Climate and Health: Conquering Water Borne Diseases in the 21st Century

March 17, 2022

Open Network for Water-Related Diseases, GCRF
Nansen Environmental Research Centre, India

Rita R. Colwell, Ph.D., D.Sc.
Distinguished University Professor
University of Maryland College Park
Data collected and summarized from:
Sherman, I. 2007 Twelve Disease that Changed Our World, American Society for Microbiology, USA
Zimmerman, B.E. and Zimmerman., DJ 2003 Killer Germs, McGraw Hill, USA
*Source of virus debated, hence used prevalent name of disease, *SARS-CoV-1, *SARS-CoV-2
## Water-related diseases

<table>
<thead>
<tr>
<th>Disease</th>
<th>Cases per year</th>
<th>Deaths per year</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amoebiasis</td>
<td>48,000,000</td>
<td>110,000</td>
</tr>
<tr>
<td>Arsenic</td>
<td>28-35m exposed to drinking water with elevated levels</td>
<td></td>
</tr>
<tr>
<td>Diarrhoeal disease, Including cholera</td>
<td>1.5 billion</td>
<td>1,800,000</td>
</tr>
<tr>
<td>Dracunuliasis (guinea worm)</td>
<td>&gt; 5000</td>
<td>-</td>
</tr>
<tr>
<td>Fluorosis</td>
<td>26 million (China)</td>
<td>-</td>
</tr>
<tr>
<td>Giardiasis</td>
<td>500,000</td>
<td>Low</td>
</tr>
<tr>
<td>Hepatitis A</td>
<td>1,500,000</td>
<td>-</td>
</tr>
<tr>
<td>Intestinal helminths</td>
<td>133,000,000</td>
<td>9400</td>
</tr>
<tr>
<td>Malaria</td>
<td>396,000,000</td>
<td>1,300,000</td>
</tr>
<tr>
<td>Schistosomiasis</td>
<td>160,000,000</td>
<td>&gt; 10,000</td>
</tr>
<tr>
<td>Trachoma</td>
<td>500,000,000</td>
<td>-</td>
</tr>
<tr>
<td>Typhoid</td>
<td>500,000</td>
<td>25,000</td>
</tr>
</tbody>
</table>
Cholera: A Global Disease

- Acute water-related diarrheal disease
- Seventh pandemic started in 1960s
- Occurs in more than 50 countries affecting approximately 7 million people
- Bengal Delta is known as “native homeland” of cholera outbreaks
- Since cholera bacteria
  - exist naturally in aquatic habitats
  - evidence of new biotypes emerging,
  > it is highly unlikely that cholera will be eradicated but clearly can be controlled by provision of safe drinking water.
Map of Chesapeake Bay – beginning of the cholera chronicle
1965-1975 An early contribution of marine microbiology to human health: Determination of the *Vibrio cholerae* life cycle
The culprit – *Calanus* copepod host
Model for the Transmission of Vibrio cholerae from the Environment to Humans

**Physical & Chemical Characteristics of Water**
- temperature
- sunlight
- rainfall
- pH
- dissolved oxygen
- salinity & nutrients

**Fecal Shedding**
returns V. cholerae to the water.

**Biological Characteristics**
- algae bloom
- phytoplankton bloom

**Zooplankton Bloom**
(enters into non-culturable state)

**V. Cholerae**
viable but non-culturable state in the water column & attached to particulates. Commensal or symbiotic relationships.

**Transmission of V. Cholerae**
to humans via ingested water containing colonized copepods or other vectors.
Villagers in Bangladesh collect filtered water in the same pond used for bathing.
Why Prediction?

Schematic representation of the disease control measures implemented at the beginning (Scenario A) and after the peak (Scenario B) of an outbreak, and potential cases averted.
Cholera and SST in the Indian Ocean 1985 - 2000

Six-month SST lead: $R^2 = 0.72$

Lobitz et al., 2000, PNAS Vol. 97, No. 4 pp. 1438-1443
What is reported about cholera and macro-scale processes?

