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

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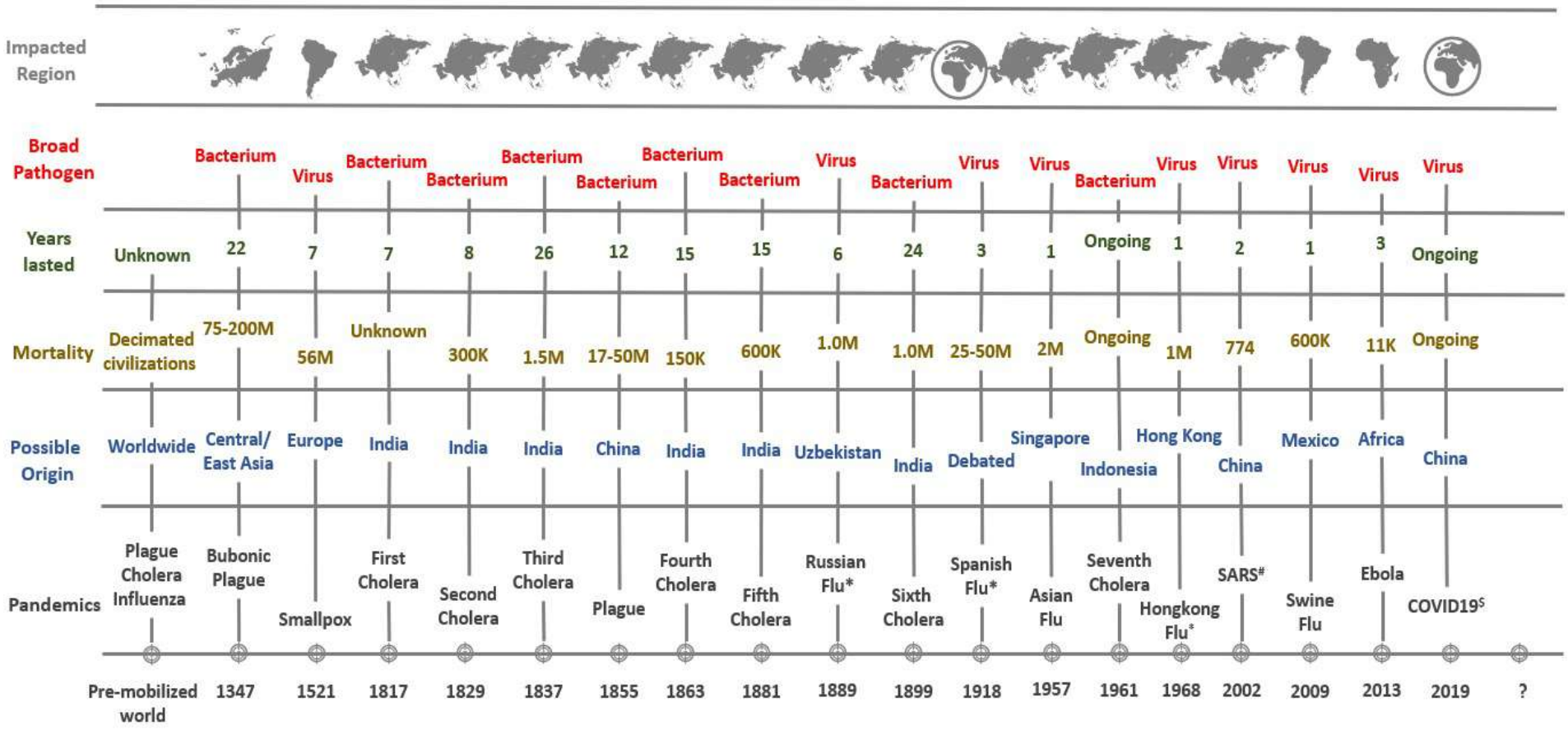
Distinguished University Professor
University of Maryland College Park



Data collected and summarized from
Sherman., I. 2007 Twelve Disease that Changed Our World, American Society for Microbiology, USA
Zimmerman, B.E. and Zimmerman., D.J 2003 Killer Germs, McGraw Hill, USA
*Source of virus debated, hence used prevalent name of disease, #SARS-CoV-1, $SARS-CoV-2

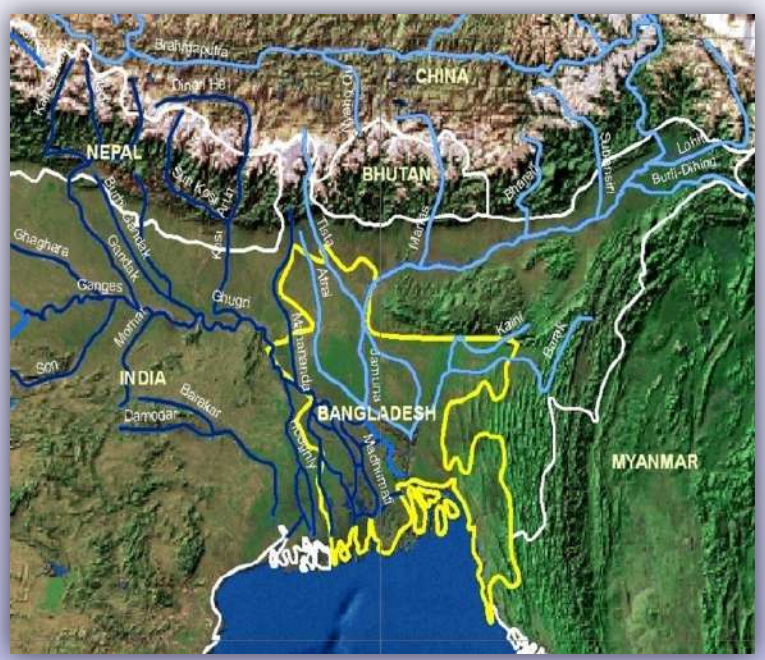
Jutla and Colwell

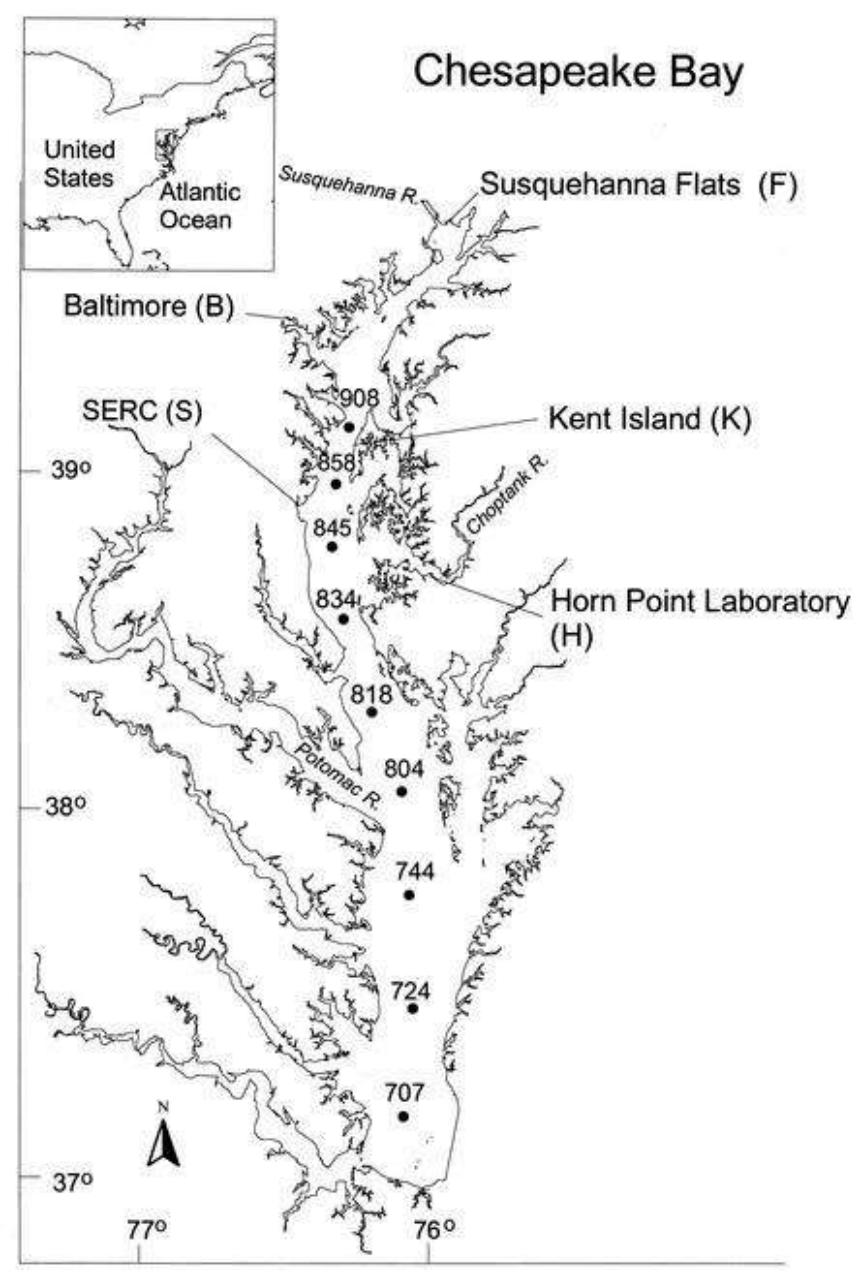
Water-related diseases

	Cases per year	Deaths per year
Amoebiasis	48,000,000	110,000
Arsenic	28-35m exposed to drinking water with elevated levels	
Diarrhoeal disease, Including cholera	1.5 billion	1,800,000
Dracunuliasis (guinea worm)	> 5000	-
Fluorosis	26 million (China)	-
Giardiasis	500,000	Low
Hepatitis A	1,500,00	-
Intestinal helminths	133,000,000	9400
Malaria	396,000,000	1,300,000
Schistosomiasis	160,000,000	> 10,000
Trachoma	500,000,000	-
Typhoid	500,000	25,000

Cholera: A Global Disease

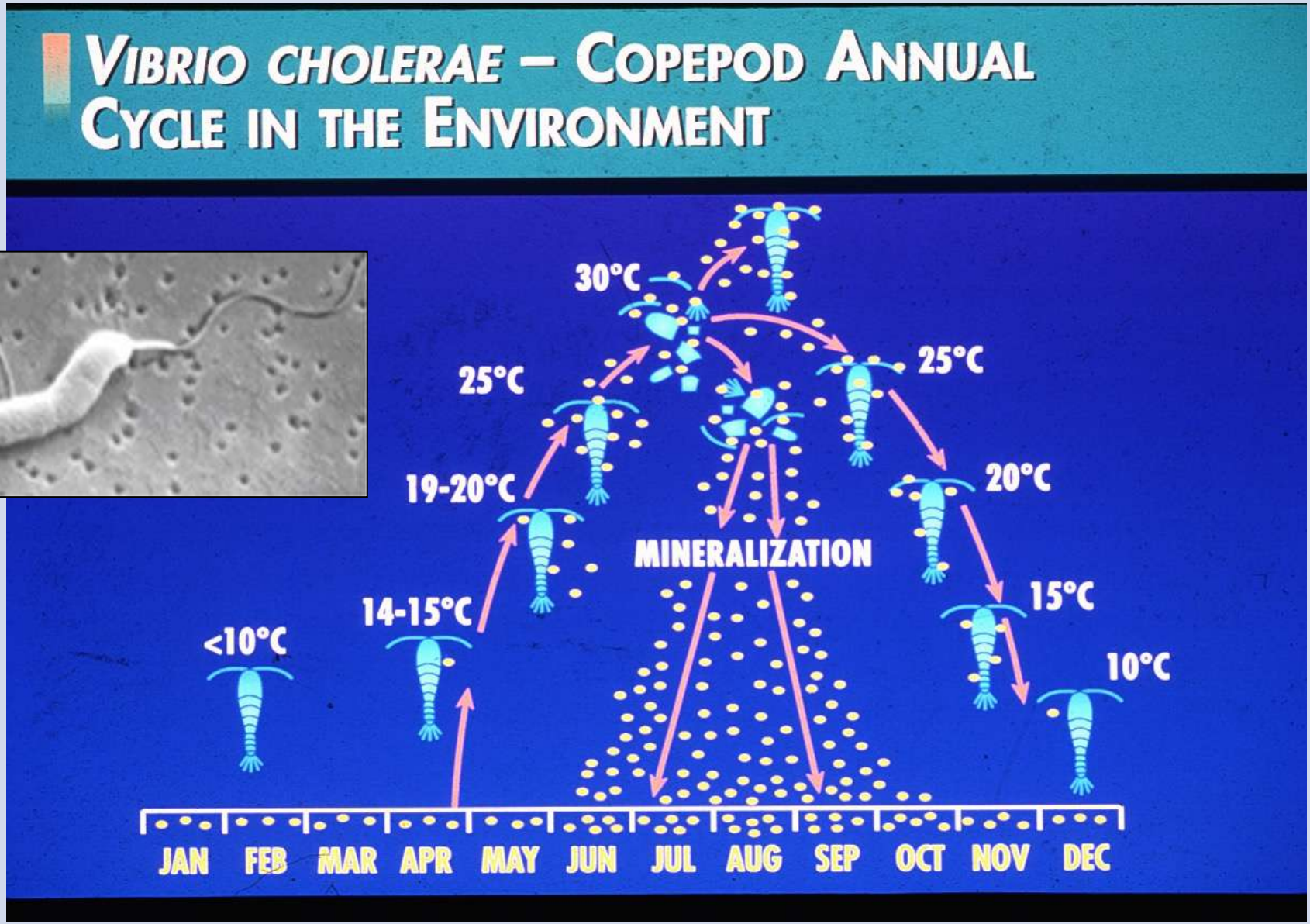
- Acute water-related diarrheal disease
- Seventh pandemic started in 1960s
- Occurs in more than 50 countries affecting approximately 7 million people
- Bengal Delta is known as “native homeland” of cholera outbreaks
- Since cholera bacteria
  - exist naturally in aquatic habitats
  - evidence of new biotypes emerging, ***it is highly unlikely that cholera will be eradicated but clearly can be controlled by provision of safe drinking water.***





