



A framework for predicting endemic cholera using satellite derived environmental determinants



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ABSTRACT

Cholera remains one of the most prevalent water-related infections in many tropical regions of the world. Macro-environmental processes provide a natural ecological niche for *Vibrio cholerae* and because powerful evidence of new biotypes is emerging, it is unlikely that the bacteria will be fully eradicated. Consequently, to develop effective intervention and mitigation strategies, it is necessary to develop cholera prediction models with several months' lead time. Almost all cholera outbreaks originate near the coastal areas and cholera bacteria exhibit a strong relationship with coastal plankton. Using chlorophyll as a surrogate for plankton bloom in coastal areas, recent studies have postulated a relationship between chlorophyll and cholera incidence. Here, we show that seasonal cholera outbreaks in the Bengal Delta can be predicted two to three months in advance with an overall prediction accuracy of over 75% by using satellite-derived chlorophyll and air temperature data. Such high prediction accuracy is achievable because the two seasonal peaks of cholera are predicted using two separate models representing distinctive macro-scale environmental processes. We have shown that interannual variability of pre-monsoon cholera outbreaks can be satisfactorily explained with coastal plankton blooms and a cascade of hydro-coastal processes. Post-monsoon cholera outbreaks, on the other hand, are related to macro-scale monsoon processes and subsequent breakdown of sanitary conditions. Our results demonstrate that satellite data over a range of space and time scales are effective in developing a cholera prediction model for the Bengal Delta with several months' lead time. We anticipate our modeling framework and findings will provide the impetus to explore the utility of satellite derived macro-scale variables for cholera prediction in other cholera endemic regions.

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1. Introduction

Cholera, an acute water-borne diarrheal disease, continues to be a significant global health threat. The ongoing seventh pandemic of cholera, which started in 1960s, has been reported in over 50 countries and has affected more than 7 million people (Gleick, 2008). The disease remains one of most prevalent water-borne infections in many tropical regions, specifically in coastal areas of South Asia, Africa, and Latin America. The life cycle of the bacterium *Vibrio cholerae*, the causative agent for cholera outbreaks, is intricately linked to two different processes: *micro*- and *macro*-environmental processes, which have vastly different spatial and

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temporal scales of interacting variables. Here, we define *micro* as microbiological, genetic, and human intestinal processes and related variables, while *macro* refers to hydrological, ecological, climatic, and coastal processes and their related variables. Despite steady accumulation of knowledge on *V. cholerae* in these two environments, our ability to adequately predict the next cholera epidemic remains limited. We recognize the importance of micro-environmental processes in understanding cholera dynamics in order to develop effective vaccines and treatment protocols. However, since *V. cholerae* thrives in a wide range of natural environmental conditions, and since evidence of new biotypes is emerging (Siddique et al., 1994), it is unlikely that this disease will be defeated by medicine alone. Rather, we need a new approach—an early cholera warning system with several months' lead time—to minimize the impact of this devastating disease by predicting where and when it will occur and then initiating effective prevention strategies. Thus, our approach attempts to identify

the macro-environmental processes and variables that have sufficient temporal and spatial “memory” to allow the development of an early cholera warning system.

Cholera in the Bengal Delta shows two seasonal peaks: one in spring (defined as the average cholera incidence in March–April–May months) and another in autumn (defined as the average cholera incidence in September–October–November months) (Jutla et al., 2010). Cholera have been associated with a wide range of environmental variables, such as sea surface temperature (SST) (Lobitz et al., 2000; Cash et al., 2008), sea surface height (Lobitz et al., 2000), monsoon precipitation (Hashizume et al., 2008), coastal plankton (Magny et al., 2008; Emch et al., 2008; Lobitz et al., 2000; Tamplin et al., 1990), air and water temperature (Islam et al., 2009; Huq et al., 2005), and coastal salinity (Miller et al., 1982). Because of the presence and survival of cholera bacteria in marine environments, the relationship between coastal plankton and cholera has also been explored (Griffith et al., 2006; Huq and Colwell, 1996; Colwell, 1996; Lobitz et al., 2000; Tamplin et al., 1990; Islam et al., 1999; Worden et al., 2006; Alam et al., 2006; Emch et al., 2008; Jutla et al., 2010).

