescaled by using the parameter ξ to reflect the burden of infection in the population. Rescaling is described in detail by Tien and Earn (18). The parameter γ is the inverse of the mean duration of infectiousness (that is, the recovery rate in persons who survive and time to death in those who do not), and μ is the birth rate and noncholera mortality rate, which can effectively be ignored on the short time frame associated with this epidemic.

The force of infection (λ) in the ith patch is:

$$\lambda_i = \beta_{Xi} x_i + \beta_{Wi} w_i + \sum_{j=1}^{10} \theta_{ij} x_j \quad \{i : i \neq j\}$$

β_{Xi} and β_{wi} represent the transmission rate from infectious persons and water in the ith patch to susceptible persons in the ith patch, and θ_{ij} represents the influence of infection prevalence in the jth patch on incidence in the ith patch, according to the relation:

$$\theta_{ij} = \kappa \frac{p_i p_j}{d^n}$$

Here, κ is a scalar multiplied by the gravity matrix representing between-patch coupling, p_i and p_j are population sizes, d is the distance between 2 patches, and n is a power that determines the strength of the dependence of transmission rate on distance.

Model Parameterization

The R_0 for cholera can be expressed in terms of infectiousness of water sources and infectiousness of person-to-person contact, and it is inversely related to the rate of recovery from disease and the all-cause mortality rate in the population (18), such that for a single-patch model:

$$R_0 = \frac{\beta_1 + \beta_W}{\gamma + \mu}$$

We assumed that cholera could be transmitted through either contaminated water or close contact but that waterborne transmission was a far more important method of transmission. Because both β_I and μ are small relative to β_w and γ:

$$R_0 \sim \frac{\beta_W}{\gamma}$$

Optimization of Control Strategies

Vaccination

We introduced vaccination into the model by moving persons from the susceptible compartment to the recovered (immune) compartment when vaccination was completed. We assumed that the vaccine was administered equally across the population in a given department (that is, we did not preferen-

tially allocate vaccine to susceptible persons, but vaccination had no effect on infectious or recovered persons):

$$\frac{ds_i}{dt} = \mu - \lambda_i s_i - v_i s_i - \mu s_i$$

$$\frac{dx_i}{dt} = -\gamma x_i + \lambda_i s_i - \mu x_i$$

$$\frac{dr_i}{dt} = \gamma r_i + v_i s_i - \mu r_i$$

$$\frac{dw_i}{dt} = \xi(x_i - w_i)$$

Here, v_i is the probability of vaccination within a department.

Provision of Clean Water

We also explored the relative effect of replacing vaccination with provision of clean water to the same number of people who could be vaccinated and the number of people who would need to receive clean water to have the same effect on epidemic spread as that achievable through vaccination. We assumed that clean water was introduced at the same time as vaccination and continued for the model run (up to 2 years). Provision of clean water reduced the number of persons who were susceptible to infection through contaminated water, without changing their susceptibility to infection through person-to-person transmission, such that:

$$\frac{ds_i}{dt} = \mu - \lambda_i s_i + \beta_{wi} w_i c_i s_i - \mu s_i$$

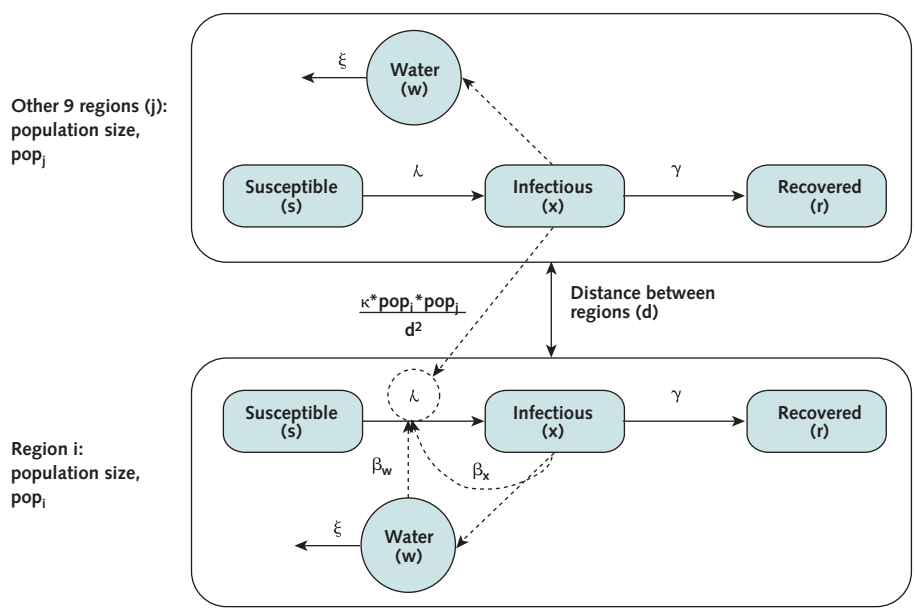
$$\frac{dx_i}{dt} = -\gamma x_i + \lambda_i s_i - \beta_{wi} w_i c_i s_i - \mu x_i$$

$$\frac{dr_i}{dt} = \gamma r_i + v_i s_i - \mu r_i$$

$$\frac{dw_i}{dt} = \xi(x_i - w_i)$$

Here, c_i is the probability of provision of clean water within a department. As with vaccination, there was no preferential provision of clean water to susceptible persons.