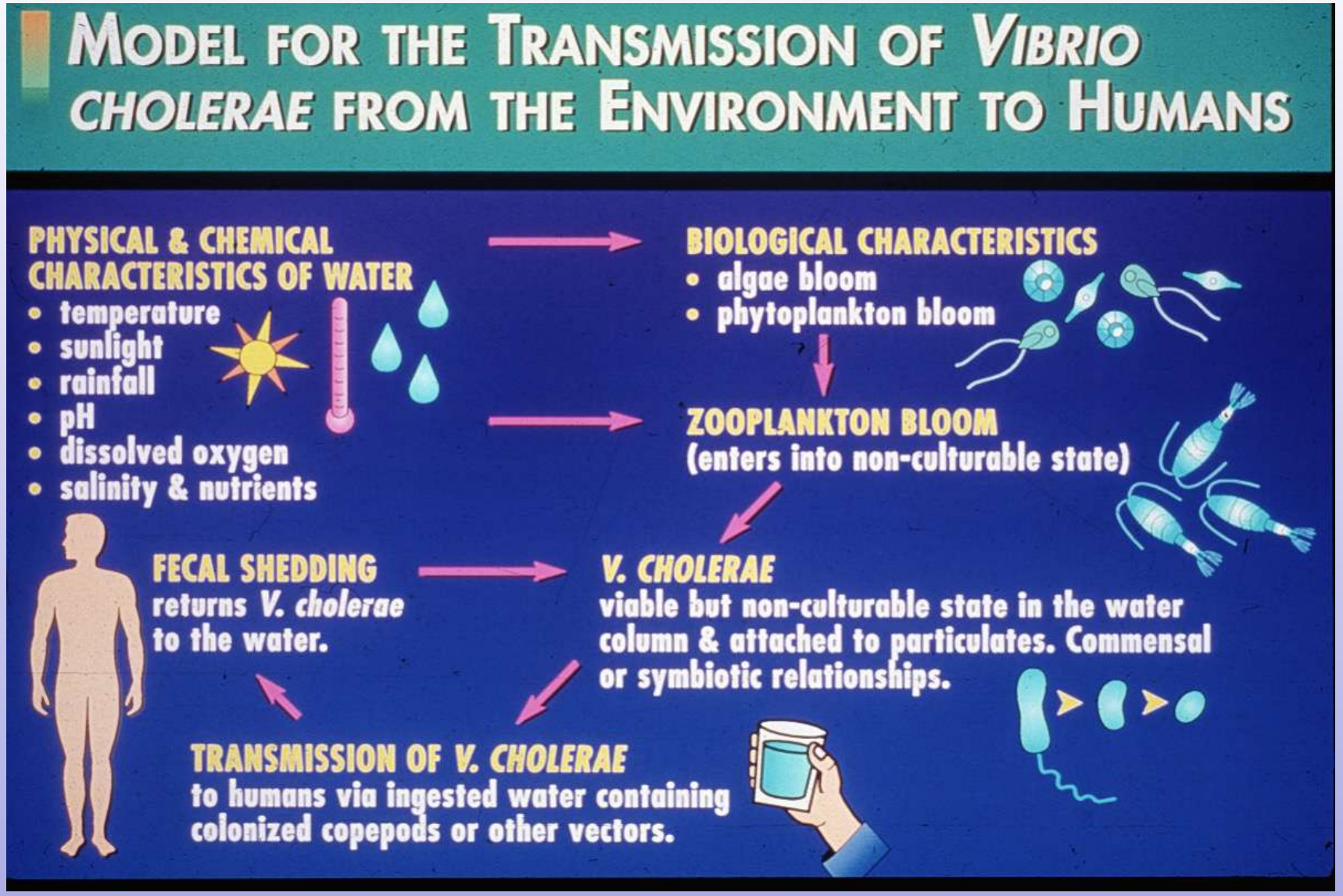
Map of Chesapeake Bay – beginning of the cholera chronicle

1965-1975 An early contribution of marine microbiology to human health: Determination of the *Vibrio cholerae* life cycle



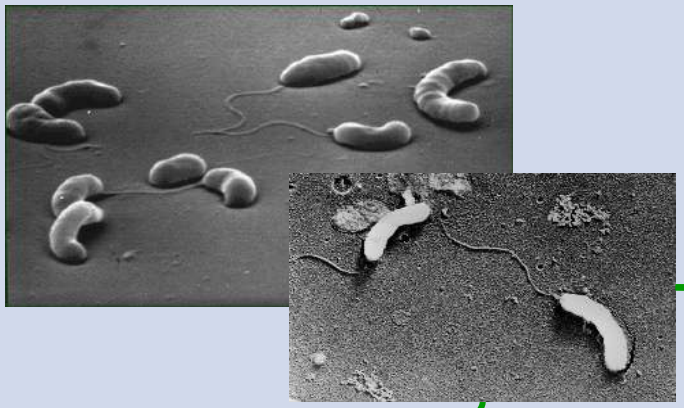
The culprit – *Calanus* copepod host

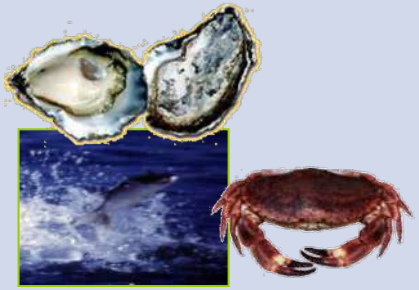
Model for the Transmission of *Vibrio cholerae* from the Environment to Humans



Villagers in Bangladesh collect filtered water in the same pond used for bathing

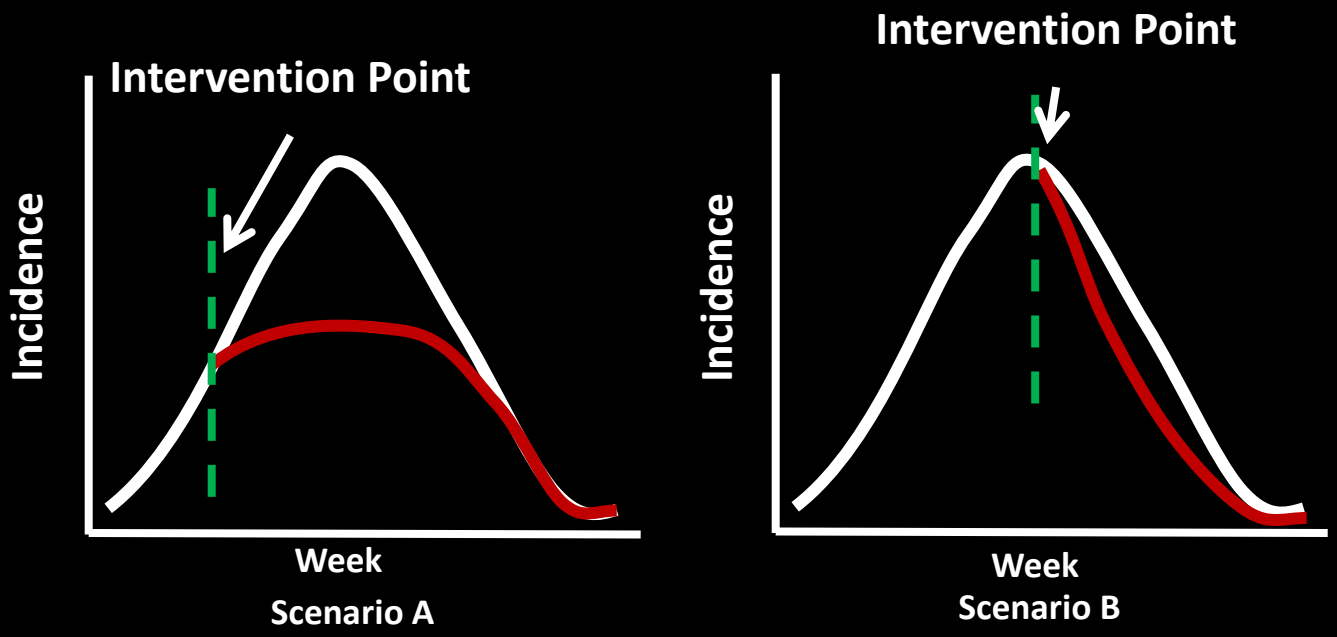
Bangladesh Model of Cholera source and Transmission



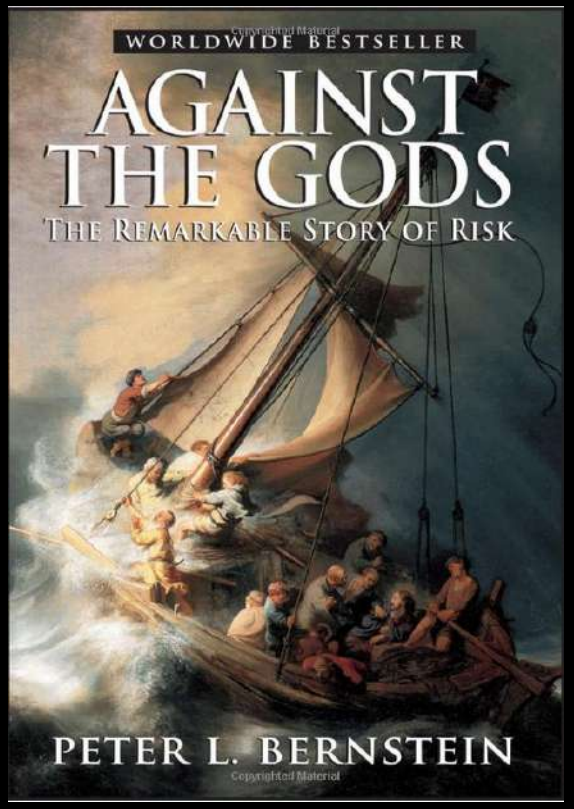


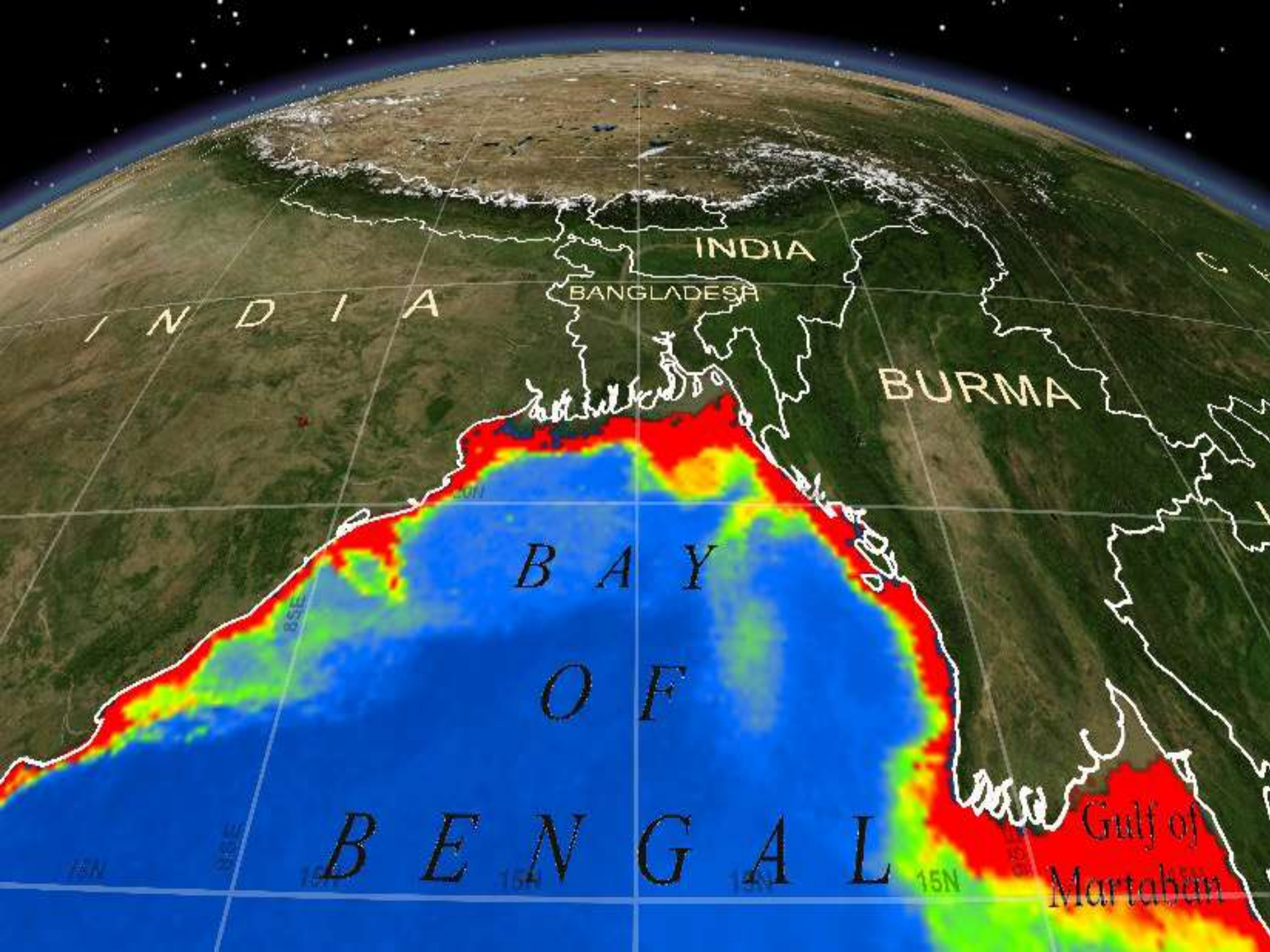
G. Constantin de Magny

Why Prediction?



