

Original Contribution

Predicting the Distribution of *Vibrio* spp. in the Chesapeake Bay: A *Vibrio cholerae* Case Study

Guillaume Constantin de Magny,¹ Wen Long,^{2,3} Christopher W. Brown,^{2,4} Raleigh R. Hood,³ Anwar Huq,⁵ Raghu Murtugudde,² and Rita R. Colwell^{1,5,6}

¹University of Maryland Institute for Advanced Computer Studies, Biomolecular Sciences Bldg #296 room 3104H, College Park, MD 20742

²Earth System Science Interdisciplinary Center, University of Maryland, College Park, MD

³Horn Point Laboratory, University of Maryland Center for Environmental Science, Cambridge, MD

⁴National Oceanic and Atmospheric Administration, College Park, MD

⁵Maryland Pathogen Research Institute, University of Maryland, College Park, MD

⁶Department of Environmental Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD

Abstract: *Vibrio cholerae*, the causative agent of cholera, is a naturally occurring inhabitant of the Chesapeake Bay and serves as a predictor for other clinically important vibrios, including *Vibrio parahaemolyticus* and *Vibrio vulnificus*. A system was constructed to predict the likelihood of the presence of *V. cholerae* in surface waters of the Chesapeake Bay, with the goal to provide forecasts of the occurrence of this and related pathogenic *Vibrio* spp. Prediction was achieved by driving an available multivariate empirical habitat model estimating the probability of *V. cholerae* within a range of temperatures and salinities in the Bay, with hydrodynamically generated predictions of ambient temperature and salinity. The experimental predictions provided both an improved understanding of the *in situ* variability of *V. cholerae*, including identification of potential hotspots of occurrence, and usefulness as an early warning system. With further development of the system, prediction of the probability of the occurrence of related pathogenic vibrios in the Chesapeake Bay, notably *V. parahaemolyticus* and *V. vulnificus*, will be possible, as well as its transport to any geographical location where sufficient relevant data are available.

Keywords: *Vibrio cholerae*, forecast, Chesapeake Bay, habitat models, pathogens

INTRODUCTION

The Chesapeake Bay is the largest estuary in North America and represents a valuable socioeconomic resource for the region. The sport fishing industry alone yields nearly \$300 million annually, and both swimming and boating are supported by the beaches and safe harbors of the Bay. Vast

wetlands surround the Chesapeake Bay and its tributaries, offering haven for a rich diversity of wildlife and migratory bird populations. The Chesapeake Bay is also the largest producer of blue crabs in the world (<http://www.waterencyclopedia.com/Ce-Cr/Chesapeake-Bay.html>). Unfortunately, events associated with human activity, as well as natural environmental changes, jeopardize viability of this important natural resource.

The natural microbial flora of the Chesapeake Bay includes several species of *Vibrio*, some of which are

Correspondence to: Guillaume Constantin de Magny, e-mail: magny@umi.acs.umd.edu

pathogenic (Colwell et al., 1977). *V. parahaemolyticus* and *V. vulnificus*, for example, can cause serious enteric disease after ingestion of raw or undercooked seafood carrying these bacteria, or in some cases, fatal wound infection. *Vibrio cholerae* was first isolated from the Chesapeake Bay in 1977 (Colwell et al., 1977), and toxigenic strains of *V. cholerae* serogroup O1, the causative agent of cholera epidemics, continue to be identified in the Chesapeake Bay, after having been first reported in 1980 (Colwell et al., 1981). *V. cholerae* O1 is now known to be autochthonous to the Bay and its tidal tributaries (Heidelberg et al., 2002; Louis et al., 2003; Grim et al., 2008). Cholera was once considered “America’s greatest scourge” (Chambers, 1938), after its widespread ravages in 1849 from New York to New Orleans. However, with improvement in sanitation and public health by the early 1900 s, cholera gradually disappeared, with reappearance in the United States in 1973 in Texas (Weissman et al., 1974). Since then, sporadic cases have been reported each year in the United States and confirmed as indigenous in origin (Blake, 1994).

The precise mechanisms and environmental interactions that give rise to increased numbers of *V. cholerae* in an aquatic environment have yet to be fully understood, and this is coupled with the fact that it is not yet possible to construct mechanistic models for prediction of their presence and abundance with exquisite accuracy. Habitat preferences of *V. cholerae* have been characterized reasonably well, and statistically significant empirical relationships have already been established between presence of *V. cholerae* and selected environmental factors, such as sea-surface temperature and salinity (Lipp et al., 2002; Louis et al., 2003). Temperature and salinity affect the growth rate of *V. cholerae* and are associated with higher rates of isolation of *V. cholerae* from environmental samples. Optimal salinity for growth of *V. cholerae* is between 5‰ and 25‰, but *V. cholerae* can both exist and thrive in freshwater (Singleton et al., 1982; Heidelberg et al., 2002; Louis et al., 2003). With sufficient dissolved organic matter present, *V. cholerae* can grow well at salinities as high as 45‰ (Singleton et al., 1982). Several parameters, such as pH and salinity, have been shown to affect survival and multiplication of *V. cholerae* (Singleton et al., 1982; Huq et al., 1984).

The appearance of culturable *V. cholerae* in the Chesapeake Bay occurs under certain environmental conditions (Heidelberg et al., 2002; Louis et al., 2003). The abundance of vibrios increases seasonally during warmer months of the year, when pathogenic vibrios pose an increased risk of

infection for humans, more so with global warming (Lipp et al., 2002). As an increasingly larger percentage of the population occupies the coastal regions of the world, exposure to pathogenic *Vibrio* spp. will also increase (Goudarzi, 2006) (see also http://www.livescience.com/environment/060718_map_settle.html). Therefore, a prediction system for *V. cholerae* and related vibrios would be highly advantageous for prevention and mitigation of *Vibrio* infections, on both short- and long-time scales. Short-term predictions can enhance first responder capability, while longer term forecasts can be used to simulate potential consequences of climate change on microbial pathogens, not only in the Chesapeake Bay, but also in other estuaries globally. In addition, retrospective predictions or hindcasts can be used to explore the causes associated with *Vibrio* population increases and aid in anticipating the potential impact of climate change on their distribution. Understanding connections between the oceans and human health is crucial to address emerging and reemerging diseases (Watkins and Huq, 2002).

In the study reported here, a system was developed and implemented that generates predictions of the likelihood of *V. cholerae* in the Chesapeake Bay by exploiting what is known about the optimal physical habitat of *V. cholerae* and taking advantage of recent advances in technology and telecommunications to retrieve, simulate, and forecast relevant environmental conditions. The prediction system identifies geographic locations in the Chesapeake Bay where environmental conditions coincide with the preferred physical habitat of *V. cholerae*. This general approach has also proven to be effective for predicting the likelihood of encountering sea nettles (*Chrysaora quinquecirrha*), a stinging jellyfish in the Chesapeake Bay (Decker et al., 2007), and is being implemented for several harmful algal bloom species. In this article, we introduce the prediction system and its products, and examine their potential applications. In particular, we employed hindcasts of *V. cholerae* probability to explore the relationship between river flow and *V. cholerae* presence in the Bay.

MATERIALS AND METHODS

Daily hindcasts, nowcasts, and 3-day forecasts of the likely presence of *Vibrio cholerae* in the Chesapeake Bay were generated by identifying geographic locations in the Bay where ambient conditions coincide with its preferred range of sea-surface temperature (SST) and salinity. A habitat

suitability model, developed previously for *V. cholerae* O1 in the Bay (Louis et al., 2003), was implemented with real-time SST and salinity grid cells simulated by the Regional Ocean Modeling System (Wilkin et al., 2005) configured for the Chesapeake Bay.