Our recent studies have established that biannual peaks of cholera incidence in the Bengal Delta are influenced by two separate macro-environmental processes (Akanda et al., 2009, 2011). Existence of such processes for cholera and three other complementary observations motivate us to explore the utility of satellite-derived macro-environmental variables to develop a cholera prediction model: (i) almost all cholera outbreaks originate near the coastal areas, including the reemergence of cholera in Latin America in 1991 (Jutla et al., 2010; Magny et al., 2008; Emch et al., 2008; Lobitz et al., 2000; Tamplin et al., 1990); (ii) laboratory studies suggest a significant positive correlation between plankton abundance and pathogenic cholera bacteria (Colwell and Spira, 1992; Huq et al., 1990; Tamplin et al., 1990); and (iii) remote sensing provides unprecedented coverage of space-time measurements of plankton in coastal regions around the world (Uz and Yoder, 2004; Jutla et al., 2011). The overall objective of the this study was to develop a cholera prediction model using remote sensing information and limited ancillary data with two to three months' prediction lead time; and suggest a plausible pathway that provide an explanation for an environment conducive to cholera outbreak and transmission.

2. Current state of knowledge for predicting cholera

With increased availability of new sensors and remote sensing data, the opportunity to employ satellite derived data to develop predicting mechanisms for water-related diseases has increased significantly. Outbreaks of several water-related diseases such as malaria (Hay et al., 1998; Adimi et al., 2010; Elipe et al., 2007), Rift Valley Fever (Linthicum et al., 1999), Cholera (Magny et al., 2008), Cryptosporidium (Jagai et al., 2009) and Schistosomiasis (Malone et al., 2001) has been predicted through macro-environmental determinants using the latest advances in satellite remote sensing. Efforts to develop prediction models for cholera outbreak

probably started with Rogers (1958), who suggested that absolute humidity (quantity of water in a particular volume of air) might demarcate regions of epidemic and endemic cholera. Lobitz et al. (2000) was perhaps one of the first studies to use remote sensing data to explore a possible connection between SST, phytoplankton, and cholera incidence by using 16 months' of satellite data from one pixel in the Bay of Bengal. Table 1 shows three key studies that have attempted to develop cholera simulation models using micro- and macro-environmental variables. Magny et al. (2008) and Emch et al. (2008) used plankton data from the coastal Bay of Bengal region to explore the relationship between plankton and cholera incidence. Magny et al. (2008) associated cholera incidence time series with coastal chlorophyll data and reported one month's lag between cholera incidence and coastal plankton, but did not elaborate on the strength of the relationship or the plausible physical mechanism for such an association. A closer look at the regressive model structure of Magny et al. (2008) reveals that the persistence effects of the previous season's cholera incidence exceed the role of environmental processes. In other words, their model resembles a moving average type model (Table 1 in Magny et al., 2008). Using the same data, Emch et al. (2008) reported two-month lags coastal chlorophyll and cholera incidence in Bangladesh. Part of the reason for disparity in the results of Magny et al. (2008) and Emch et al. (2008) can be attributed to the choice of spatial and temporal scales of plankton data. Our study indicates that there is significant spatial variability of plankton in the Bay of Bengal; consequently, substantial spatial averaging is required before plankton data can be used to establish a cholera–chlorophyll relationship (Jutla et al., 2012). Magny et al. (2008) and Emch et al. (2008) assumed that chlorophyll, SST, and rainfall affect the disease outbreaks throughout a given year, whereas our previous studies (Akanda et al., 2009, 2011) have indicated presence of strong asymmetrical role of hydroclimatological processes in the cholera outbreaks in the Bengal Delta. Pascual et al. (2008) developed a semi-mechanistic model for simulating endemic cholera in the Bengal Delta. Their model structure involves biological variables such as disease rates and immunity levels, which are not easy to measure. In addition, Pascual et al. (2008) reported a strong correlation between cholera incidence and ENSO for three summer months only—June, July, and August—which are the three lowest cholera incidence months. While predicting the cholera outbreaks using ENSO, Pascual et al. (2008) suggested that the model failed to predict cholera outbreaks in two of five strong El Niño events. Matsuda et al. (2008) developed a regression model based on the cholera incidence time series in children who were less than 10 years old using precipitation and air temperature in Bangladesh. The authors indicated that their model cannot be generalized to the entire population; they also did not elaborate as to why precipitation and air temperature should be used as predictor variables for outbreaks of cholera.

Our analysis of the above mentioned existing cholera models (Emch et al., 2008; Pascual et al., 2008; Magny et al., 2008) indicates lack of predictive capabilities in the endemic regions because these models (i) do not capture the asymmetric hydro-climatic influence

Table 1
Available cholera prediction models.

S. No	Author	Model type	Variables	Scale (spatial, temporal)
1	Magny et al. (2008)	Regression-based	Previous season cholera incidence, chlorophyll, precipitation, SST	Monthly, regional (two cities)
2	Pascual et al. (2008)	Semi-mechanistic	Population, biological variables (immunity levels, susceptibility rates), ENSO	District level, monthly
3	Matsuda et al. (2008)	Regression-based	Rainfall, air temperature	Monthly, prediction of cholera for children, district level

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