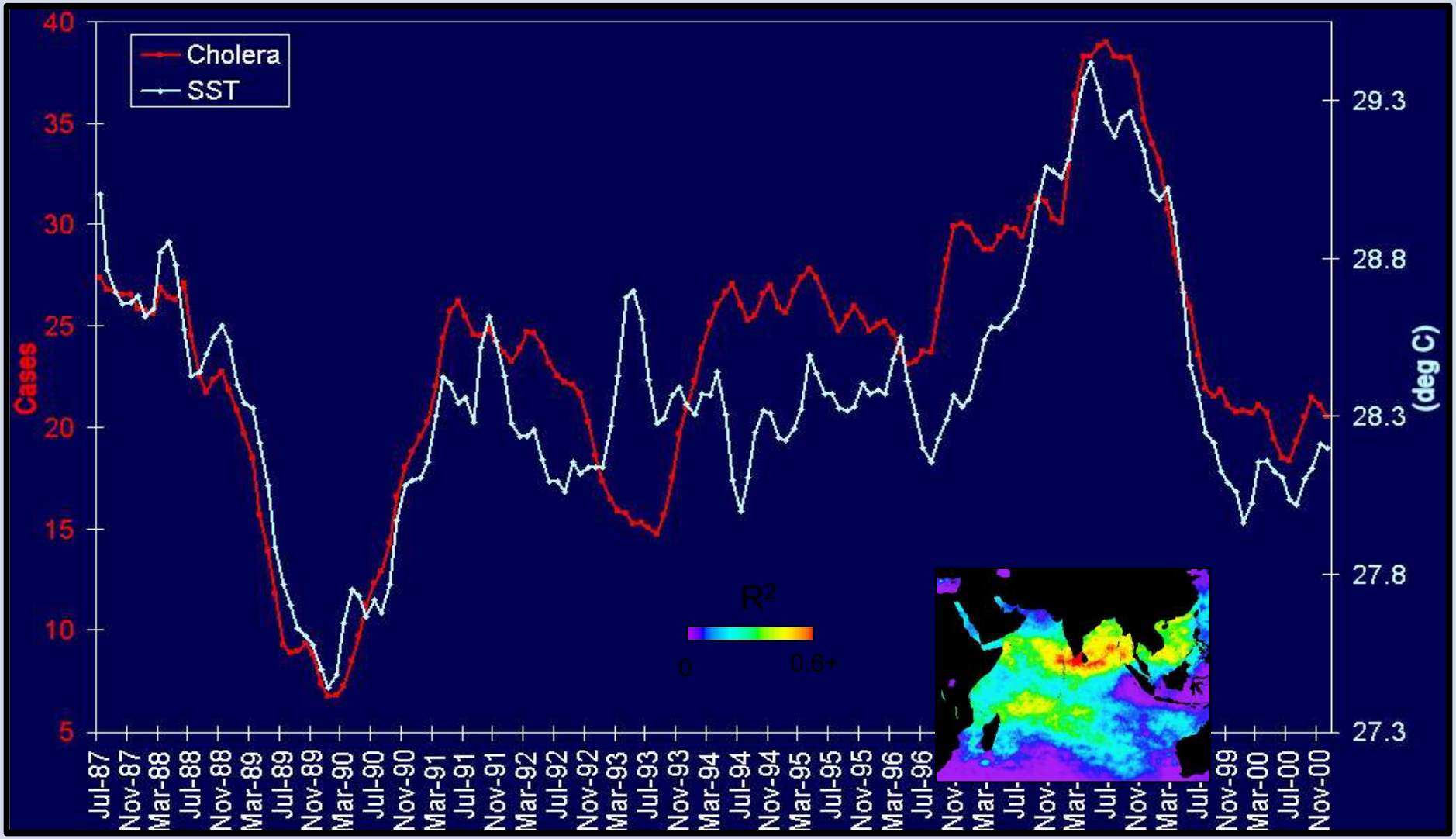
Schematic representation of the disease control measures implemented at the beginning (Scenario A) and after the peak (Scenario B) of an outbreak, and potential cases averted.




INDIA
BANGLADESH
INDIA
BURMA
BAY
OF
BENGAL
Gulf of
Martaban
15N

Cholera and SST in the Indian Ocean 1985 - 2000

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

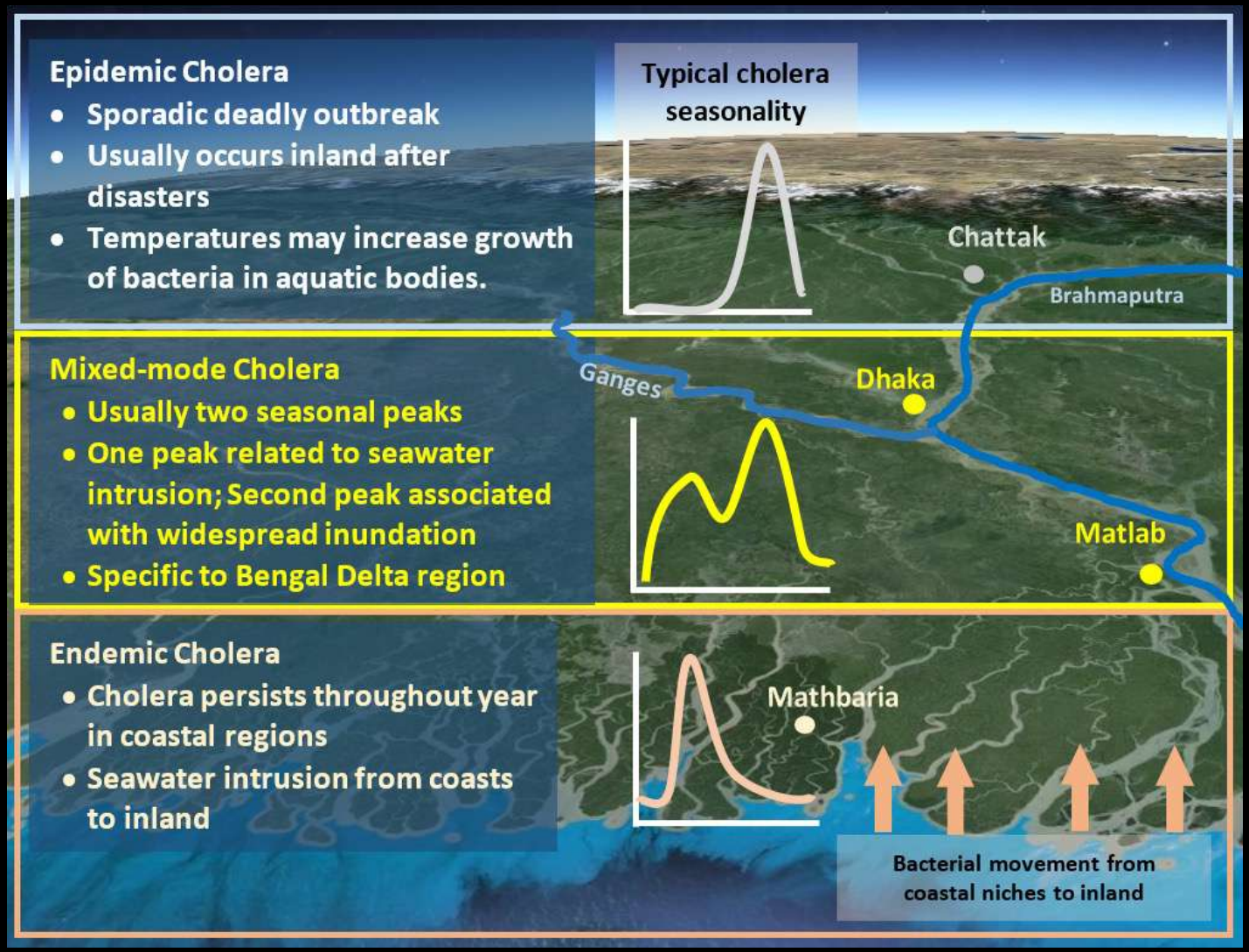


Lobitz et al., 2000, PNAS Vol. 97, No. 4 pp. 1438-1443

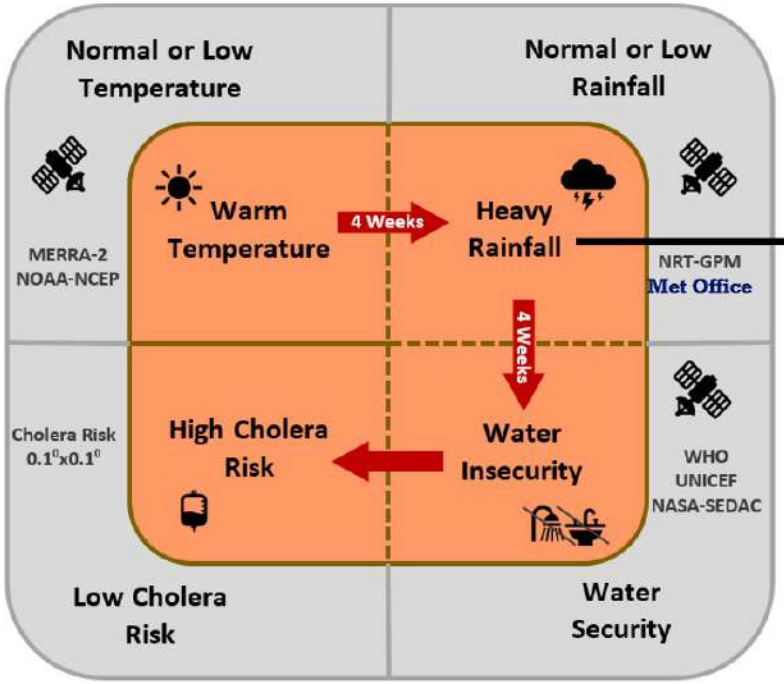
What is reported about cholera and macro-scale processes?

Cholera outbreaks have been linked to environmental and climate variables

- **precipitation (*Hashizume et al. 2008*)**
- **floods (*Koelle et al., 2005*)**
- **river level (*Emch et al., 2008*)**
- **sea surface temperature (*Colwell*, 1996; *Lobitz et al., 2000*)**
- **coastal salinity (*Miller et al., 1982*)**
- **dissolved organic material (*Worden et al., 2005*)**
- **fecal contamination (*Islam et al., 2006)***
- **chlorophyll (*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.
Typical cholera seasonality
Chattak
Brahmaputra
Mixed-mode Cholera
• Usually two seasonal peaks
• One peak related to seawater intrusion; Second peak associated with widespread inundation
• Specific to Bengal Delta region
Ganges
Dhaka
Matlab
Endemic Cholera
• Cholera persists throughout year in coastal regions
• Seawater intrusion from coasts to inland
Mathbaria
Bacterial movement from coastal niches to inland

Epidemic Mode of Cholera



Warm temperature= above climatological average temperature
Heavy rainfall= above climatological average precipitation
Water insecurity=lack of access to water and sanitation access
High cholera risk=probability of cholera greater than 50%