***Vibrio cholerae* Empirical Habitat Suitability Model**

An existing logistical regression model (Eq. 5 in Table 7 of Louis et al., 2003) was employed to predict the likelihood of the presence of *V. cholerae* in the Chesapeake Bay. The logit model for *V. cholerae* was derived from data gathered using a direct fluorescent-antibody assay (DFA O1) ($Vchol_{DFA}$) method that detects both culturable and viable but non-culturable (VBNC) *V. cholerae* O1 serogroup (Chaiyanan et al., 2001). VBNC organisms exhibit detectable metabolic function, but are not culturable by conventional laboratory culture methods (Xu et al., 1982). The empirical habitat model is based on temperature (T), salinity (S), and an interactive term between temperature and salinity:

$$\log it(Vchol_{DFA}) = -1.1939 + 0.1233 \times T - 0.1997 \times S - 0.0324 \times T \times S \quad (1)$$

The probability of *V. cholerae* presence from the model was estimated using $p = e^{\log it} / [e^{\log it} + 1]$, where $\log it$ refers to the logit of the model.

Agreement between observed value and the value predicted by the logistic model was 76.9% ($n = 108$) (Louis et al., 2003). The habitat suitability model is forced by simulated SST and sea-surface salinity in the Chesapeake Bay using the Chesapeake Bay Regional Ocean Modeling System (ChesROMS).

Chesapeake Bay Regional Ocean Modeling System

ChesROMS is an open source Chesapeake Bay implementation of the Regional Ocean Modeling System (ROMS), a community ocean model developed and maintained by Rutgers University (<http://www.myroms.org/>). ROMS/ChesROMS is a free-surface, terrain-following, primitive equations model widely used by the scientific community for a diverse range of applications. The physical model is based on finite difference for curvilinear orthogonal grids (Arakawa and Lamb, 1977) and vertically terrain-following sigma coordinates, with time integration split into external mode and internal mode for primitive hydrodynamic variables, including surface elevation, velocity, and many

passive and active tracers (e.g., temperature, salinity, etc.). ChesROMS uses historical reanalyses, near-real time observations, and forecast data to provide model external forcing, such as atmospheric momentum and heat fluxes, river outflow and ocean sea level, to simulate salinity, temperature, and other physical variables in the Bay to enable hindcasts, nowcasts, and forecasts of *V. cholerae*.

ChesROMS (v1.2) consists of a 150×100 cell horizontal grid and 20 layers vertically to yield spatial resolutions in the horizontal that range from 500 m to 5 km and in the vertical ranging from 0.2 to 1.5 m. Additional information about ROMS and ChesROMS can be found at <http://ches.communitymodeling.org/models/ChesROMS/index.php> (Xu et al., manuscript in preparation).

ChesROMS is the hydrodynamic component of the Chesapeake Bay Prediction System. The prediction system is comprised of a suite of Unix Shell scripts, Perl scripts, Fortran and C programs, NCL programs, MATLAB scripts, and GIS shape files that automatically perform the tasks of compiling the model input files from observations, running the model, processing the model output, and displaying the graphical products on a dynamic, interactive website.

Model Predictions

Forecasts

Both short- and long-term forecasts of *V. cholerae* probability of occurrence were generated by applying the habitat suitability model with forecasted SST and salinity. Forcings for short-term forecasts were acquired from the same database used to generate hindcasts, except atmospheric forcing quantities, including 3-hourly winds, net shortwave and downward longwave radiations, air temperature, relative humidity, and pressure, obtained from the National Center for Environmental Prediction (NCEP) North American Mesoscale (NAM) model. For long-term forecasts, downscaling with a regional Earth System Model was performed with the Weather Research and Forecasting (WRF) model coupled to the NOAA (http://www.emc.ncep.noaa.gov/mmb/gcp/noahslm/README_2.2.htm) Land-Surface Model (LSM) (Ek et al., 2003) to drive ChesROMS, where seasonal to interannual forecasts from NCEP provide boundary conditions (Murtugudde, 2009b). The same arrangement is also used for decadal projections by downscaling Intergovernmental Panel on Climate Change (IPCC) scenarios.

Hindcasts

The prediction system generated daily retrospective predictions, or hindcasts, of *V. cholerae* probability ($V_{chol_{DFA}}$) for a 15-year period from 1991 to 2005. Nine tidal constituents from the Advanced Circulation Model for Coastal Ocean Hydrodynamics (ADCIRC) model and non-tidal water levels were combined to provide boundary sea-surface height change to the model. The non-tidal water level data were retrieved from the NOAA National Ocean Service webpage, which provides historical and real-time observed data by monitoring stations located at Wachapreague, Virginia, and Duck, North Carolina. Numerically, the Chapman condition for surface elevation and the Flather condition for barotropic velocity were applied to the barotropic component (depth-averaged, fast propagating surface wave mode) at the open-ocean boundary. For the baroclinic component, radiation condition was used for velocity and radiation condition with nudging for temperature and salinity. Daily freshwater discharge data for nine major tributaries from the United States Geological Survey (USGS) stream water monitoring website were applied at upstream river boundaries. Monthly climatological temperature and salinity from the World Ocean Atlas (WOA, 2001) database were used, with a nudging technique to prescribe temperature and salinity changes at the mouth of Chesapeake Bay. Atmospheric forcing, including 3-hourly winds, net shortwave and downward longwave radiation, air temperature, relative humidity, and atmospheric pressure were obtained from the North American Regional Reanalysis (NARR) produced at NCEP (<http://www.emc.ncep.noaa.gov/mmb/rrean/>).

Variability of *V. cholerae* in the Chesapeake Bay

The 15-years of daily hindcasts were used to pinpoint “hotspots” of predicted *V. cholerae* presence in the Chesapeake Bay, to examine the seasonal and interannual variability of their likely presence in these locations, and to explore the potential factor(s) behind the variability. The year 2005 was selected as baseline because it possessed the smallest anomalies in *V. cholerae* probabilities over the 15-year period (1991–2005) examined. Regions in the Chesapeake Bay with the highest probability of presence of *V. cholerae* were located by identifying where the annual sum of probabilities of daily predictions was greater than 30 in the year 2005. Over the 15,000 pixels of the model grid, 4702 correspond to water for which the range of the yearly

sum is from 0 to 244.48, and was greater than 30 for 776 pixels (16.5%), representing areas where the variability is concentrated. To illustrate the temporal variability of *V. cholerae* probability in the Bay, we computed the spatial mean probability for *V. cholerae* presence in these “hot-spot” regions.

Wavelet analysis was performed on the time-series of daily hindcasts to extract the significant frequency modes of *V. cholerae* probability and determine its underlying dynamics with simulated water-surface SST and sea-surface salinity, and actual river flow. Wavelet analysis was employed because ecological and environmental time-series are typically nonstationary, i.e., their dominant periodic components change over time, and these characteristics may render traditional correlation or spectral techniques, such as Fourier analysis, inappropriate to analyze the temporal trend of local variations in the frequency and periodicity of the variable in question, in this case *V. cholerae* probability, in the time series. Wavelet analysis is an extensively used technique in ecology and epidemiology to explore the spatial and temporal dynamics of time-series (Grenfell et al., 2001; Broutin et al., 2005; Constantin de Magny et al., 2007; Cazelles et al., 2008; Kausrud et al., 2008). The Morlet wavelet was employed (Cazelles et al., 2008) with wavelet decomposition for the periodic band between 0.3 (= 4 months) and 5 years for the 15-year period (1991–2005). River flows were examined because salinity distribution in the Chesapeake Bay is largely driven by riverine input of freshwater. They also represent a relatively independent variable, as the simulated SST and salinity were employed to derive the probability of *V. cholerae* presence, though the same river flow data were used to force ROMS.