Appendix Figure 1. **Model overview.**



For each of the 10 departments in Haiti, the population is divided into "susceptible," "infectious," and "recovered." Infection spreads through contact of susceptible with infectious persons both within a given department and in other departments, as well as through contamination of water sources. Additional model details are provided in the **Appendix**.

Appendix Figure 2. **Map of Haiti, showing the 10 departments and locations of capital cities.**

Appendix Table 1. **Dates and Ranks of First Laboratory-Confirmed Case of Cholera, by Department***

Department	Date	Rank
Artibonite	21 October 2010	1
Ouest	23 October 2010	2
Centre	24 October 2010	3
Nord	25 October 2010	4
Nord-Ouest	26 October 2010	5
Sud	10 November 2010	6
Nord-Est	13 November 2010	7
Sud-Est	14 November 2010	8
Nippes	18 November 2010	9
Grand'Anse	19 November 2010	10

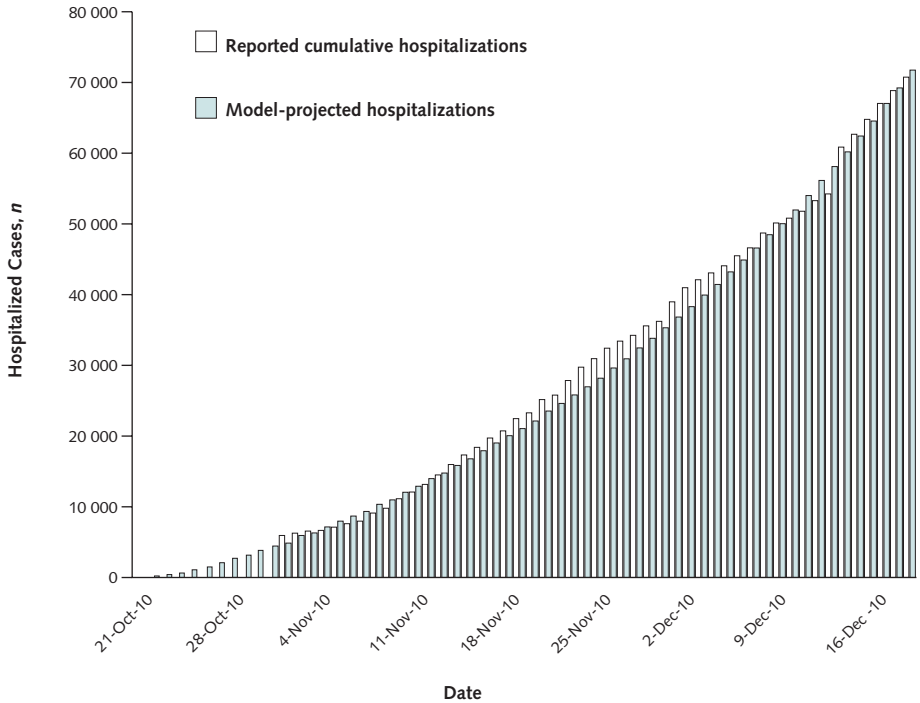
* Data from the U.S. Centers for Disease Control and Prevention (15).

Appendix Table 2. **Best-Fit Parameter Values Based on Model Fit to MSPP Hospitalization Data**

Parameter	Description	Plausible Range	Best-Fit Value
β_i	Transmissibility, case	0.010 to 0.100	0.010
β_w	Transmissibility, water	0.789 to 0.945	0.944
ξ^{-1}	Mean survival of pathogen in water (weeks)	2.743 to 5.949	5.910
γ^{-1}	Mean duration of infectiousness (days)	2.376 to 3.013	2.913
κ	Gravity constant	6.76×10^{-13} to 8.92×10^{-12}	6.83×10^{-12}
R_0	Basic reproductive number	2.07 to 2.78	2.78

MSPP = Ministère de la Santé Publique et de la Population.

Appendix Figure 3. **Model projections of overall hospitalized cases in Haiti and reported cumulative hospitalizations from MSPP data.**

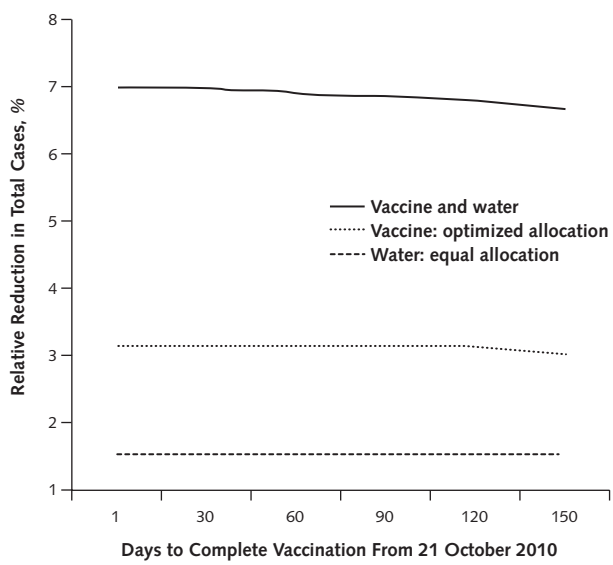


The model was well-calibrated to reported cumulative hospitalizations. MSPP = Ministère de la Santé Publique et de la Population.