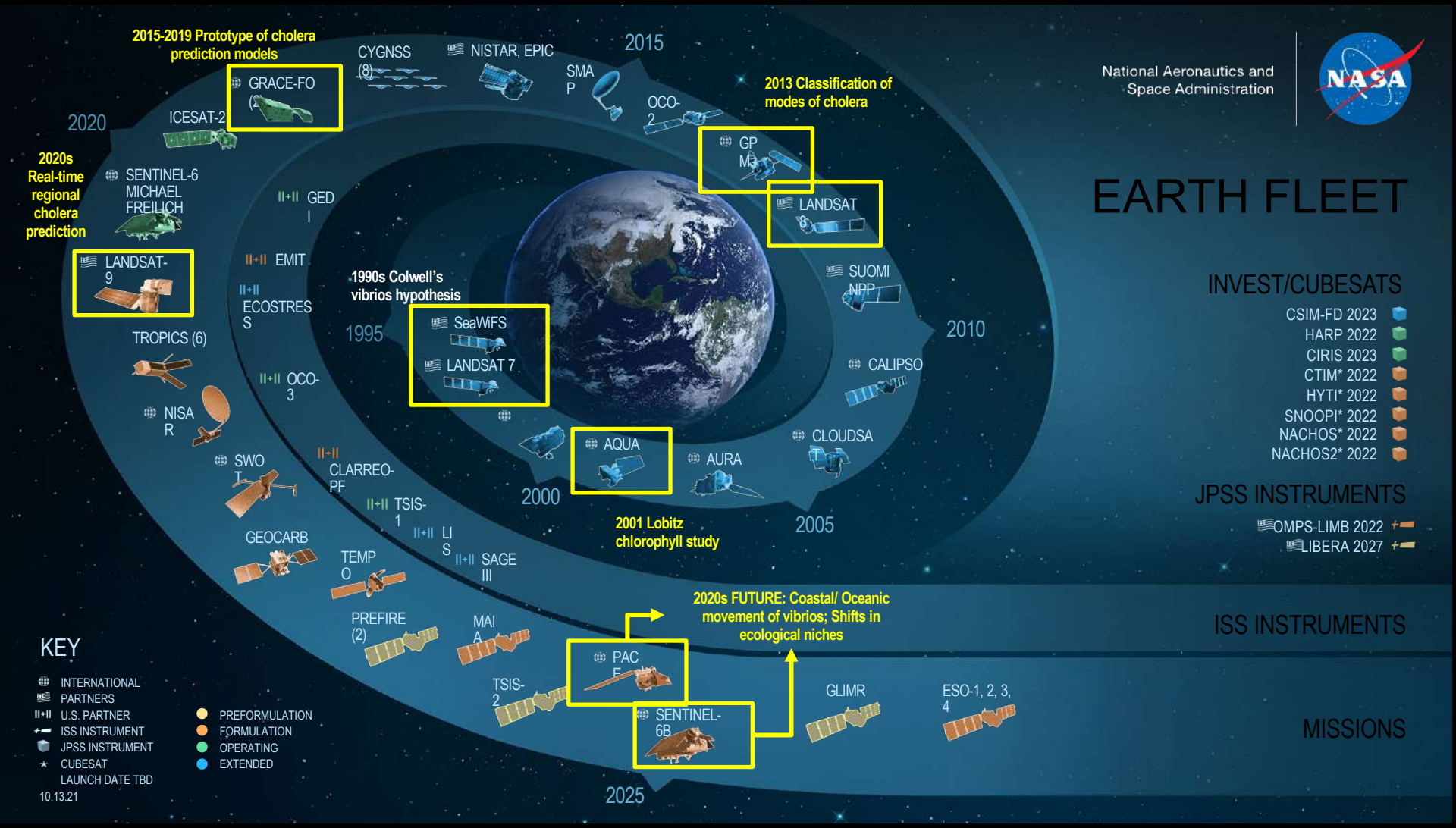
- Sporadic outbreak
- Usually occurs following floods or inundation of large landscapes
- Warm temperatures may increase growth of bacteria in aquatic bodies.

Accumulated rainfall above threshold

Challenge

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

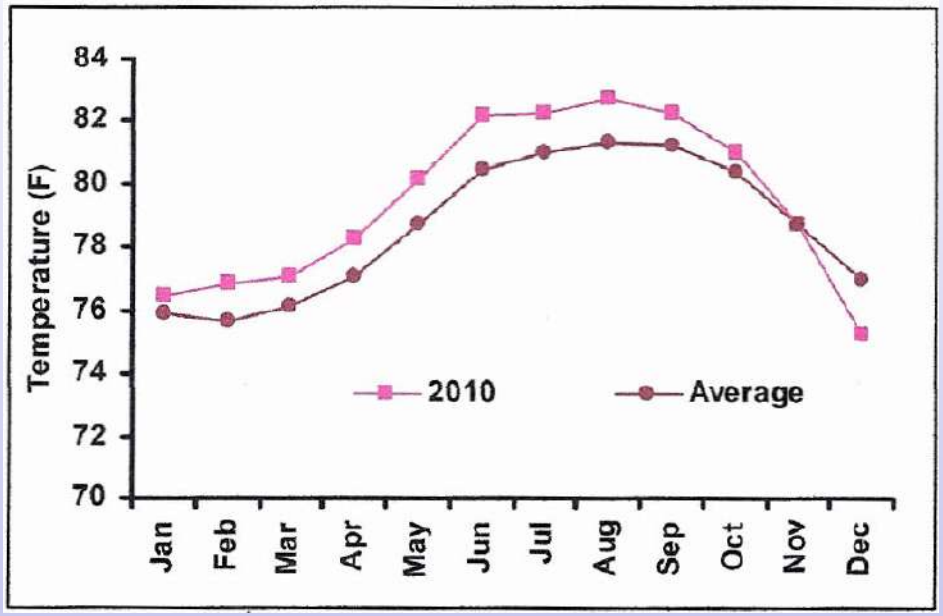
Jutla et al., 2017, ASCE JWRPM


2015-2019 Prototype of cholera prediction models
GRACE-FO (2)
CYGNSS (8)
NISTAR, EPIC
SMAP
2015
OCO-2
2013 Classification of modes of cholera
GPM
LANDSAT 8
2020
ICESAT-2
2020s Real-time regional cholera prediction
SENTINEL-6 MICHAEL FREILICH
GEDI
EMIT
LANDSAT-9
ECOSTRESS
1990s Colwell's vibrios hypothesis
SeaWiFS
LANDSAT 7
1995
SUOMI NPP
2010
TROPICS (6)
OCO-3
CALIPSO
NISAR
AQUA
AURA
CLOUDSAT
SWOT
CLARREO-PF
TSIS-1
2000
2001 Lobitz chlorophyll study
2005
GEOCARB
LIS
SAGE III
TEMPO
2020s FUTURE: Coastal/ Oceanic movement of vibrios; Shifts in ecological niches
PREFIRE (2)
MAIA
PACE
TSIS-2
SENTINEL-6B
GLIMR
ESO-1, 2, 3, 4
2025
National Aeronautics and Space Administration
NASA
EARTH FLEET
INVEST/CUBESATS
CSIM-FD 2023
HARP 2022
CIRIS 2023
CTIM* 2022
HYTI* 2022
SNOOPI* 2022
NACHOS* 2022
NACHOS2* 2022
JPSS INSTRUMENTS
OMPS-LIMB 2022
LIBERA 2027
ISS INSTRUMENTS
MISSIONS
KEY
INTERNATIONAL
PARTNERS
U.S. PARTNER
ISS INSTRUMENT
JPSS INSTRUMENT
CUBESAT
LAUNCH DATE TBD
10.13.21
PREFORMULATION
FORMULATION
OPERATING
EXTENDED

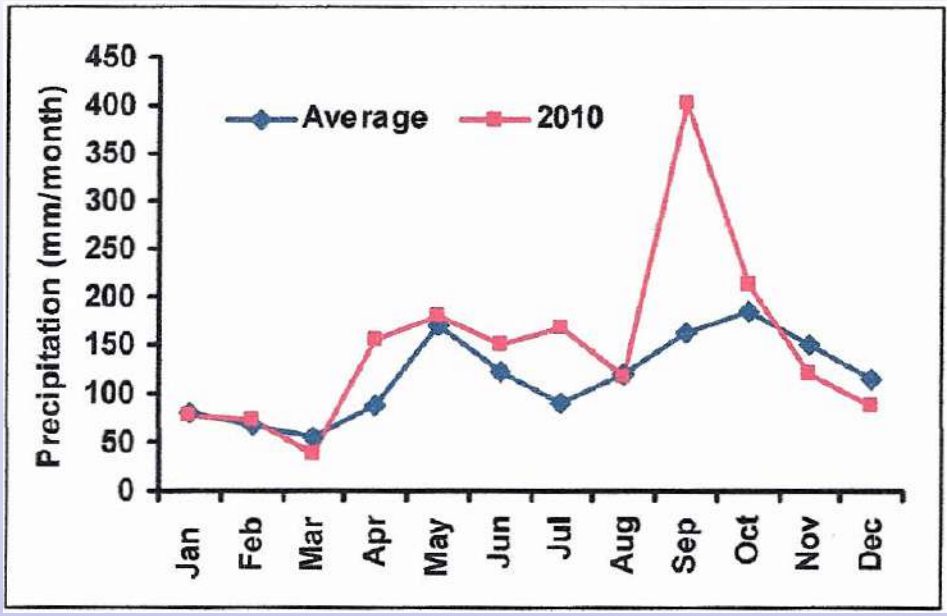
Could we have predicted the Haiti Cholera outbreak?

- **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.**

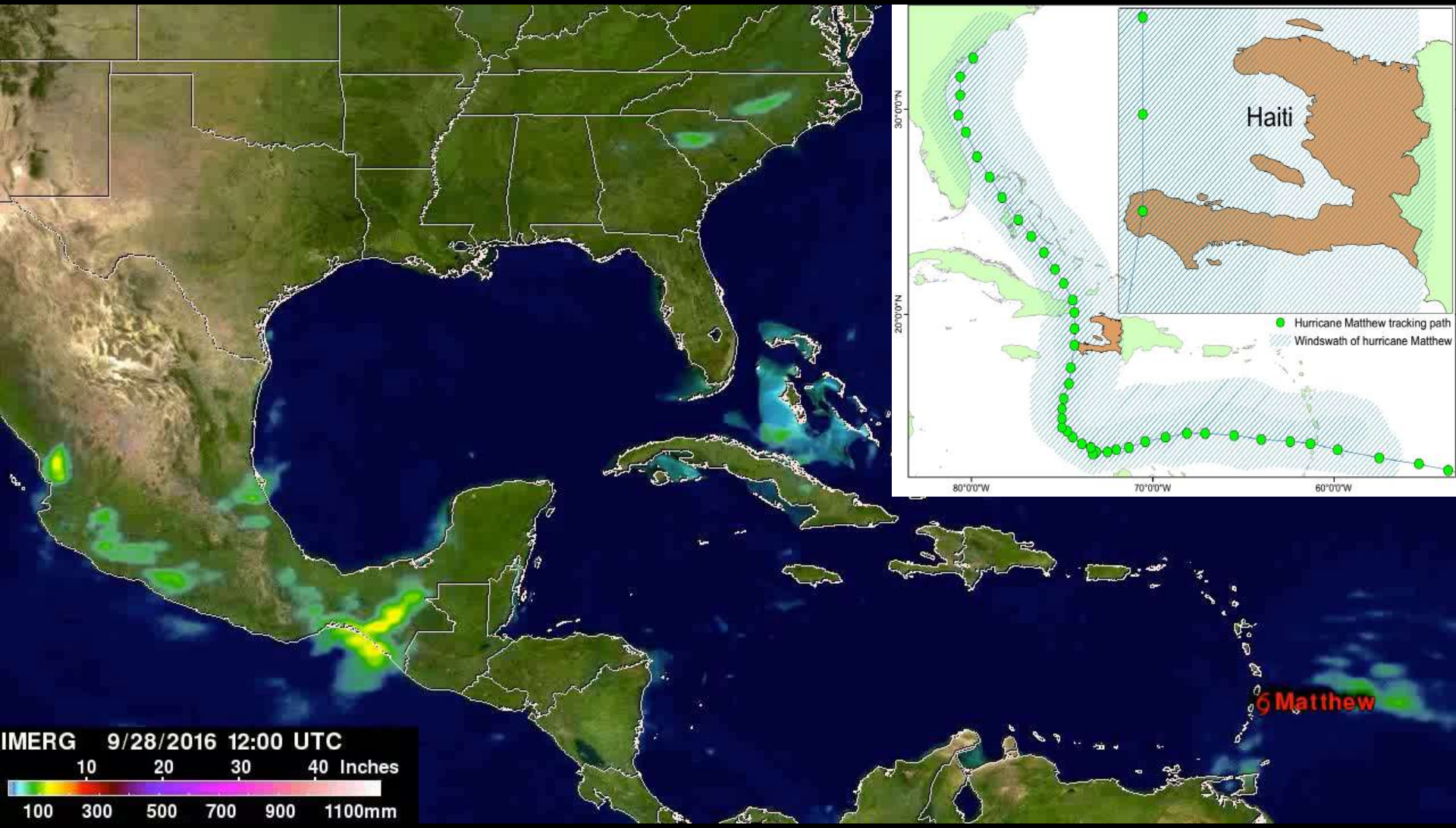
Antarpreet Jutla, Elizabeth Whitcombe, Nur Hasan, Bradd Haley, Ali Akanda, Anwar Huq, Munir Alam, R. Bradley Sack and Rita Colwell. 2013. Environmental factors influencing epidemic cholera. Amer J Trop Med Hyg 89(3) 597-607