RESULTS

Forecasts

Experimental short-term predictions, i.e., nowcasts and 3-day forecasts of *V. cholerae* likelihood in the Chesapeake Bay (Fig. 1), are created and staged on the “Mapping Pathogens in the Chesapeake Bay” website for dissemination (<http://155.206.18.162/pathogens/>). The website supports typical capabilities, e.g., zooming and panning, and will shortly stage shapefiles of the forecasts for water quality experts and coastal managers. The same habitat model is employed to routinely issue experimental 16-day forecasts

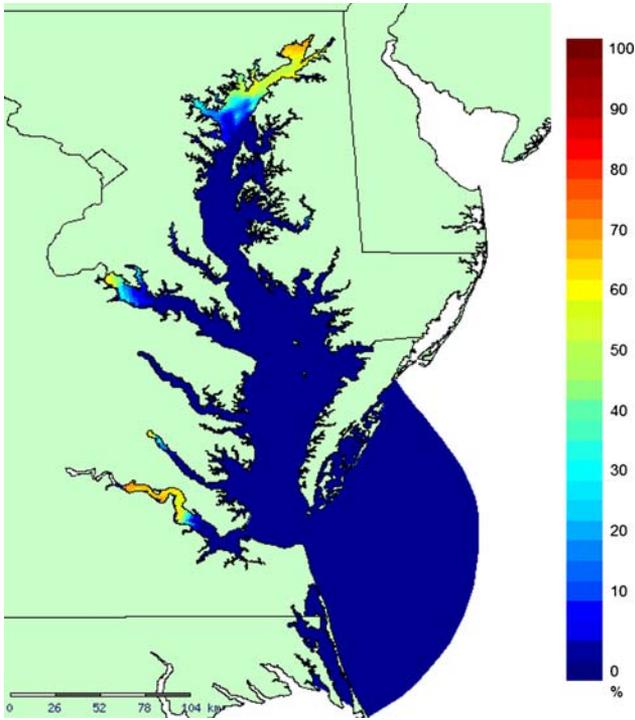


Figure 1. Nowcast illustrating the likelihood of *Vibrio cholerae* O1 presence for June 9, 2007 generated by the Chesapeake Bay pathogen prediction system. Land is colored green and state lines are given in black.

of *V. cholerae* generated with the dynamically downscaled atmospheric forcing supplied by WRF (not shown).

Hindcasts

Daily hindcasts of the likelihood of *V. cholerae* from 1991 to 2005 indicate the highest probabilities of *V. cholerae* were generally located in the outflow of the Susquehanna River and the upper reaches of the Potomac, Rappahannock, York, and James Rivers on the west side of the Bay, and the Choptank River on the eastern shore during the months of late spring and early summer. Probabilities were generally very low (<5%) in the main stem of the Bay south of Baltimore, and the remaining embayments and rivers on the eastern shore. For example, the area where annual accumulative probability was equal to, or exceeded, 30 in 2005 was greatest in the outflow of the Susquehanna (455 model grid cells), followed by the upper reaches of the western estuaries (261 grid cells) and Choptank River (20 grid cells) (Fig. 2a), and the predicted daily mean probability of *V. cholerae* exceeded 0.50 from April to July in all regions (Fig. 2b–d), though with considerable variability between and within individual locations. Daily

probabilities decreased dramatically, for instance, in the Choptank River (Fig. 2b) in July, though reduced more gradually in the western estuaries and Susquehanna outflow (Fig. 2c, d).

The patterns of predicted *V. cholerae* probability observed in 2005 are a result of the temporal variations of SST and salinity at the three identified “hotspot” locations (Fig. 3). The patterns of mean SST are similar among all regions, with a minimum observed in February, a progressive and regular increase through the summer months of July and August, followed by a decrease in September. Sea-surface temperature exhibited little variance in all regions. Mean predicted salinity also followed a similar pattern in all regions, gradually increasing from low in April to high in October, though importantly, the maximum mean salinity achieved was higher in the Choptank area ($\sim 10\text{‰}$) than the Susquehanna Flat and western estuaries ($\sim 6\text{‰}$) (Fig. 3). Variances of predicted salinities were also much larger than that for SSTs in all regions. The difference between the pattern of predicted mean probability of *V. cholerae* in the Choptank and at the two other sites appears to be the result of different salinity patterns. Predicted *V. cholerae* increases during the early spring (Fig. 2), due to increases in SST, while salinity remains low (Fig. 3). However, when salinity exceeded a threshold of approximately 4‰ , the predicted *V. cholerae* probability decreased. In the Choptank, the probability declined to zero when the salinity rose to greater than 8‰ .

In summary, the predicted likelihood of *V. cholerae* follows closely the pattern of water SST when salinity remains low, as expected from the habitat suitability model employed (Eq. 1). The likelihood of *V. cholerae* presence at salinities greater than 8‰ is low, even at optimum water SST.

Considerable interannual variability in hindcasts of daily area mean *V. cholerae* likelihood exists between 1991 to 2005 for the three hotspots identified previously (Fig. 4). The Choptank region, in particular, experiences a larger swing in average *V. cholerae* probabilities, with maximum predicted area mean probabilities ranging from approximately 0.1 in 2002 to 0.9 in 2003. The annual likelihood of *V. cholerae* in the three hotspot regions follows a similar pattern, with some years exhibiting greater probabilities and others less (Fig. 5). Positive anomalies were observed simultaneously in the three locations for the years 1994, 1996, 2003, and 2004, and negative anomalies for the years 1991, 1992, 1995, and