Appendix Table 3. **Number of Persons Needing Clean Water to Achieve a Reduction in Case Counts of Cholera Equal to That Achievable Through Vaccination**

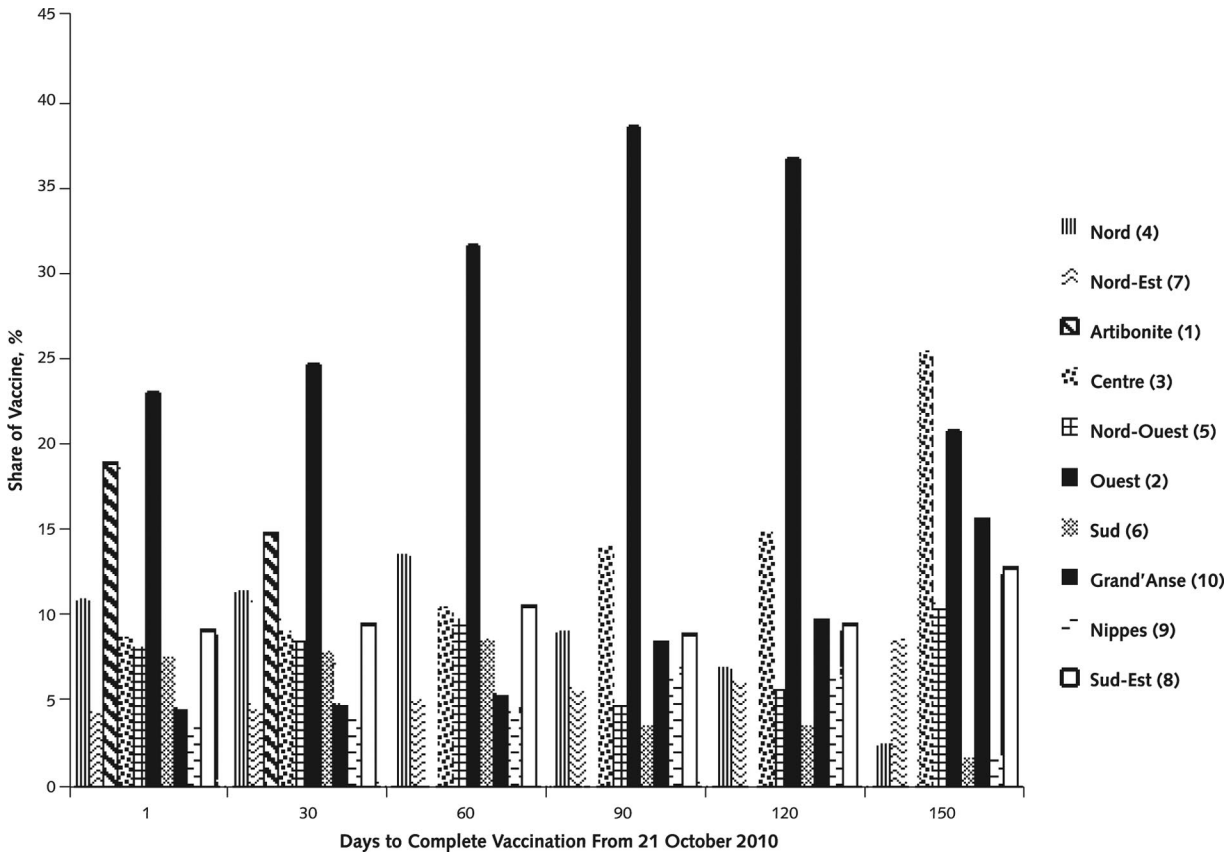
Days Since 21 October 2010	Relative Reduction in Total Cases, %	Vaccine: Optimized Allocation (Doses), *n*	Water: Equal Allocation (People), *n*	Water: Proportionate Allocation (People), *n*
1	3.09	500 000	866 840	995 996
30	3.10	500 000	867 883	997 382
60	3.10	500 000	868 823	998 773
90	3.09	500 000	870 044	1 001 230
120	3.08	500 000	872 021	1 007 110
150	3.04	500 000	871 655	1 016 010

Appendix Figure 4. **Projected effect of equal allocation of clean water to all departments, optimized allocation of vaccine, and a combination of these strategies.**



The combination strategy demonstrates a superadditive effect.

Appendix Figure 5. **Optimized allocation of limited vaccine resources, by department, according to time to complete vaccination.**



Optimized allocation of vaccine focuses largely on Ouest department, because of its large population, and Centre department, which serves as a "crossroads" for cholera spread. As vaccination is increasingly delayed, larger shares are allocated to peripheral regions where epidemics occurred later. Numbers in parentheses represent the ordering of outbreaks.