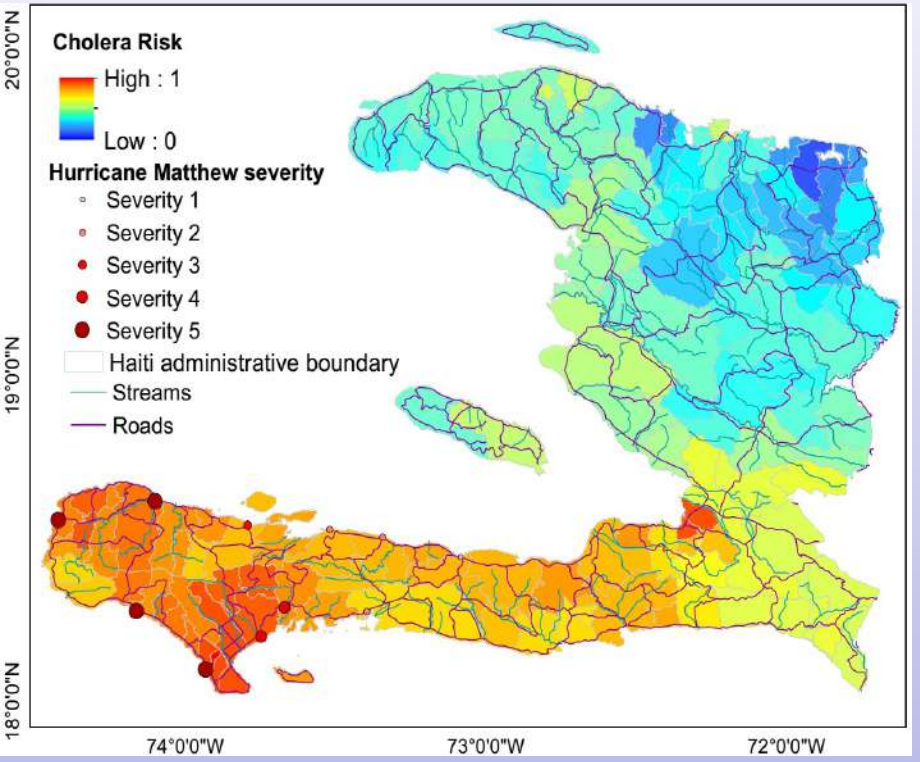
Air temperature in Haiti in 2010 compared with historical air temperature data

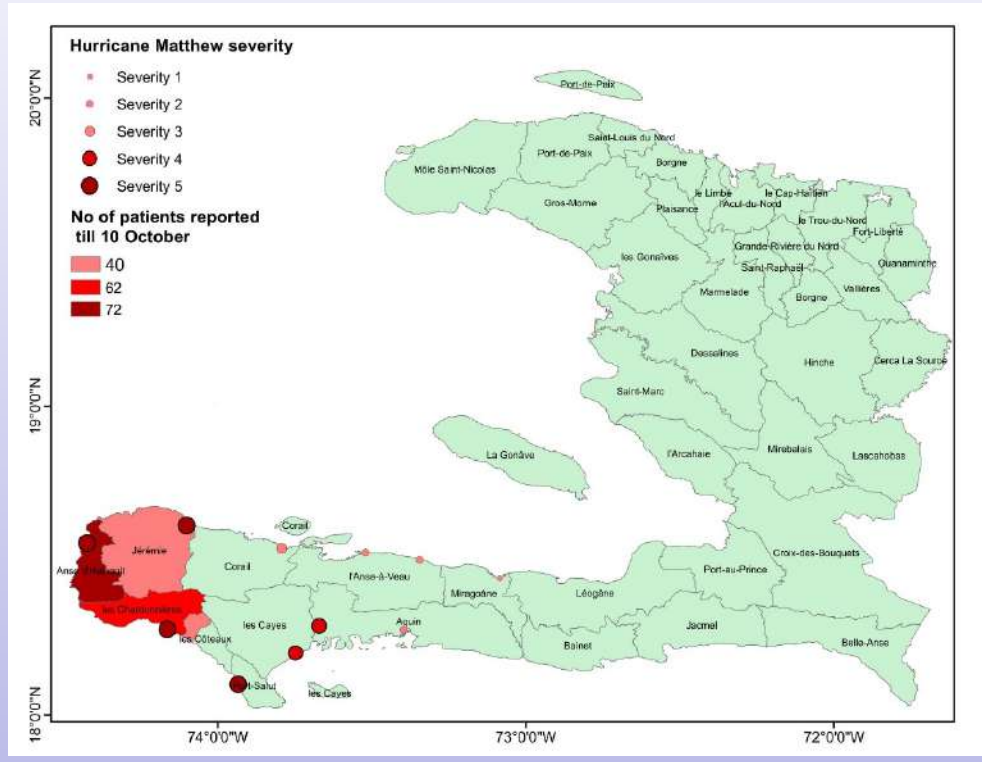


Monthly rainfall in Haiti in 2010 compared with historical rainfall data


Haiti
Hurricane Matthew tracking path
Windswath of hurricane Matthew
80°0'0"W
70°0'0"W
60°0'0"W
20°0'0"N
30°0'0"N
Matthew
IMERG 9/28/2016 12:00 UTC
10 20 30 40 Inches
100 300 500 700 900 1100mm

Cholera in Haiti



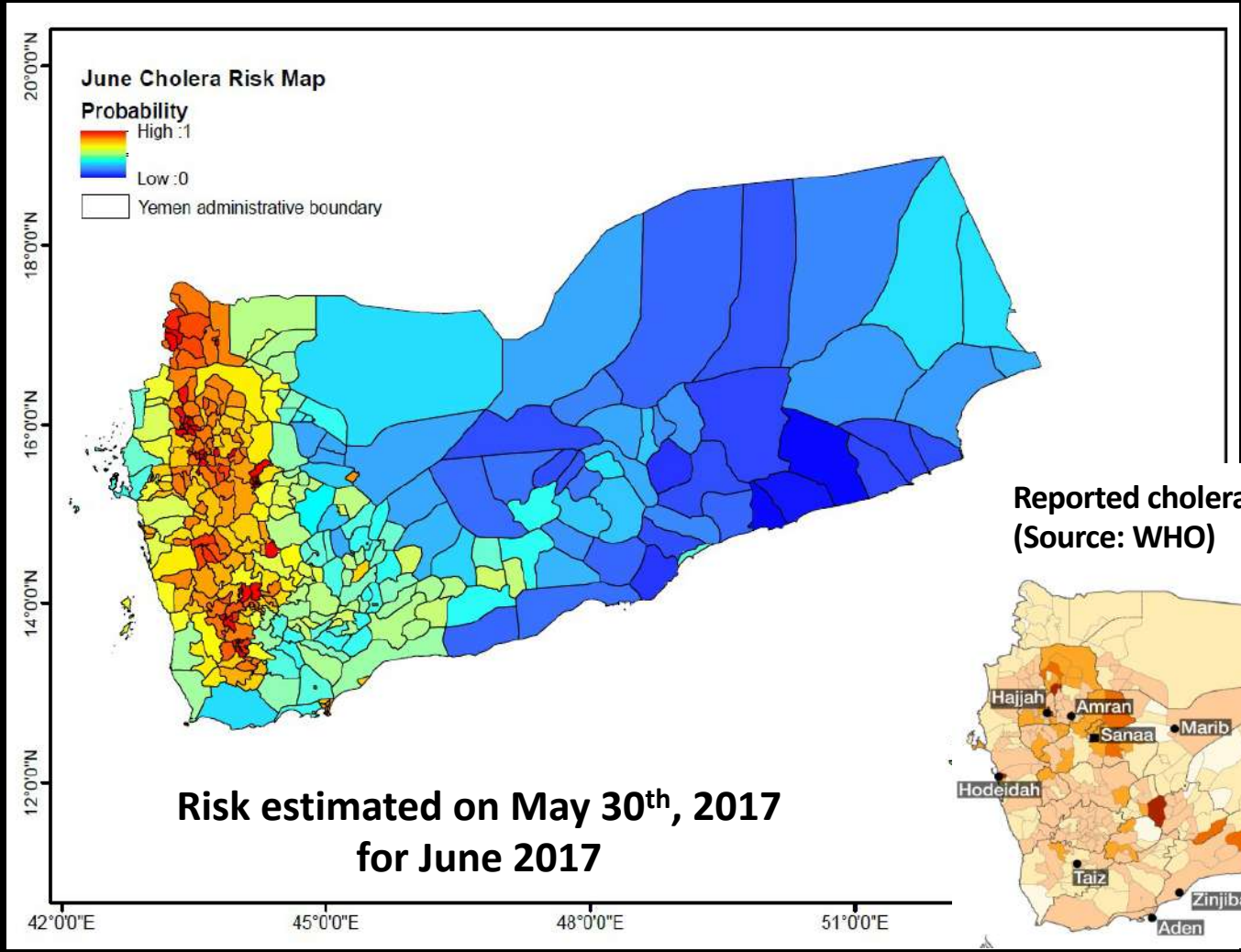


Prediction of October 2015 cholera depending on Hurricane Matthew severity

Actual cholera in October 2015 following Hurricane Matthew

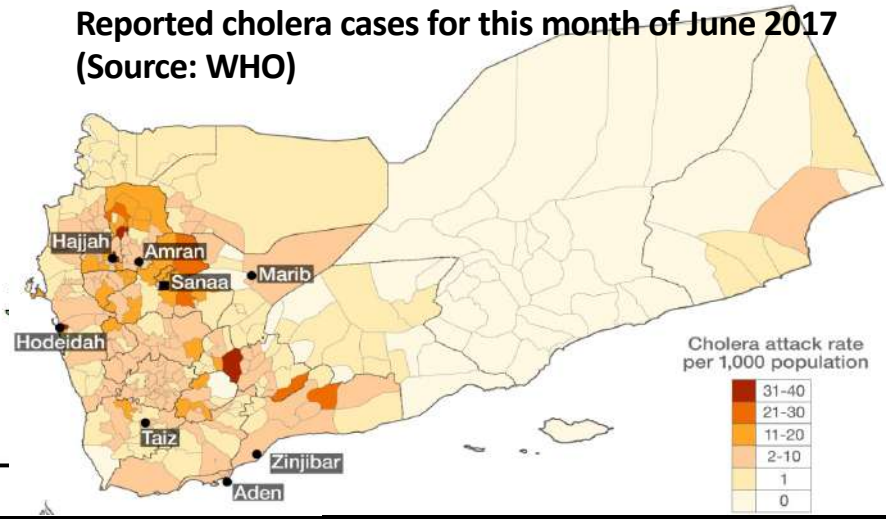
Khan et al., 2018 ASCE JWRPM

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

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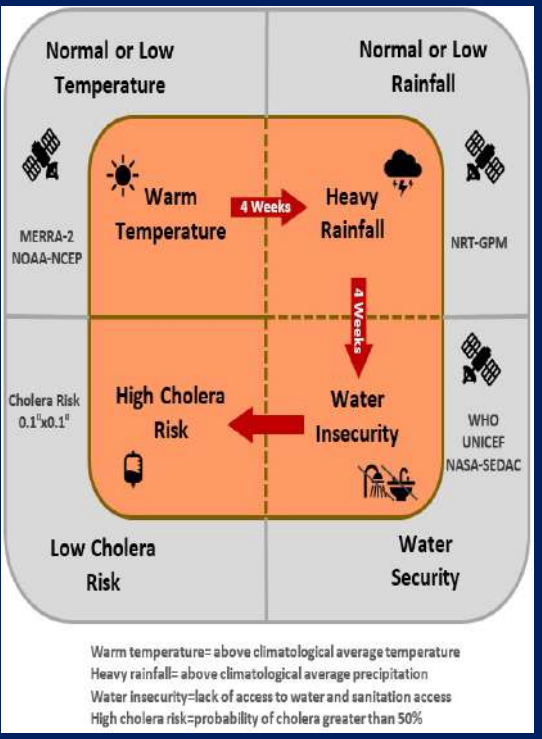

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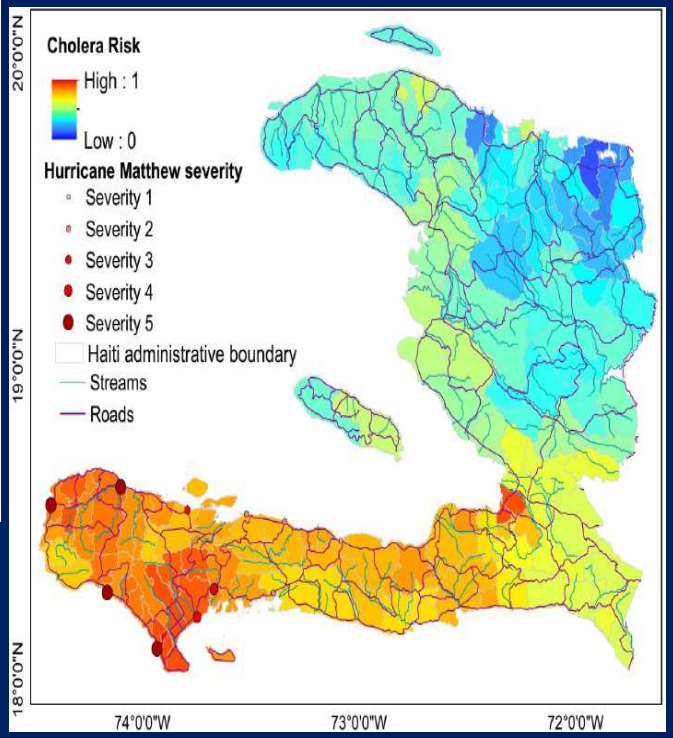