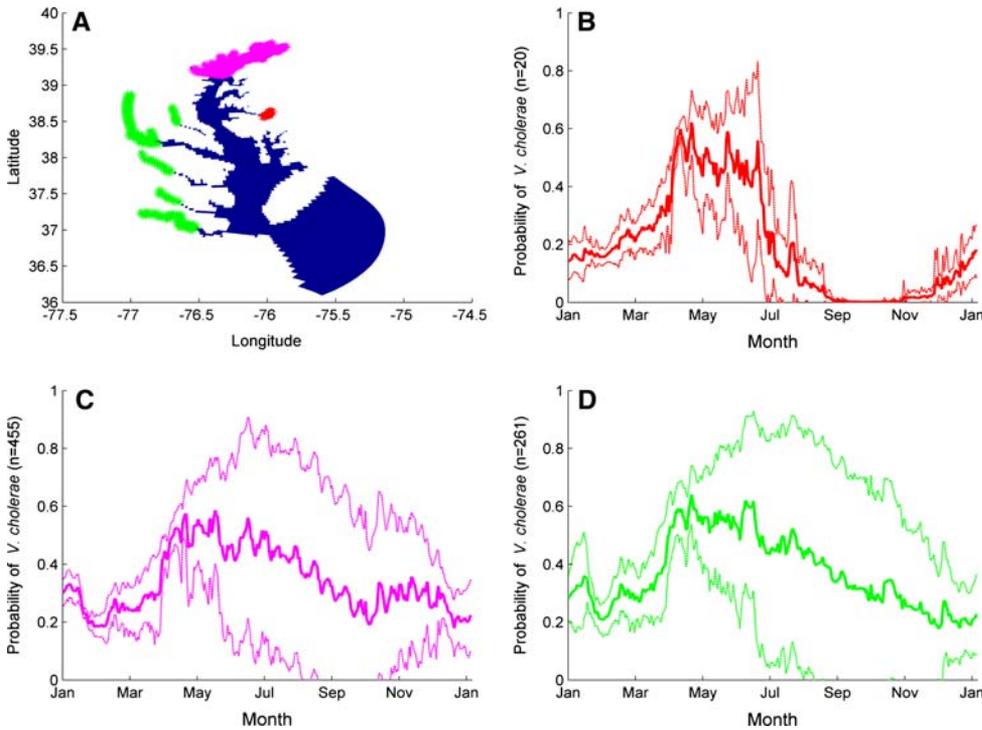


Figure 2. a Locations where the annual sum of *V. cholerae* probabilities ($V_{chol_{DEA}}$) in 2005 were greater than 30. Mean (*bold line*) and \pm standard deviation (*line*) of *V. cholerae* probability in the b Choptank River estuary, c Susquehanna flat area, and d Western estuaries in 2005.

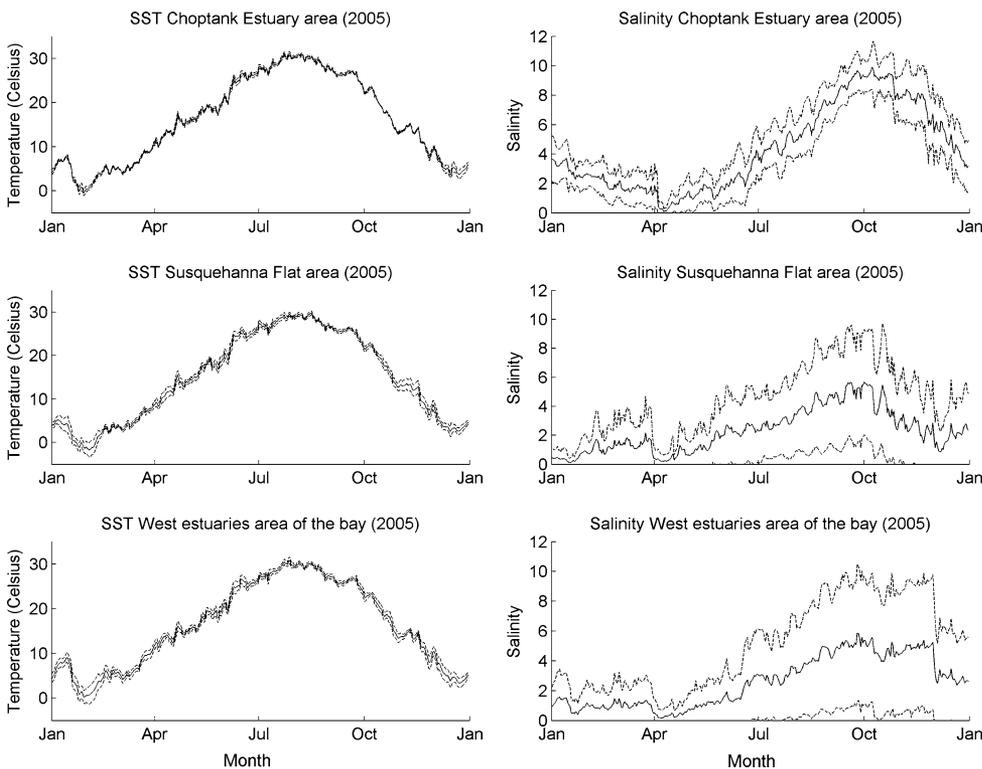


Figure 3. Daily mean (*solid line*) and \pm standard deviation (*dashed line*) of simulated sea-surface temperature and salinity by the hydrodynamic model (ROMS) for the Choptank estuary (*top panel*), Susquehanna flats (*middle*), and Western estuaries (*bottom*).

1999 through 2002. Annual anomalies of the *V. cholerae* predictions are correlated negatively with anomalies in salinity and positively with river flow in all regions. Consequently, the likelihood of *V. cholerae* is expected to

be higher than normal during periods of greater than average river flow, which creates lower than average salinity conditions. For instance, 1996 was a wet year and predicted *V. cholerae* probabilities were higher than

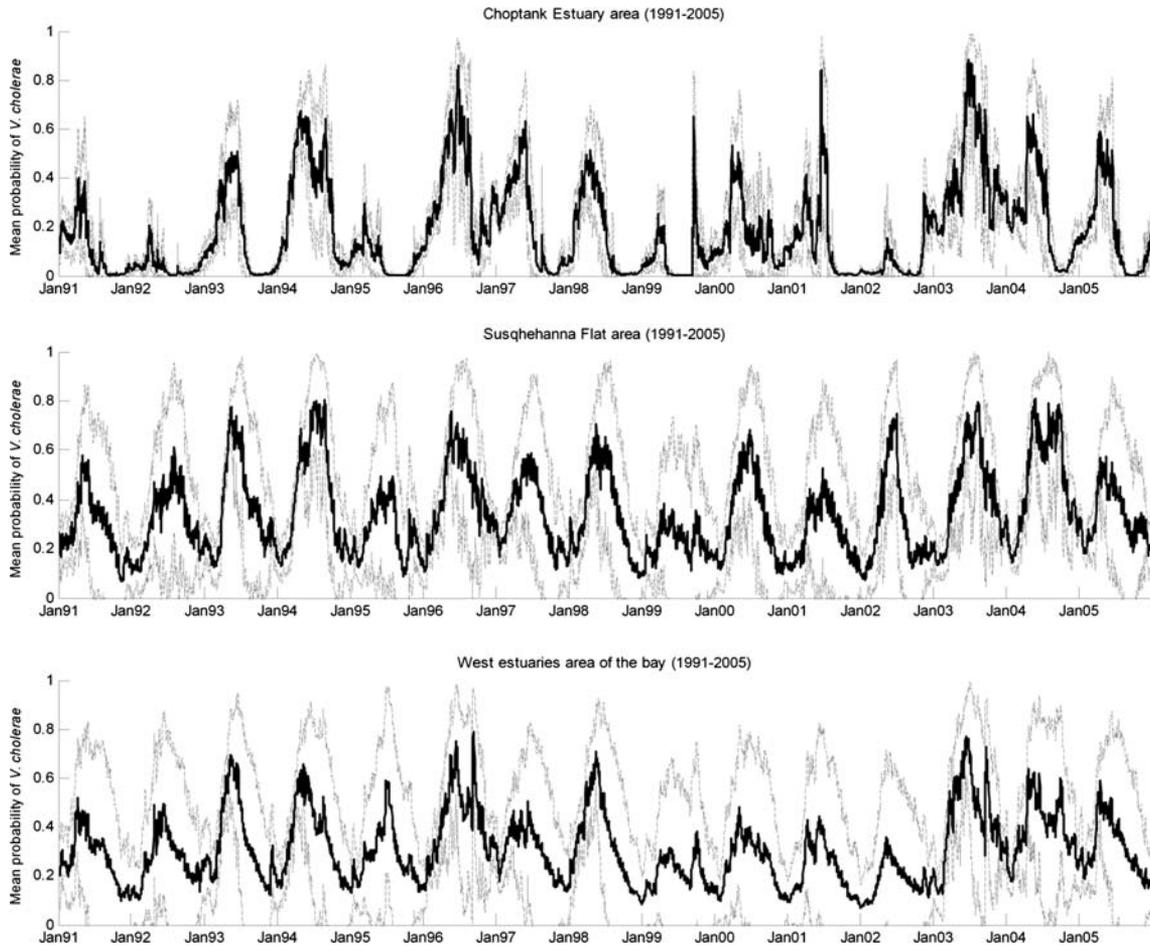


Figure 4. Daily mean (solid bold line) and \pm standard deviation (dashed line) of predicted *Vibrio cholerae* O1 presence from 1991 to 2005 in the Choptank River estuary (top panel), Susquehanna flats (middle), and Western estuaries (bottom).