Cholera outbreaks have been linked to environmental and climate variables:

- precipitation \((\text{Hashizume et al. 2008})\)
- floods \((\text{Koelle et al., 2005})\)
- river level \((\text{Emch et al., 2008})\)
- sea surface temperature \((\text{Colwell, 1996; Lobitz et al., 2000})\)
- coastal salinity \((\text{Miller et al., 1982})\)
- dissolved organic material \((\text{Worden et al., 2005})\)
- fecal contamination \((\text{Islam et al., 2006})\)
- chlorophyll \((\text{Lobitz et al., 2000, Magny et al., 2008})\)
Epidemic Cholera
- Sporadic deadly outbreak
- Usually occurs inland after disasters
- Temperatures may increase growth of bacteria in aquatic bodies.

Mixed-mode Cholera
- Usually two seasonal peaks
- One peak related to seawater intrusion; Second peak associated with widespread inundation
- Specific to Bengal Delta region

Endemic Cholera
- Cholera persists throughout year in coastal regions
- Seawater intrusion from coasts to inland

Typical cholera seasonality

Bacterial movement from coastal niches to inland
Epidemic Mode of Cholera

- Sporadic outbreak
- Usually occurs following floods or inundation of large landscapes
- Warm temperatures may increase growth of bacteria in aquatic bodies.

Accumulated rainfall above threshold

Challenge
- Disease (prevalence) data
- Time invariant algorithm
- Search for self-adaptive algorithm

Jutla et al., 2017, ASCE JWRPM
Could we have predicted the Haiti Cholera outbreak?

- The 2010 cholera outbreak in Haiti indicated the disease remains a global threat.

- Framework for developing cholera prediction models in cholera endemic (ER) and non-endemic regions (NER)

- The sharp contrast in mortality rates between ER and NER exists not because we do not know how to treat cholera patients, but because of a persistent “knowledge barrier” between ER and NER.

- We propose a pragmatic and adaptive framework which hypothesizes that convergence of three enabling situations - Inception, Environmental Conditions, and Transmission - are necessary for a cholera outbreak to become an epidemic.

Air temperature in Haiti in 2010 compared with historical air temperature data

Monthly rainfall in Haiti in 2010 compared with historical rainfall data
Cholera in Haiti

Prediction of October 2015 cholera depending on Hurricane Matthew severity

Actual cholera in October 2015 following Hurricane Matthew

Khan et al., 2018 ASCE JWRPM
Real-time cholera prediction for Yemen

Risk estimated on May 30th, 2017 for June 2017

Reported cholera cases for this month of June 2017 (Source: WHO)
Epidemic Cholera

- Sporadic outbreak
- Usually occurs following floods or inundation of large landscapes
- Warm temperatures may increase growth of bacteria in aquatic bodies.

Prediction of October 2015 cholera depending on Hurricane Matthew severity

Real-time cholera prediction for Yemen
NEXT GEN SEQUENCING AND METAGENOMICS
Shotgun whole (meta)genome sequencing

Biological specimen → Community DNA → DNA Sequencing

GenBook Biomarker Matching → CosmosID Database

Identified → All Microbes

CosmosID AR/VF Database

Microbial Identification & Pathogen Characterization
Strain is the Clinically Informative and Actionable Unit
Microbiome Analysis of Acute Diarrheal Patients Compared with Healthy Individuals

pre-publication results
Study Cohort

@ 2% Surveillance (every 50th patient) at the National Institute of Cholera and Enteric Diseases (NICED), Calcutta, India

<table>
<thead>
<tr>
<th>Study Phases</th>
<th>Total # of Samples</th>
<th>Known Etiology</th>
<th>Unknown Etiology</th>
<th>Healthy Control</th>
</tr>
</thead>
<tbody>
<tr>
<td>PHASE I</td>
<td>9</td>
<td>9</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PHASE II</td>
<td>28</td>
<td>0</td>
<td>18</td>
<td>10</td>
</tr>
<tr>
<td>PHASE III</td>
<td>37</td>
<td>17</td>
<td>10</td>
<td>10</td>
</tr>
</tbody>
</table>