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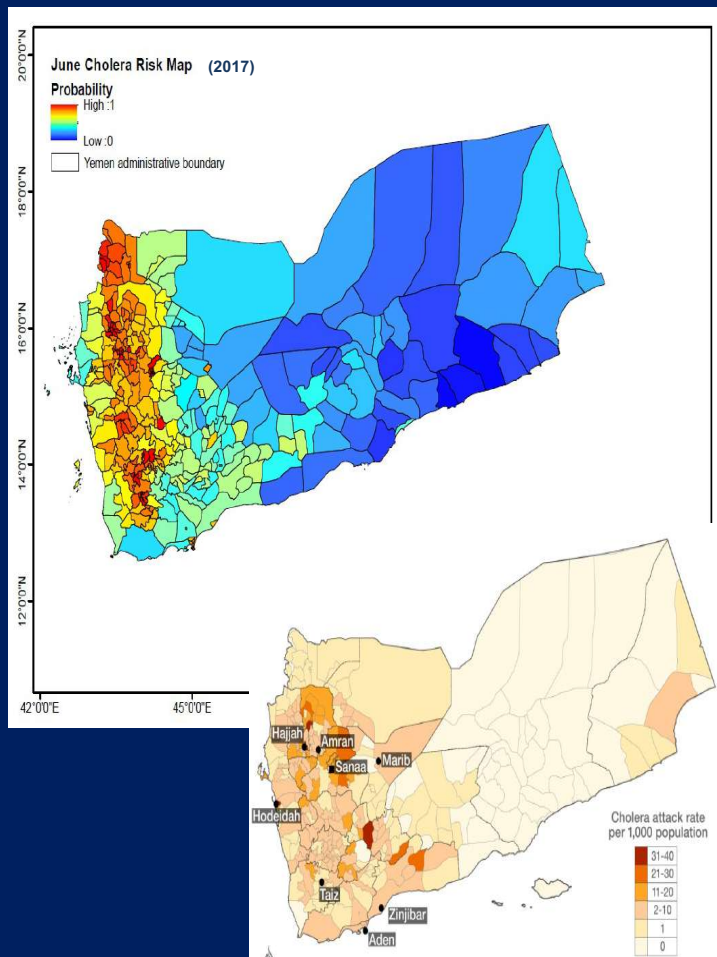
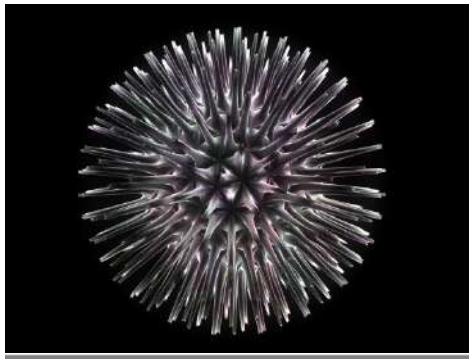
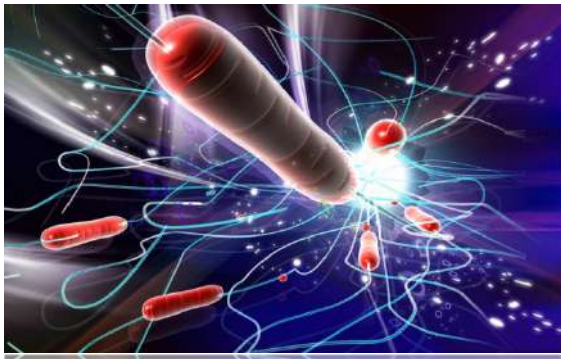




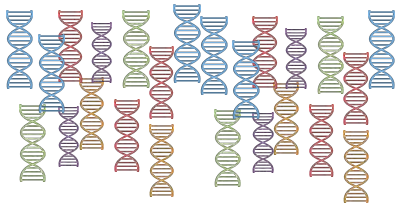


NEXT GEN SEQUENCING AND METAGENOMICS

Shotgun whole (meta)genome sequencing

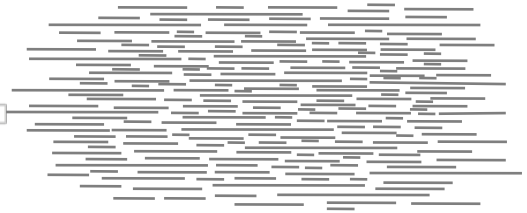
Biological specimen

Community DNA

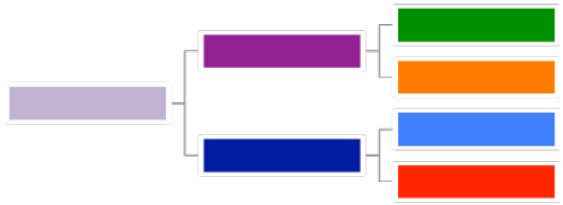


DNA Sequencing

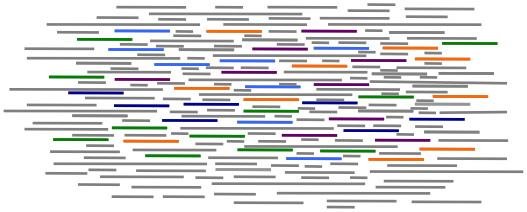
Raw Sequence Reads



CosmosID Database



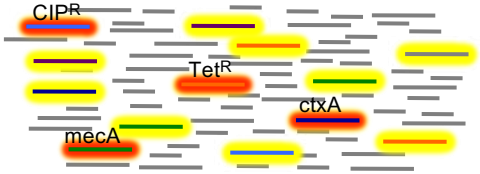
GenBook Biomarker Matching



Identified

All Microbes

CosmosID AR/VF Database



Microbial Identification & Pathogen Characterization

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Unlocking The Microbiome

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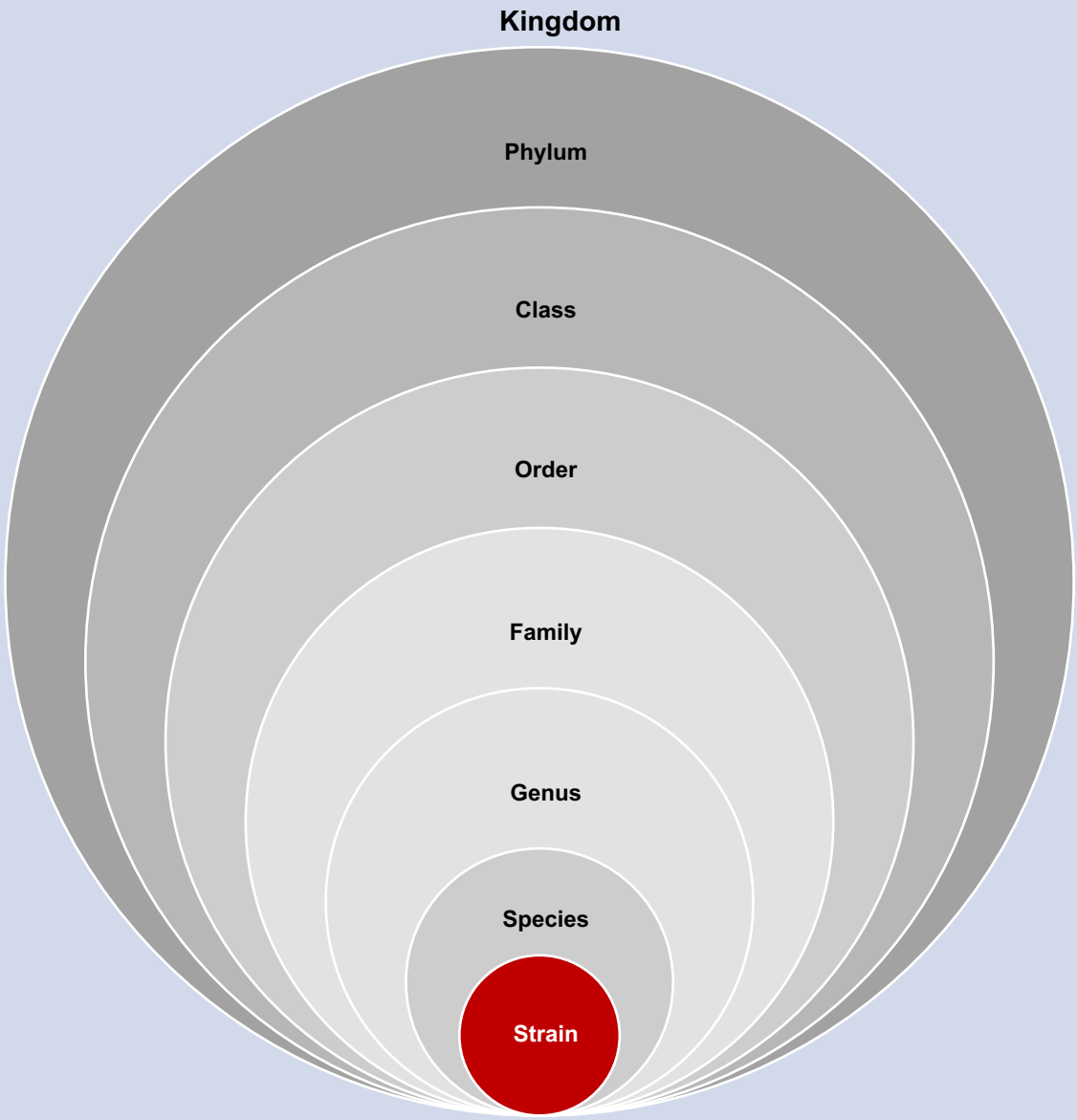
Strain is the Clinically Informative and Actionable Unit



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Microbiome Analysis of Acute Diarrheal Patients Compared with Healthy Individuals

pre-publication results

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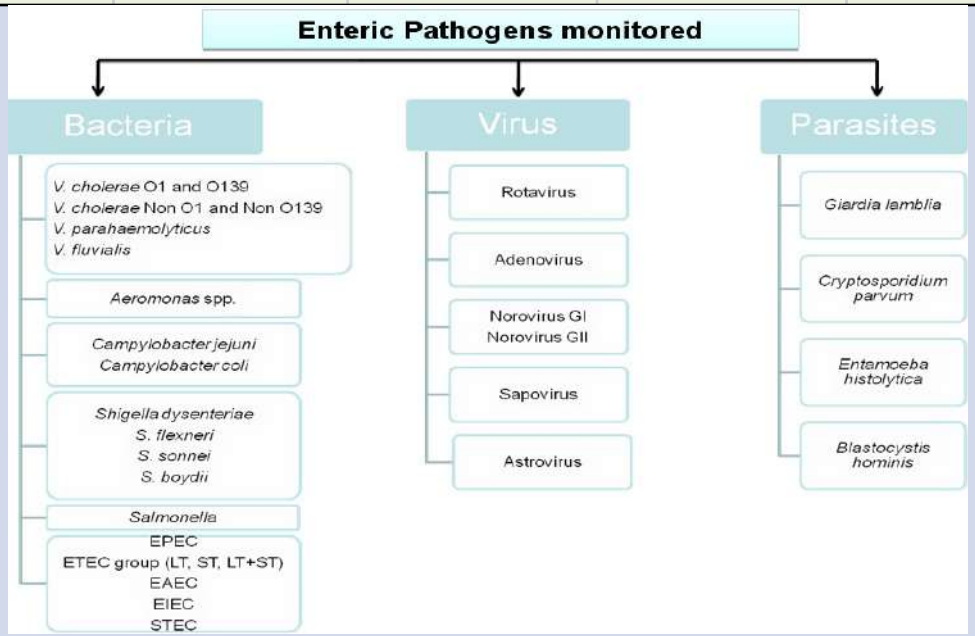
Study Cohort

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

Study Phases	Total # of Samples	Known Etiology	Unknown Etiology	Healthy Control
PHASE I	9	9	0	0
PHASE II	28	0	18	10
PHASE III	37	17	10	10



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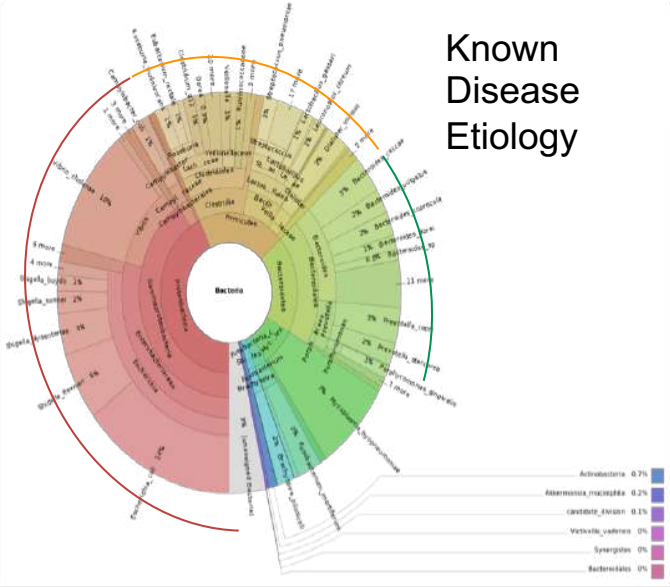
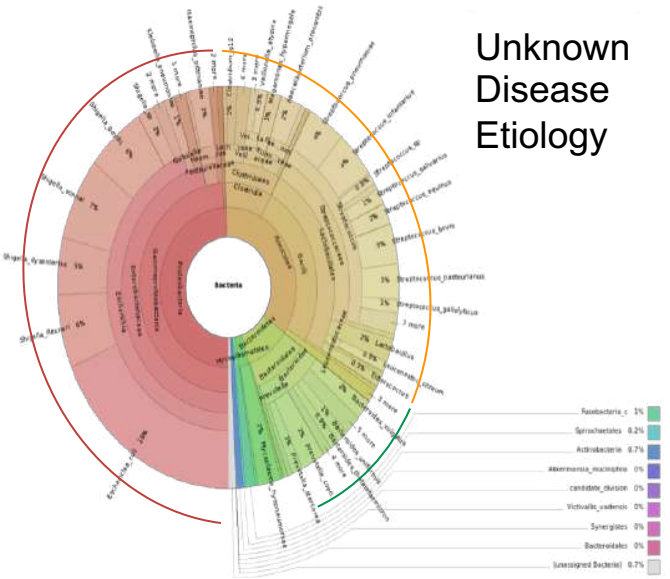
Microbial Community in Healthy vs Diarrheal Patients