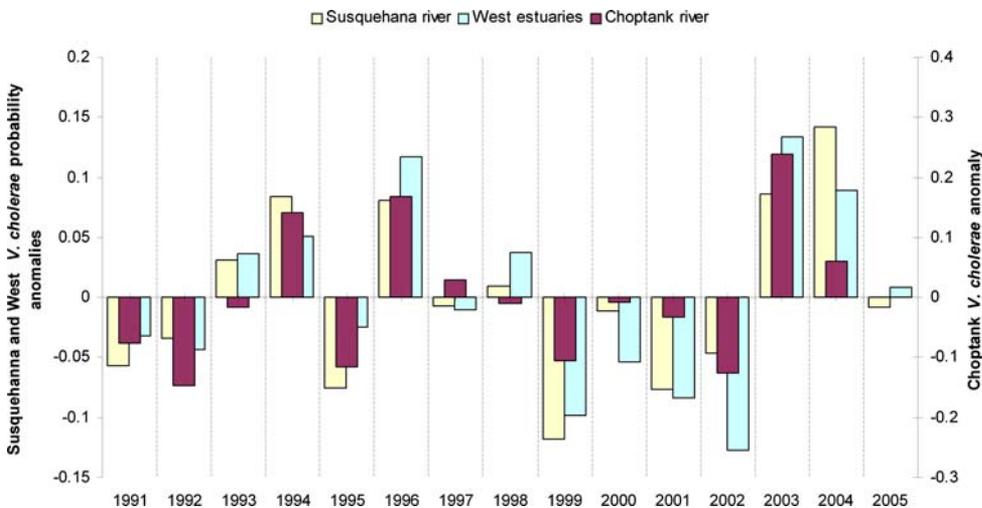


Figure 5. Annual anomaly of *Vibrio cholerae* probability for the period between 1991 and 2005 in the Choptank River, Susquehanna estuary, and Western estuaries. Anomalies of *V. cholerae* probabilities are plotted on the left y-axis for Susquehanna estuary and Western estuaries, and on the right y-axis for Choptank River.

normal, while 1999 was a dry year and predicted probabilities were reduced greatly relative to the norm. Years 1997, 1998, and 2005 appeared to be close to the norm,

with 2005 being the closest. No significant relationships were observed between annual anomalies of *V. cholerae* and SST.

Wavelet analysis, illustrating the evolution of periodic components over time in signal, of the hindcasts of *V. cholerae* probability, simulated SST and salinity, and river flows, reveal a complex nonlinear dynamics, with strong seasonality, multiyear oscillations, and nonstationarity over the 15-years (1991–2005) examined (Fig. 6). The annual cycle of the *V. cholerae* time series, present and significant in all three locations, was more pronounced in the Susquehanna and western estuaries areas than in the Choptank River. The Choptank displayed more interannual variability than the other two regions, exhibiting statistically significant common modes of oscillation of *V. cholerae* probability at periods of both 2 years and 3.5–4 years (Fig. 6, top row). Seasonal to interannual variability was also evident at these periodic ranges in simulated salinity (Fig. 6, second row), whereas the seasonal pattern dominated in simulated sea-surface temperature (Fig. 6, third row). The wavelet power spec-

tra of river discharge of the three regions were similar to the salinity spectra (Fig. 6, fourth row). Some of the observed differences in variability between regions may arise from reduced variability caused by averaging a larger number of estimates in the Susquehanna ($n = 455$) and western estuaries ($n = 261$), than the Choptank ($n = 20$), reflected by higher standard deviation of the spatial means for these locations (not shown).

As expected, the wavelet power spectra of *V. cholerae* predictions were a combination of variability observed in surface salinity and SST in the three hotspot regions. More specifically, salinity dominated interannual variability of *V. cholerae* prediction while the annual cycle was reinforced by SST (Fig. 6). More importantly, the scales of variability in *V. cholerae* predictions were very similar to the significant oscillating modes of river runoff—the main driver of the salinity in these tributary estuaries—in each of the three regions.