Enteric Pathogens monitored

- **Bacteria**
  - *V. cholerae* O1 and O139
  - *V. cholerae* Non O1 and Non O139
  - *V. parahaemolyticus*
  - *V. fluvialis*
  - *Aeromonas* spp.
  - *Campylobacter jejuni*
  - *Campylobacter coli*
  - *Shigella dysenteriae*
    - *S. flexneri*
    - *S. sonnei*
    - *S. boydii*
  - *Salmonella*
    - *EPEC*
    - *ETEC* group (LT, ST, LT+ST)
    - EAEC
    - EIEC
    - STEC

- **Virus**
  - Rotavirus
  - Adenovirus
  - Norovirus GI
  - Norovirus GII
  - Sapovirus
  - Astrovirus

- **Parasites**
  - *Giardia lamblia*
  - *Cryptosporidium parvum*
  - *Entamoeba histolytica*
  - *Blastocystis hominis*
Microbial Community in Healthy vs Diarrheal Patients

Known Disease Etiology

Unknown Disease Etiology

γ-Proteobacteria
Firmicutes
Bacteroidetes

Healthy Control Local Population

HMP
Crohn’s Disease and the Microbiome

Total n = 39

14 Crohns
8 Female
6 Male

25 Healthy
9 Female
16 Male

• 1: Crohn’s data come from SRA Bioproject PRJNA46321 "Metagenomic Analysis of the Structure and Function of the Human Gut Microbiota in Crohn's Disease"

• 2: Healthy data come from SRA Bioproject PRJNA48479 “Human Microbiome Project (HMP) Metagenomic WGS Projects, deeper sequencing of the human microbiome samples: Production Phase”
Species Enrichment in Healthy vs Crohn’s

Analysis provided by CosmosID
Celiac Disease and the Microbiome

Longitudinal (intrasubject) analysis for microbial species. A paired Wilcoxon (Wilcoxon signed rank) test was used to identify microbial species whose abundance differentially changes between a preonset time point (−18, −15, −12, −9, −6, and −3 mo) and CD onset. Any species for which a statistically significant (P value < 0.05) change is observed in at least one time point in (A) cases and (B) controls is reported here. Box plots for significant features are shown in SI Appendix, Fig. S2. Time points at which a significant change is observed are shown in SI Appendix, Fig. S5. Here, we report only species for which significant changes are uniquely observed in cases or in controls.
Clostridium

- Increased abundance has been associated with symptoms of ASD
- Byproducts of Clostridium are thought to contribute to symptoms of ASD
  - β2-toxin
  - Propionic acid
Ruminococcus bromii

- Major metabolizer of resistant starches
- Ruminococcus bromii allows for the cross-feeding of many other bacteria:
  - Eubacterium rectale (a butyrate producer)
  - Ruminococcus gnatus (an acetate, lactate and formate producer)
Is COVID-19 polymicrobial and systemic?

How does coronavirus kill? Clinicians trace a ferocious rampage through the body, from brain to toes

Meredith Wadman, Jennifer Couzin-Frankel, Jocelyn Kaiser, Catherine Matacic. Science, Apr. 17, 2020, 6:45 PM

Identification of Bacteria and Viruses Present in Respiratory Samples in which SARS-CoV-2 has been Detected
SARS Cov-2 viral RNA has been detected in 48.1% of stool samples

Cheung et al., (2020). Gastrointestinal Manifestations of SARS-CoV-2 Infection and Virus Load in Fecal Samples from the Hong Kong Cohort and Systematic Review and Meta-analysis. Gastroenterology. Pre-Proof
Positive Stool Samples Detected After Respiratory Sample Tested Negative During Recovery

COVID-19 tracking in wastewater
Results from Frederick, Maryland sites, 2020
Case Study: Mount St. Mary’s University

- Twice weekly sampling of dormitory effluent
- Covid spike triggered testing of individual students
- 221 students tested
  - 10 positive
  - 9 asymptomatic
- “It could have become quite a spreading event,” said Donna Klinger, a spokeswoman for the university
- Coronavirus positive students isolated and wastewater tests done twice weekly
A decision-making initiative for protecting human health and enhancing the resilience of coastal communities under current and changing environments.
SARS-CoV-2 (COVID-19)