DIARRHEAL PATIENTS

HEALTHY INDIVIDUALS



Known Disease Etiology

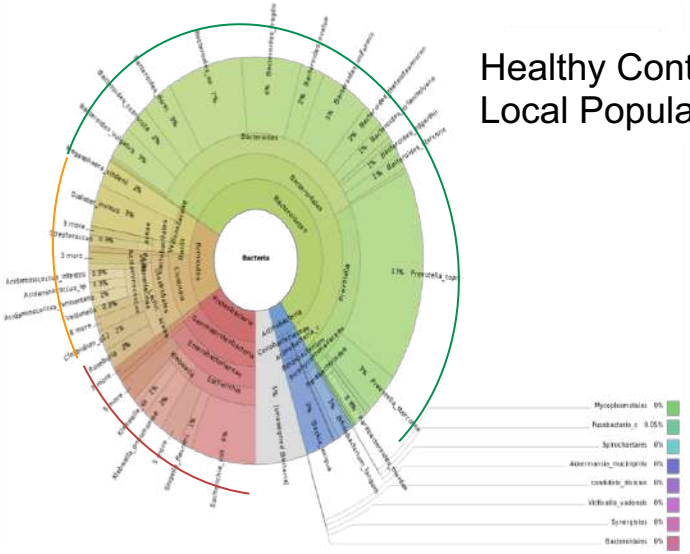


Unknown Disease Etiology

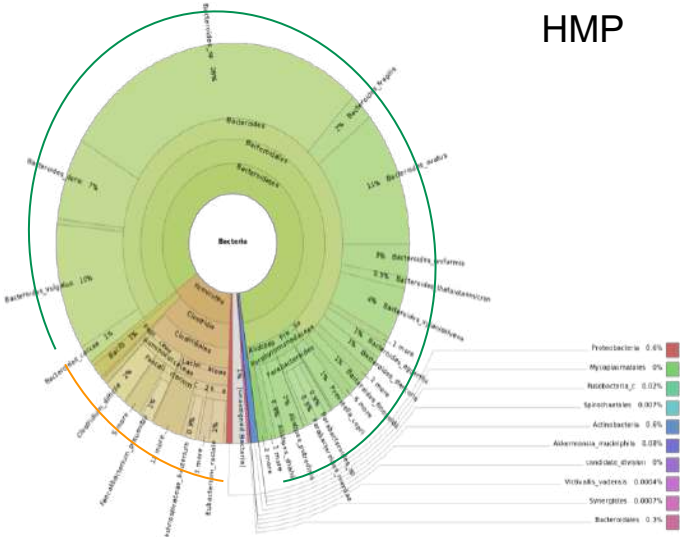
γ- Proteobacteria

Firmicutes

Bacteroidetes

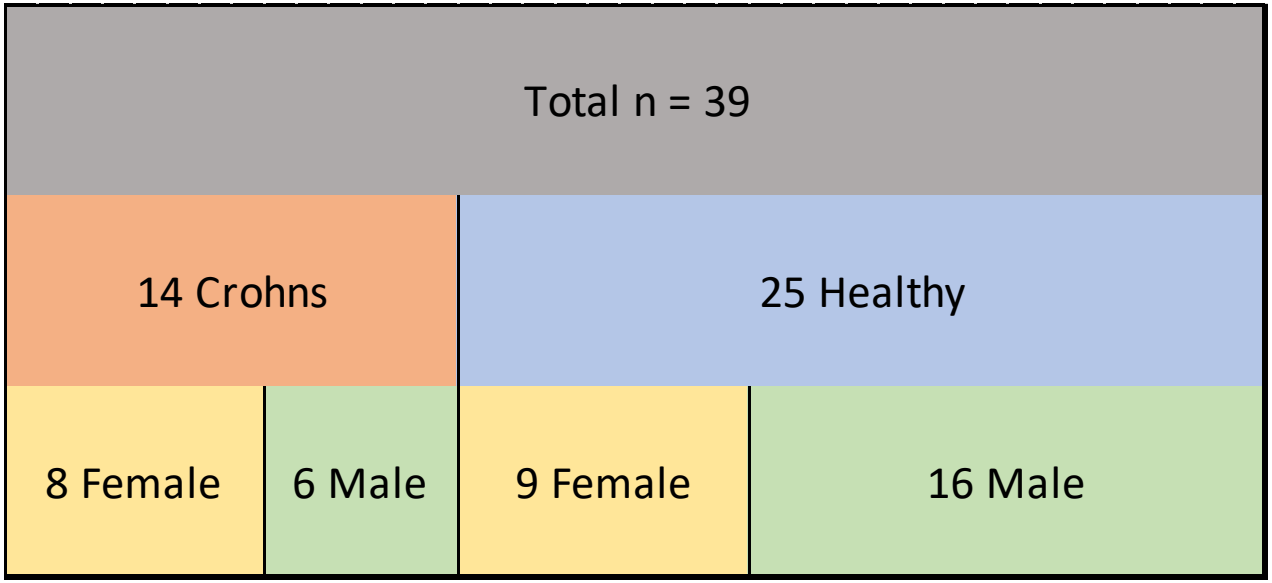


Healthy Control Local Population



HMP

Crohn's Disease and the Microbiome



- 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"

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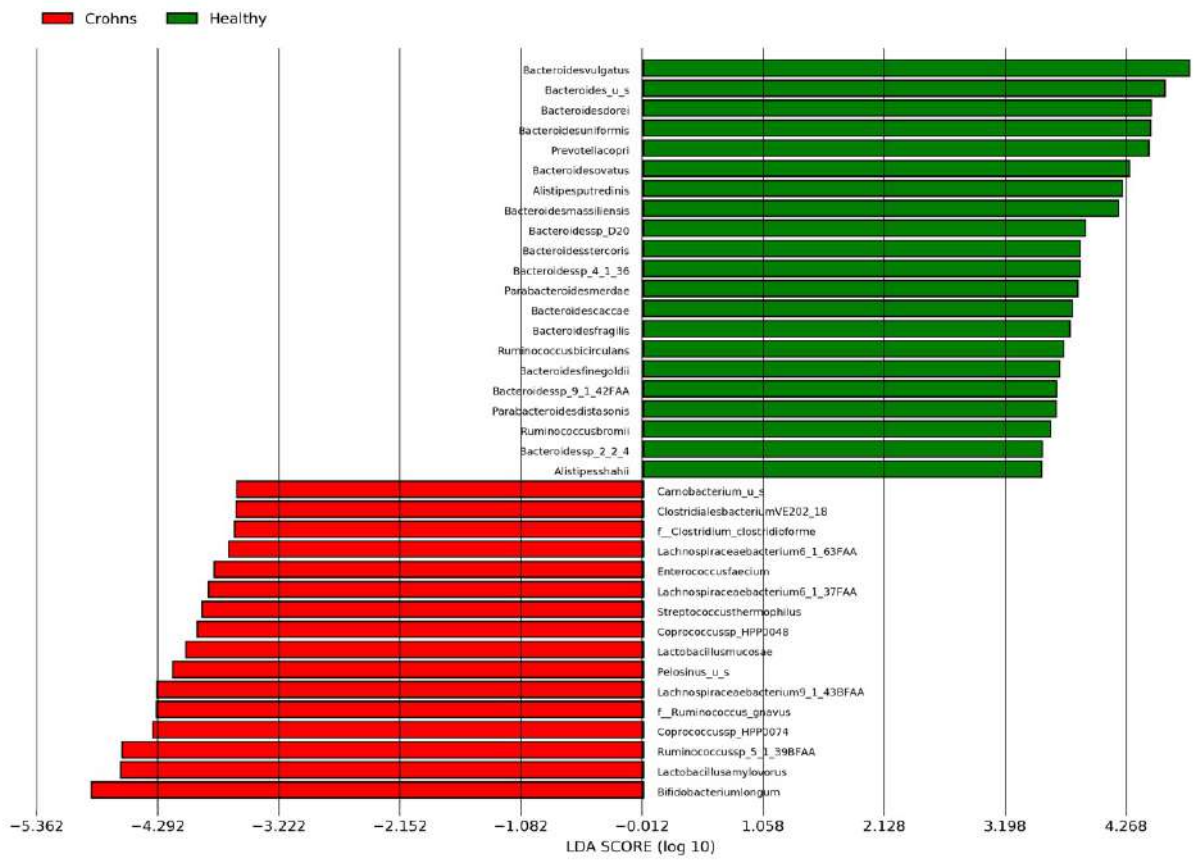
Species Enrichment in Healthy vs Crohn's



Analysis provided by CosmosID

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Celiac Disease and the Microbiome

Leonard, M.M., Karathia, H., Pujolassos, M. et al. Multi-omics analysis reveals the influence of genetic and environmental risk factors on developing gut microbiota in infants at risk of celiac disease. Microbiome 8, 130 (2020).

HARVARD MEDICAL SCHOOL

MASSACHUSETTS GENERAL HOSPITAL

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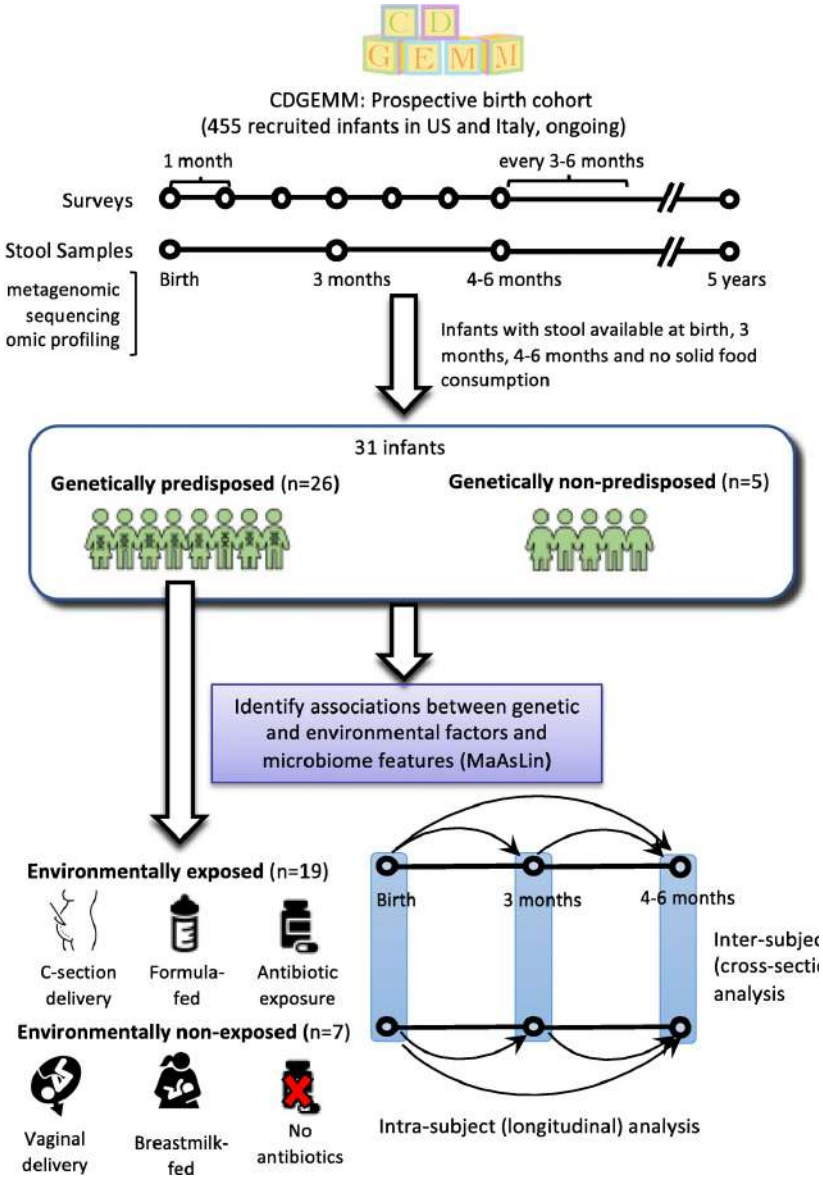
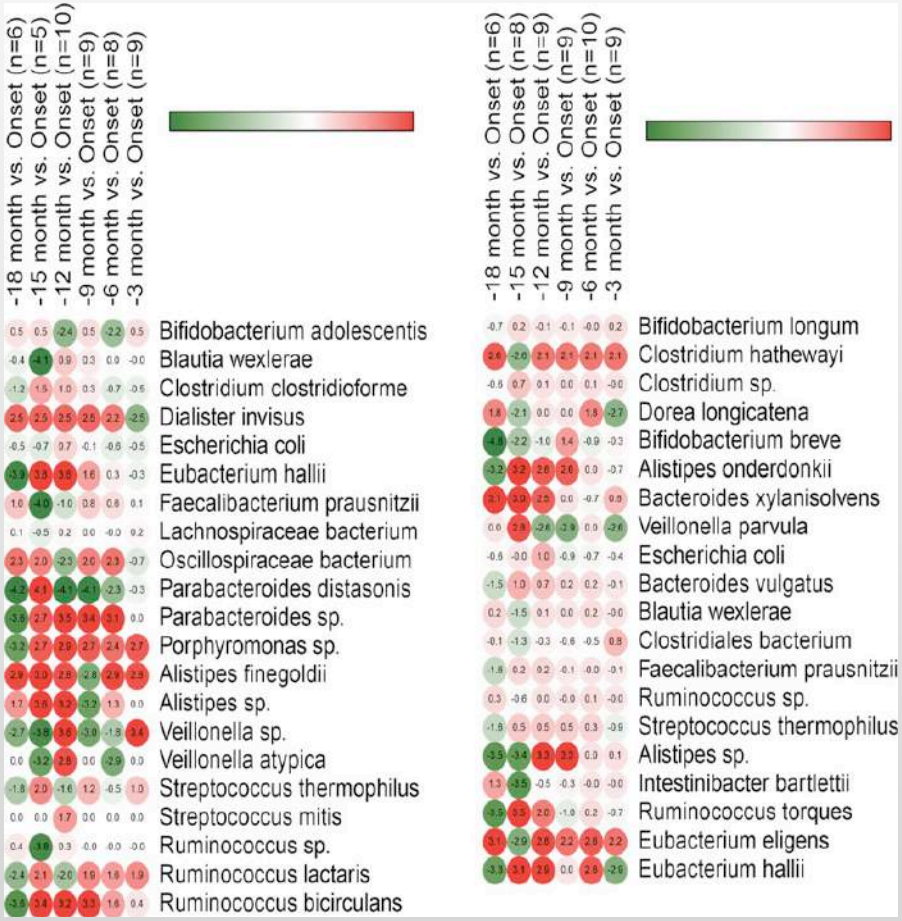
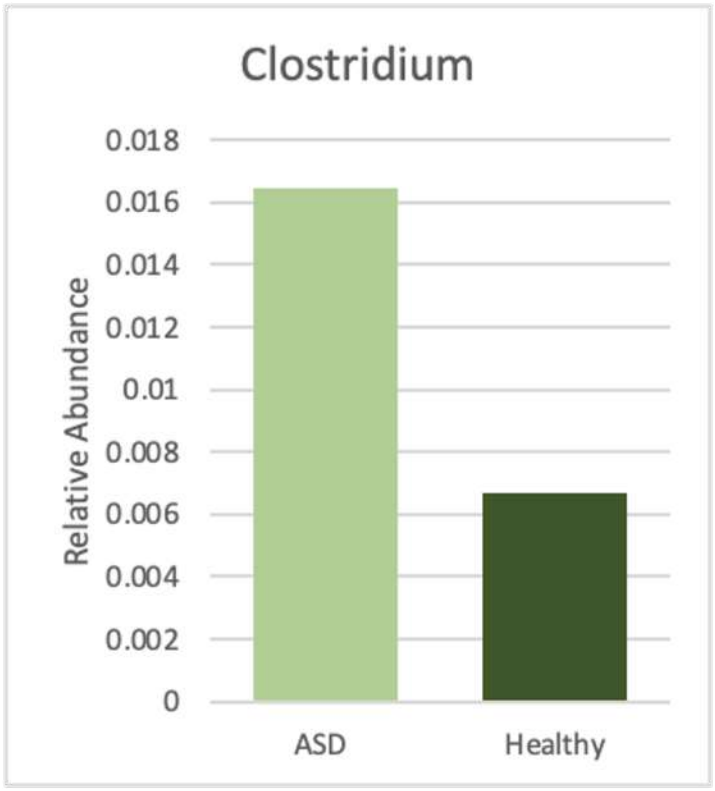