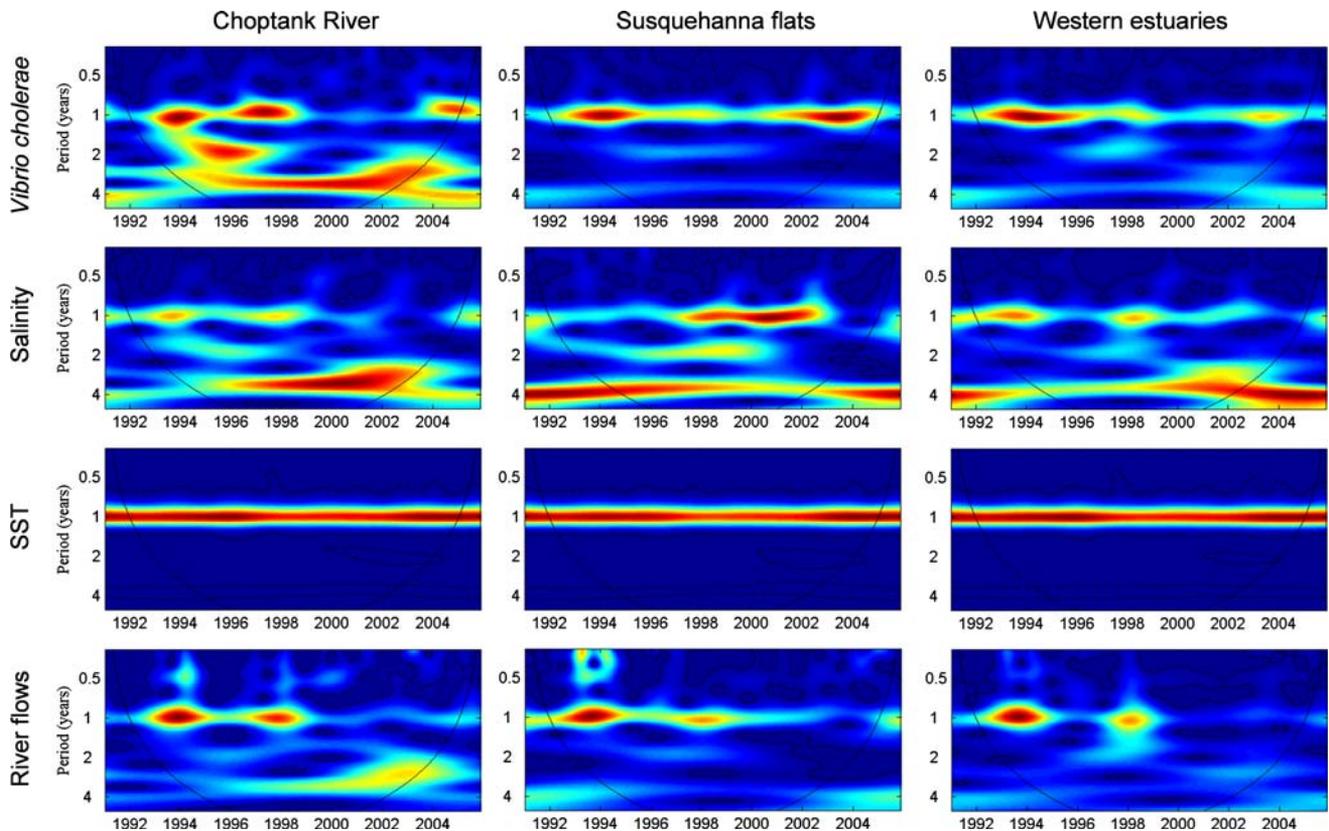


Figure 6. Wavelet power spectra of *V. cholerae* probability (first row), simulated salinity (second) and sea-surface temperature (third), and river flow (fourth) in the Choptank River (left column), Susquehanna flats (middle), and Western estuaries (right). The black

dashed lines delineate the $\alpha = 5\%$ significant levels computed based on 500 bootstrapped series. The solid black lines represent the cone of influence, indicating the region is not influenced by edge effects. Power values range from low values in dark blue to high in dark red.

DISCUSSION

The capability to predict *Vibrio cholerae* is invaluable and offers many potential benefits. Once validated, the short-term forecasts will be useful in identifying locations of probable *Vibrio* presence. This capability will enable individuals and public health agencies to efficiently direct sampling of microbial populations for research and management activities, and government agencies to guide pathogen monitoring programs and enhance first responder capabilities, thereby minimizing the impact of *V. cholerae* on recreational and commercial activities in the Chesapeake Bay and its tributaries. Thus, the system provides a basic understanding and early warning system for increase in those microbial populations that threaten human health and, thereby, will help to mitigate deleterious effects on the health of both humans and the ecosystem.

Long-term forecasts of the probability of *Vibrio cholerae* and other pathogenic *Vibrio* spp. can be used to: (1) examine potential implications of management policies, such as land-use change and agricultural practices, on *Vibrio* populations; (2) anticipate the potential impact of extreme climate events on *Vibrio* populations; and (3) explore the potential response of *Vibrio* distribution to prescribed climate change scenarios and plan for associated threats to public and ecosystem health.

The probability of *Vibrio cholerae* presence is related positively to river flow through its effect on salinity. Increasing regional precipitation, without changing other factors, will increase freshwater flow into the Bay and consequently increase the probability of *V. cholerae*. This is particularly important in the context of climate change, which is expected to increase temperature and the intensity and frequency of extreme climate events, such as heavy rainfall, intense tropical storms, and hurricanes (Boesch, 2008). These events will directly influence river flow and the entire ecosystem function, increasing the probability of contact between natural pathogenic bacterial populations in the Chesapeake Bay and the human population.

Global climate change has been correlated with adverse health effects via exposure pathways associated with frequency or intensity of extreme climate and hydrological events, such as heat waves, floods, and droughts (Patz et al., 2000). Related studies employing a global climate model (GCM) have projected change in the global climate, even in those regions that may experience reduction in mean precipitation (Frei et al., 2006; Madsen and Figdor, 2007).

Changes in precipitation extremes in the United States are already apparent in the weather records and are becoming more frequent and more intense (Gleason et al., 2008). In the Chesapeake region, the sea level has been projected to rise, as a result of global warming, approximately 10 inches by 2030 and up to 25 inches by 2100 (Boesch, 2008).

The large salinity gradient, from oligohaline in the upper estuary to polyhaline in the lower Bay, makes it a challenge to predict future salinity change influenced by global climate change. According to the above analysis, areas where *V. cholerae* has a suitable habitat are mainly in the low salinity environment. The physical balance between fresh water river loading and salinity intrusion from tidal mixing, estuarine exchange flow, and sea level rise, dictates the salinity regime where *V. cholerae* is forecasted. While sea level rise is most likely to increase the salinity of the upper Chesapeake Bay (Najjar et al., 2000; Neff et al., 2000), river flow is largely influenced by precipitation and snowpack melting within the watershed. In the mid-Atlantic, the annual streamflow change is 1.5–2.0 times the annual precipitation change on a fractional basis (Sankarasubramanian et al., 2001). Hence, the implications of climate change effect on stream flow and the salinity regime in tributaries of the Chesapeake Bay watershed are highly sensitive to climate change. While the sea level rise in the Chesapeake Bay and cultural eutrophication have a clear increasing trend along with the temperature (Kemp et al., 2005; Chesapeake Bay Foundation, 2007), very little is known about the climatic connection of the Chesapeake Bay or its watershed response to modes of climate variability such as the El Niño–Southern Oscillation (ENSO) (Trenberth, 1997), the North Atlantic Oscillation (NAO) (Hurrell et al., 2001), or the Pacific Decadal Oscillation (PDO) (Mantua et al., 1997). There may be some modulation of the high-frequency variability by ENSO as seen in a very short time-series on the water level at the head of the Bush River in the upper Chesapeake Bay (Pasternack and Hinnov, 2003). Miller and Harding (2007) note significant differences in spring blooms following a warm/dry or a wet/cool winter in situ and remotely sensed chlorophyll, but they do not attribute the winter conditions to NAO or ENSO. Our own analyses showed small, albeit statistically significant, correlations between total runoff into the Bay and the PDO index, and between the surface chlorophyll and the ENSO index (not shown). For ecosystem forecasting, we need to extract seemingly weak climatic connections (Taylor et al., 2002). This will require development of a high-resolution dynamic,

or statistical downscaling, in the framework of regional Earth System modeling for mechanistic and empirical forecasts tailored for human health applications, as presented as a prototype here.

With challenges in validation, uncertainties, and skill assessment remaining to be overcome, the motivation is to demonstrate the potential for Earth System prediction, and this is but one of a suite of forecasts, including sea nettles, striped bass, and some harmful algal blooms (Murtugudde, 2009b). Ecosystem forecasting will remain a challenge because the uncertainties not only cascade from physical downscaling to the impact models, but may also amplify (Giorgi and Diffenbaugh, 2008). However, it is known that ecosystems are able to amplify climatic links that may be weak in each physical variable but additive for ecosystem components (Taylor et al., 2002). The challenge is to construct ecosystem models as mechanistic as possible, so that climatic links are fully exploited. The mechanistic pathway for *V. cholerae* will likely involve incorporating specific aspects of its reservoir, i.e., copepods (Huq et al., 1983), in the ecosystem models embedded in ROMS.

Validation is obviously critical for public health applications and represents the next step in the development of a working system, i.e., more data will be gathered for other geographical locations on *V. cholerae* abundance and variability that can be directly compared with the model predictions for the Chesapeake Bay (Murtugudde, 2009a, 2010). To overcome limitations in ground truth data availability of *V. cholerae* for skill assessment of the forecast, similar sample collection and pathogen detection as was carried out by Louis et al. (2003) is now underway in a new study.