Development of prediction algorithm
In-house cholera prediction algorithm was modified for COVID-19
Algorithm is based on geographically weighted raster probabilistic dose-response assimilation technique

(Email ajutla@ufl.edu and moiz.usmani@ufl.edu for details)

Prediction of coronavirus risk

Left panel: Prediction made on April 24th 2020 and valid until May 14th, 2020.
Right panel: Actual number of COVID19 cases during those three weeks: a heuristic prediction model developed in GeoHLab
COVID-19 Risk Map
as of March 07, 2022

https://covid-ufl.hub.arcgis.com/
A Simple, Sustainable Method for Reducing Cholera
Cases of Cholera Per 1000 Population

Test Group

Control

Sari

Nylon
Safe water is a global challenge
Collaborators and Colleagues

ICDDR,B - Dhaka
- Dr. Munir Alam
- A.K. Ashraful Aziz
- Dr. A.S.G. Faruque
- Dr. M. Imadadul Huq
- Dr. Sirajul M. Islam
- Huda Khan
- Rezaur Rahman
- Dr. David Sack
- Dr. M. A. Salam
- Mr. Sarker M. Nazmul Sohel
- Dr. Peter Kim Sstreetfield
- Dr. Carel van Mels
- Dr. Mohammad Yunus

NICED, Kolkata, India
- Dr. Balakrish Nair
- Dr. T. Ramamurthy

University of Maryland
- Kyle Brumfield
- Sittipan Chayanan
- Arlene Chen
- Nipa Choopun
- Philip Clark
- Guillaume Constantin de Magny
- Christopher Grim
- Jafrul Hasan
- Anwarul Huq
- Shameem Huq
- Chenyang Jiang
- James Kaper
- Erin Lipp
- Victoria Lord
- Valerie Louis
- David Maneval
- Jennifer Newlin
- Tonya Rawlings
- Janie Robinson
- Estelle Russe-Cohen
- Paul West
- Young Gun Zo
Collaborators and Colleagues

- Richard Atwell, England
- Louisa Beck, NASA Ames
- Norma Binsztein, Argentina
- Phyllis Brayton, NIAID, NIH
- Tom Brettin, Los Alamos National Laboratory
- John Calkins, ESRI, Redlands, CA
- Jongsik Chun, Seoul, Korea
- Ric Ciccone, ISciences, Burlington, VT
- Jack Dangermond, ESRI, Redlands, CA
- William Davenport, ESRI, Redlands, CA
- Ana Gil, Lima, Peru
- Jay Grimes, Univ. of Southern Mississippi
- Dominique Hervio-Heath, Plouzane, FR
- Sunny Jiang, Univ. of California
- Crystal Johnson, Louisiana State University
- Antarpreet Jutla, Univ of Florida
- Tatsuo Kaneko, San Diego
- L. Lizaragga-Partida, Mexico
- Brad Lobitz, NASA Ames
- Patrick Monfort, Univ of Montpellier, FR
- Betty Lovelace, NCI/NIH
- Matt Luck, ISciences, Burlington, VT
- J. Glenn Morris, University of Florida
- Moiz Usmani, University of Florida
- Thomas Parris, ISciences, Burlington, VT
- Monique Pommepuy, Brest, France
- Carla Pruzzo, University of Genoa, Italy
- Irma Rivera, Univ. of Sao Paolo, Brazil
- Nell Roberts, Louisiana State University
- R. Bradley Sack, Johns Hopkins University, School of Public Health
- Fred Singleton, Gainesville, Florida
- Minnie Sochard, Catholic University, Washington, DC, USA
- Miguel Talledo, Lima, Peru
- Ron Taylor, Darmouth, College, NH
- Byron Wood, NASA Ames
- Huai-shu Xu, China
- Linda Zall, Office of the Chief Scientist
- Fred Zimmerman, ISciences, Burlington, VT
“When one tugs at a single thing in nature, he (and she) find it hitched to the rest of the universe.”

John Muir
(1838-1914)