The prediction system employed in this study will include additional pathogen species of importance, such as *V. parahaemolyticus* and *V. vulnificus*, once habitat suitability models are developed for the target species for the Chesapeake Bay. *V. parahaemolyticus* can infect individuals who ingest raw or undercooked seafood contaminated by the pathogen. Symptoms typically include diarrhea and abdominal cramps, and occasionally wound or ear infections (Daniels et al., 2000). The Food and Drug Administration (FDA) mandated the *V. parahaemolyticus* Task Force to conduct a risk assessment characterizing public health impact associated with consumption of raw oysters contaminated with *V. parahaemolyticus* (Miliotis and Watkins, 2000). Regulations are now enforced as a preventive measure to control *V. parahaemolyticus* in oysters after harvest, namely closing shellfish harvesting if

10,000 viable *V. parahaemolyticus* per gram of shellfish are present (Miliotis and Watkins, 2000). *V. vulnificus* is a widespread and important component of the bacterial population of the Chesapeake Bay (Wright et al., 1996), and is more prevalent when water temperatures are warm (Kelly, 1982; Tamplin et al., 1982; Wright et al., 1996). Reports of illness and death in the USA caused by *V. vulnificus*, resulted in the establishment by the Interstate Shellfish Sanitation Conference (ISSC) of a *V. vulnificus* interim control plan in 1995 for oysters.

The regional Earth System modeling approach described here to generate long-term forecasts responds to the need for high-resolution, downscaled fields of air and watersheds and land use change impacts on coastal water and human health (Murtugudde, 2009b). Efforts to provide an holistic approach are underway, with encouraging early successes (Lehodey et al., 2008). Regional configurations of two models (Earth Science System Interdisciplinary Center [ESSIC]—Biogeochemical Circulation Model [BOGCM] and ROMS) have been established for the Indian Ocean, including river discharge and the Indonesian throughflow. The ecological approach developed in this study can, by optimization, be expanded to address waterborne diseases regionally, nationally, and globally.

CONCLUSION

Globally, cholera has reemerged as a global killer, with an unprecedented rise in cholera cases since 1990, and has become a major public health concern for the World Health Organization (Collins, 2003). Cholera remains endemic in regions of the developing world, specifically in coastal areas of South Asia and in countries surrounding the northern Bay of Bengal, a marginal sea of the Indian Ocean. In the United States, 7 to 8 million cases of illness and 1200 deaths are attributable to waterborne infections, in general, annually (Leclerc et al., 2002). The innovative prediction system presented here is one of a suite of tools that will identify and predict coastal ocean-related public health risks from pathogens, with the objective of alleviating waterborne health risk, representing a step toward developing a robust ecological forecasting capability. Short-term predictions identify potential hot-spots likely to harbor *V. cholerae* and these can be used to develop an early warning system, thereby enhancing first responder capability. Application of this system to geographical locations of epidemiological interest, where sufficient relevant data

are available, will be especially valuable (Constantin de Magny et al., 2008). Despite the lack of historically complete sets of data for validation, the prototype system can be expanded to include additional target species and applied to other geographical regions.

ACKNOWLEDGEMENTS

GCdeM and RRC were funded in part by National Institutes of Health Grant No. 1 R01 A139129 and National Oceanic and Atmospheric Administration (NOAA) Grant No. S0660009. WL and RH were funded by NOAA Grant No. NA05NOS4781222 and NA05NOS4781226 and CWB by the NOAA Center for Satellite Applications and Research. Authors gratefully acknowledge Jiangtao Xu for her contribution to the hindcast capability.

REFERENCES

- Arakawa A, Lamb VR (1977) *Methods of computational physics*, New York: Academic Press, pp 174–265
- Blake P (1994) Endemic cholera in Australia and the United States. In: *Vibrio cholerae, cholera: molecular to global perspectives*, Wachsmuth PBIK, Olsvik O (editors), Washington, DC: American Society of Microbiology, pp 309–320
- Boesch DF (editor) (2008) *Global warming and the free state: comprehensive assessment of climate change impacts in Maryland*, Cambridge, MD: University of Maryland Center for Environmental Science
- BROUTIN H, GUÉGAN J-F, ELGUERO E, SIMONDON F, CAZELLES B (2005) Large-scale comparative analysis of pertussis population dynamics: periodicity, synchrony, and impact of vaccination. *American Journal of Epidemiology* 161:1159–1167
- CAZELLES B, CHAVEZ M, BERTEAUX D, MENARD F, VIK JO, JENOUVRIER S, et al. (2008) Wavelet analysis of ecological time series. *Oecologia* 156:287–304
- CHAIYANAN S, CHAIYANAN S, HUQ A, MAUGEL T, COLWELL RR (2001) Viability of the nonculturable *Vibrio cholerae* O1 and O139. *Systematic and Applied Microbiology* 24:331–341
- CHAMBERS JS (1938) *The conquest of cholera. America's greatest scourge*, New York: Macmillan
- CHESAPEAKE BAY FOUNDATION (2007) *Climate change and the Chesapeake Bay: challenges, impacts, and the multiple benefits of agricultural conservation work*, Annapolis, MD: Chesapeake Bay Foundation
- COLLINS AE (2003) Vulnerability to coastal cholera ecology. *Social Science and Medicine* 57:1397–1407
- COLWELL RR, KAPER J, JOSEPH SW (1977) *Vibrio cholerae, Vibrio parahaemolyticus*, and other vibrios: occurrence and distribution in Chesapeake Bay. *Science* 198:394–396
- COLWELL RR, SEIDLER RJ, KAPER J, JOSEPH SW, GARGES S, LOCKMAN H, et al. (1981) Occurrence of *Vibrio cholerae* serotype O1 in Maryland and Louisiana estuaries. *Applied and Environmental Microbiology* 41:555–558
- CONSTANTIN DE MAGNY G, GUÉGAN JF, PETIT M, CAZELLES B (2007) Regional-scale climate-variability synchrony of cholera epidemics in West Africa. *BMC Infectious Diseases* 7:20
- CONSTANTIN DE MAGNY G, MURTUGUDDE R, SAPIANO MR, NIZAM A, BROWN CW, BUSALACCHI AJ, et al. (2008) Environmental signatures associated with cholera epidemics. *Proceeding of the National Academy of Sciences of the United States of America* 105:17676–17681
- DANIELS NA, MACKINNON L, BISHOP R, ALTEKRUSE S, RAY B, HAMMOND RM, et al. (2000) *Vibrio parahaemolyticus* infections in the United States, 1973–1998. *Journal of Infectious Diseases* 181:1661–1666
- DECKER MB, BROWN CW, HOOD RR, PURCELL JE, GROSS TF, MATANOSKI JC, et al. (2007) Predicting the distribution of the scyphomedusa *Chrysaora quinquecirrha* in Chesapeake Bay. *Marine Ecology-Progress Series* 329:99–113
- EK MB, MITCHELL KE, LIN Y, ROGERS E, GRUNMANN P, KOREN V, et al. (2003) Implementation of Noah land surface model advances in the National Centers for Environmental Prediction operational mesoscale Eta model. *Journal of Geophysical Research-Atmospheres* 108:16
- FREI C, SCHOLL R, FUKUTOME S, SCHMIDLI J, VIDALE PL (2006) Future change of precipitation extremes in Europe: intercomparison of scenarios from regional climate models. *Journal of Geophysical Research—Atmospheres* 111:22
- GIORGI F, DIFFENBAUGH N (2008) Developing regional climate change scenarios for use in assessment of effects on human health and disease. *Climate Research* 36:141–151
- GLEASON KL, LAWIMORE JH, LEVINSON DH, KARL TR, KAROLY DJ (2008) A revised US climate extremes index. *Journal of Climate* 21:2124–2137
- GOUDARZI S (2006) *Flocking to the coast: world's population migrating into danger*. Available: http://www.livescience.com/environment/060718_map_settle.html (accessed March 13, 2009)
- GRENFELL BT, BJORNSTAD ON, KAPPEY J (2001) Travelling waves and spatial hierarchies in measles epidemics. *Nature* 414:716–723
- GRIM CJ, TAVIANI E, ALAM M, HUQ A, SACK B, COLWELL RR (2008) Occurrence and expression of luminescence in *Vibrio cholerae*. *Applied and Environmental Microbiology* 74:708–715
- HEIDELBERG JF, HEIDELBERG KB, COLWELL RR (2002) Seasonality of Chesapeake Bay bacterioplankton species. *Applied and Environmental Microbiology* 68:5488–5497
- HUQ A, SMALL EB, WEST PA, HUQ MI, RAHMAN R, COLWELL RR (1983) Ecological relationships between *Vibrio cholerae* and planktonic crustacean copepods. *Applied and Environmental Microbiology* 45:275–283
- HUQ A, WEST PA, SMALL EB, HUQ MI, COLWELL RR (1984) Influence of water temperature, salinity, and pH on survival and growth of toxigenic *Vibrio cholerae* serovar O1 associated with live copepods in a laboratory microcosm. *Applied and Environmental Microbiology* 48:420–424
- HURRELL JW, KUSHNIR Y, VISBECK M (2001) Climate—the North Atlantic oscillation. *Science* 291:603–605
- KAUSRUD KL, MYSTERUD A, STEEN H, VIK JO, OSTBYE E, CAZELLES B, et al. (2008) Linking climate change to lemming cycles. *Nature* 456:93–U93
- KELLY MT (1982) Effect of temperature and salinity on *Vibrio* (Benecke) *vulnificus* occurrence in a Gulf Coast environment. *Applied and Environmental Microbiology* 44:820–824
- KEMP WM, BOYNTON WR, ADOLF JE, BOESCH DF, BOICOURT WC, BRUSH G, et al. (2005) Eutrophication of Chesapeake Bay: historical trends and ecological interactions. *Marine Ecology-Progress Series* 303:1–29

- Leclerc H, Schwartzbrod L, Dei-Cas E (2002) Microbial agents associated with waterborne diseases. *Critical Reviews in Microbiology* 28:371–409
- Lehodey P, Senina I, Murtugudde R (2008) A spatial ecosystem and populations dynamics model (SEAPODYM)—modeling of tuna and tuna-like populations. *Progress in Oceanography* 78:304–318
- Lipp EK, Huq A, Colwell RR (2002) Effects of global climate on infectious disease: the cholera model. *Clinical Microbiology Reviews* 15:757–770
- Louis VR, Russek-Cohen E, Choopun N, Rivera IN, Gangle B, Jiang SC, et al. (2003) Predictability of *Vibrio cholerae* in Chesapeake Bay. *Applied and Environmental Microbiology* 69:2773–2785
- Madsen T, Figdor E (2007) *When it rains, it pours: global warming and the rising frequency of extreme precipitation in the United States*, Washington DC: Environment America Research & Policy Center, pp 48
- Mantua NJ, Hare SR, Zhang Y, Wallace JM, Francis RC (1997) A Pacific interdecadal climate oscillation with impacts on salmon production. *Bulletin of the American Meteorological Society* 78:1069–1079
- Miliotis M, Watkins W (2000) *Draft risk assessment on the public health impact of Vibrio parahaemolyticus in raw molluscan shellfish*, Washington DC: FDA
- Miller WD, Harding LW (2007) Climate forcing of the spring bloom in Chesapeake Bay. *Marine Ecology-Progress Series* 331:11–22
- Murtugudde R (2009a) Observational needs for sustainable coastal prediction and management. In: *Management and Sustainable Development of Coastal Zone Environment*, Ramanathan AL, Bhattacharya P, Nepuna B (editors), New York: Springer
- Murtugudde R (2009b) Regional Earth System Prediction: a decision-making tool for sustainability? *Current Opinion in Environmental Sustainability* 1:37–45
- Murtugudde R (2010) Observational needs for regional Earth System Prediction. In: *Proceedings of OceanObs09: Sustained Ocean Observations and Information for Society (Vol 2)*, Venice, Italy, September 21–25, 2009, Hall J, Harrison DE, Stammer D (editors), Newmarket, New Zealand: ESA Publication WPP-306
- Najjar RG, Walker HA, Anderson PJ, Barron EJ, Bord RJ, Gibson JR, et al. (2000) The potential impacts of climate change on the mid-Atlantic coastal region. *Climate Research* 14:219–233
- Neff R, Chang HJ, Knight CG, Najjar RG, Yarnal B, Walker HA (2000) Impact of climate variation and change on mid-Atlantic region hydrology and water resources. *Climate Research* 14:207–218
- Pasternack GB, Hinnov LA (2003) Hydrometeorological controls on water level in a vegetated Chesapeake Bay tidal freshwater delta. *Estuarine Coastal and Shelf Science* 58:367–387
- Patz JA, Engelberg D, Last J (2000) The effects of changing weather on public health. *Annual Review of Public Health* 21:271–307
- Sankarasubramanian A, Vogel RM, Limbrunner JF (2001) Climate elasticity of streamflow in the United States. *Water Resources Research* 37:1771–1781
- Singleton FL, Attwell R, Jangi S, Colwell RR (1982) Effects of temperature and salinity on *Vibrio cholerae* growth. *Applied and Environmental Microbiology* 44:1047–1058
- Tamplin M, Rodrick GE, Blake NJ, Cuba T (1982) Isolation and characterization of *Vibrio vulnificus* from 2 Florida estuaries. *Applied and Environmental Microbiology* 44:1466–1470
- Taylor AH, Allen JI, Clark PA (2002) Extraction of a weak climatic signal by an ecosystem. *Nature* 416:629–632
- Trenberth KE (1997) The definition of El Nino. *Bulletin of the American Meteorological Society* 78:2771–2777
- Watkins JD, Huq A (2002) The relationship between oceans and human health. In: *Critical Issues in Global Health*, Koop CE, Pearson CE, Schwarz MR (editors), San Francisco: Wiley
- Weissman JB, DeWitt WE, Thompson J, Muchnick CN, Portnoy BL, Feeley JC, et al. (1974) A case of cholera in Texas, 1973. *American Journal of Epidemiology* 100:487–498
- Wilkin JL, Arango HG, Haidvogel DB, Lichtenwalner CS, Glenn SM, Hedstrom KS (2005) A regional ocean modeling system for the long-term ecosystem observatory. *Journal of Geophysical Research-Oceans* 110:13
- Wright AC, Hill RT, Johnson JA, Roghman MC, Colwell RR, Morris JG (1996) Distribution of *Vibrio vulnificus* in the Chesapeake Bay. *Applied and Environmental Microbiology* 62:717–724
- Xu HS, Roberts N, Singleton FL, Attwell RW, Grimes DJ, Colwell RR (1982) Survival and viability of nonculturable *Escherichia coli* and *Vibrio cholerae* in the estuarine and marine-environment. *Microbial Ecology* 8:313–323