Longitudinal (intrasubject) analysis for microbial species. A paired Wilcoxon (Wilcoxon signed rank) test was used to identify microbial species whose abundance differentially changes between a preonset time point (−18, −15, −12, −9, −6, and −3 mo) and CD onset. Any species for which a statistically 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.

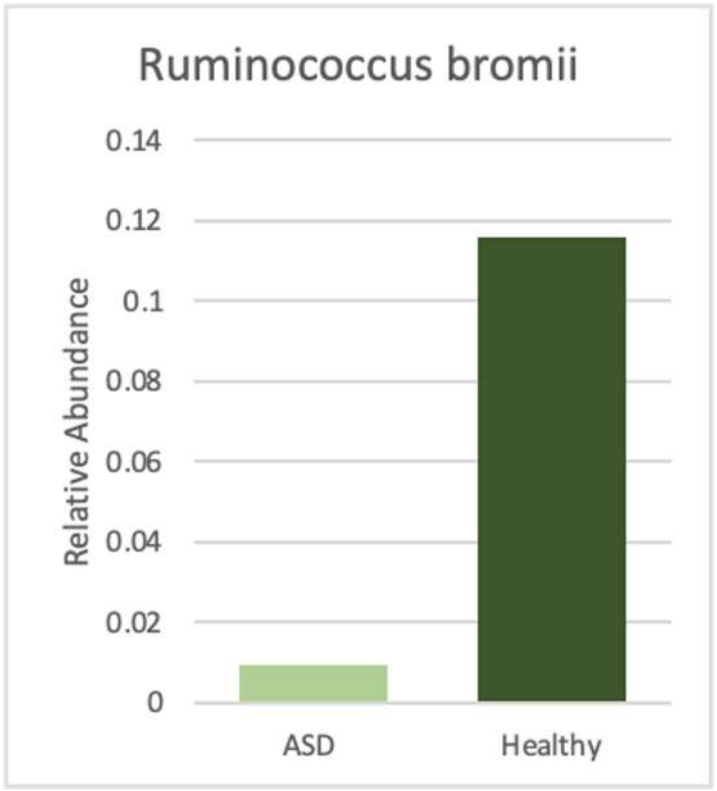
Leonard et al. 2021. Microbiome signatures of progression toward celiac disease onset in at-risk children in a longitudinal prospective cohort study. PNAS. https://doi.org/10.1073/pnas.2020322118

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

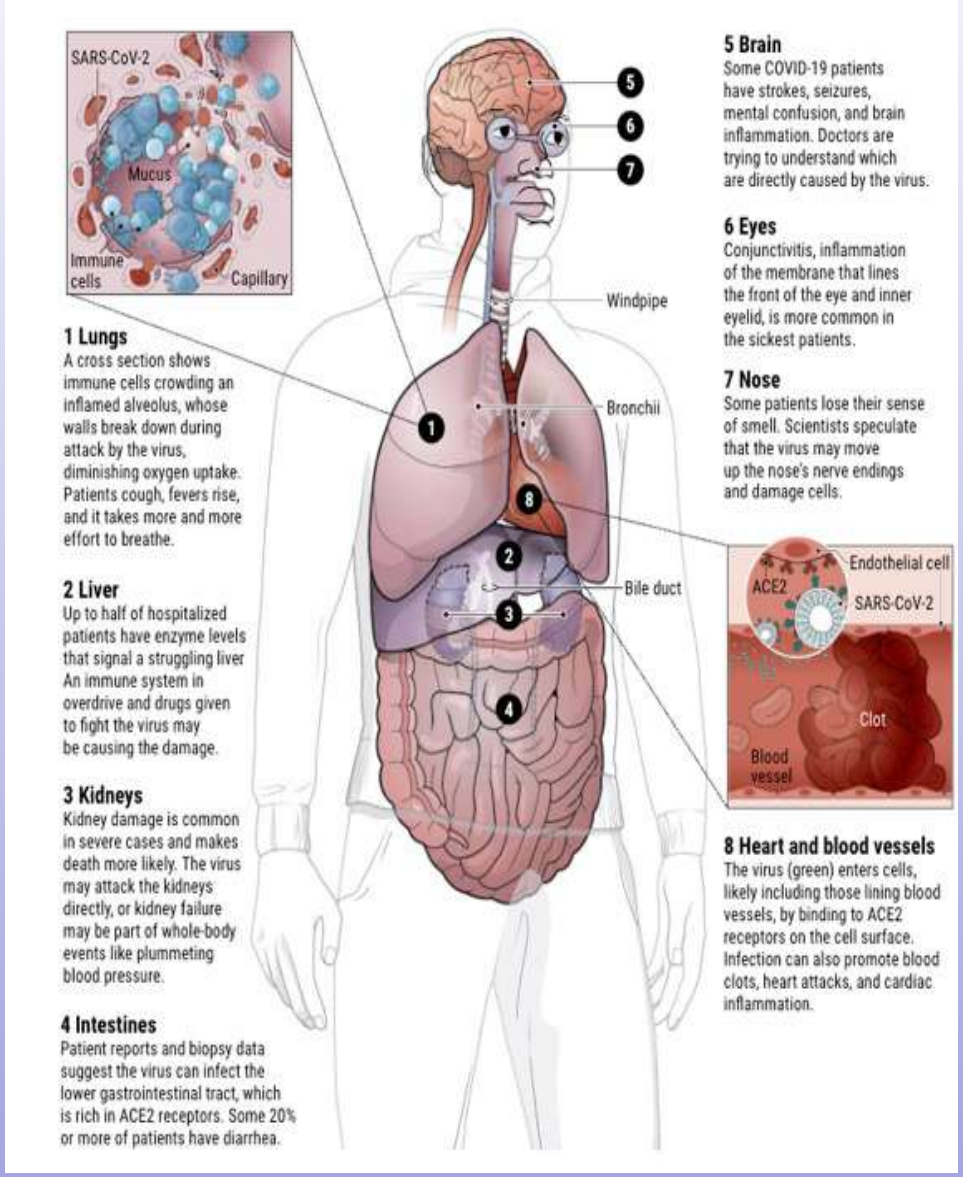


- Major metabolizer of resistant starches
- Ruminococcus bromii allows for the cross-feeding of many other bacteria:
  - Eubacterium rectale (a butyrate producer)
  - Ruminococcus gnavus (an acetate, lactate and formate producer)

Is COVID-19 polymicrobial and systemic?

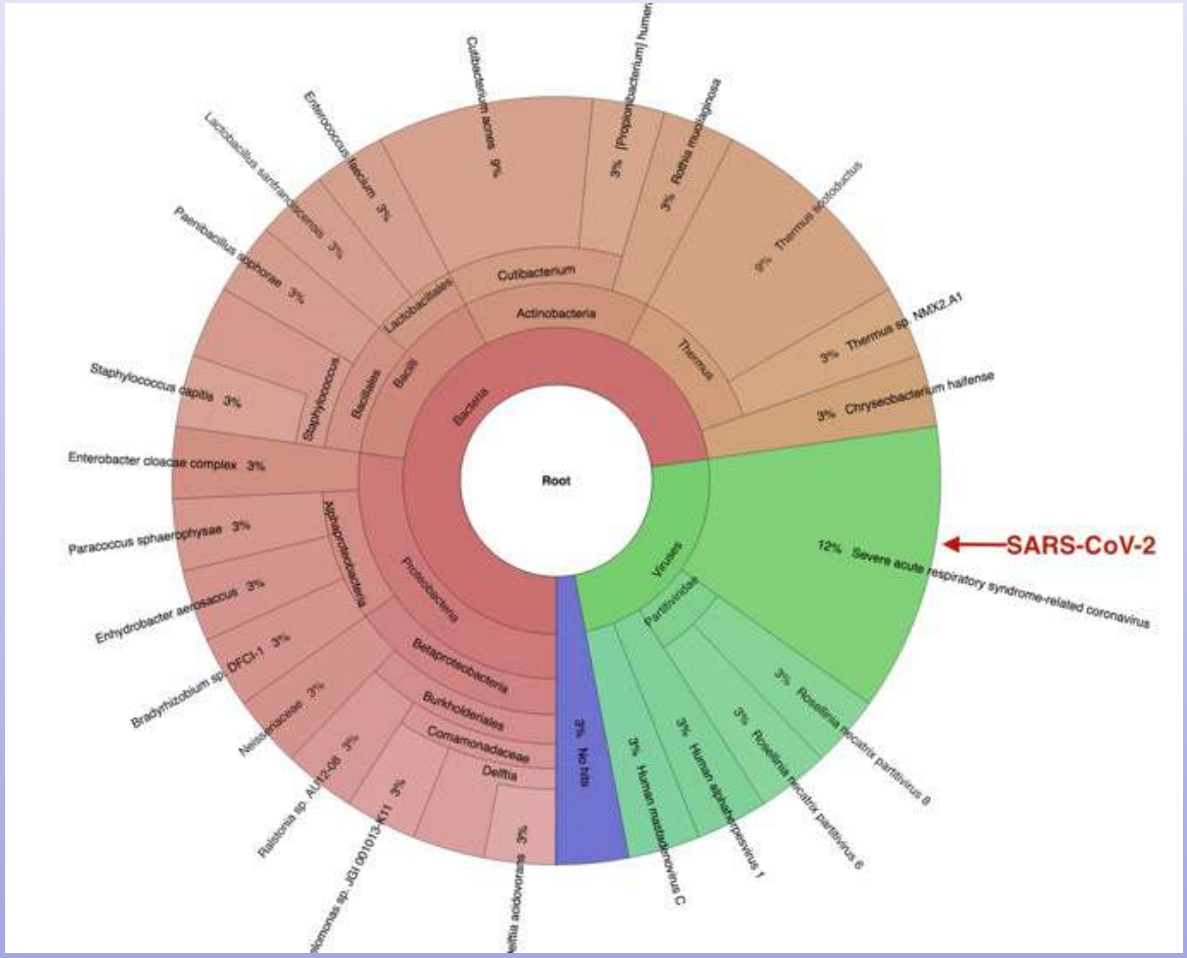
How does coronavirus kill? Clinicians trace a ferocious rampage through the body, from brain to toes

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

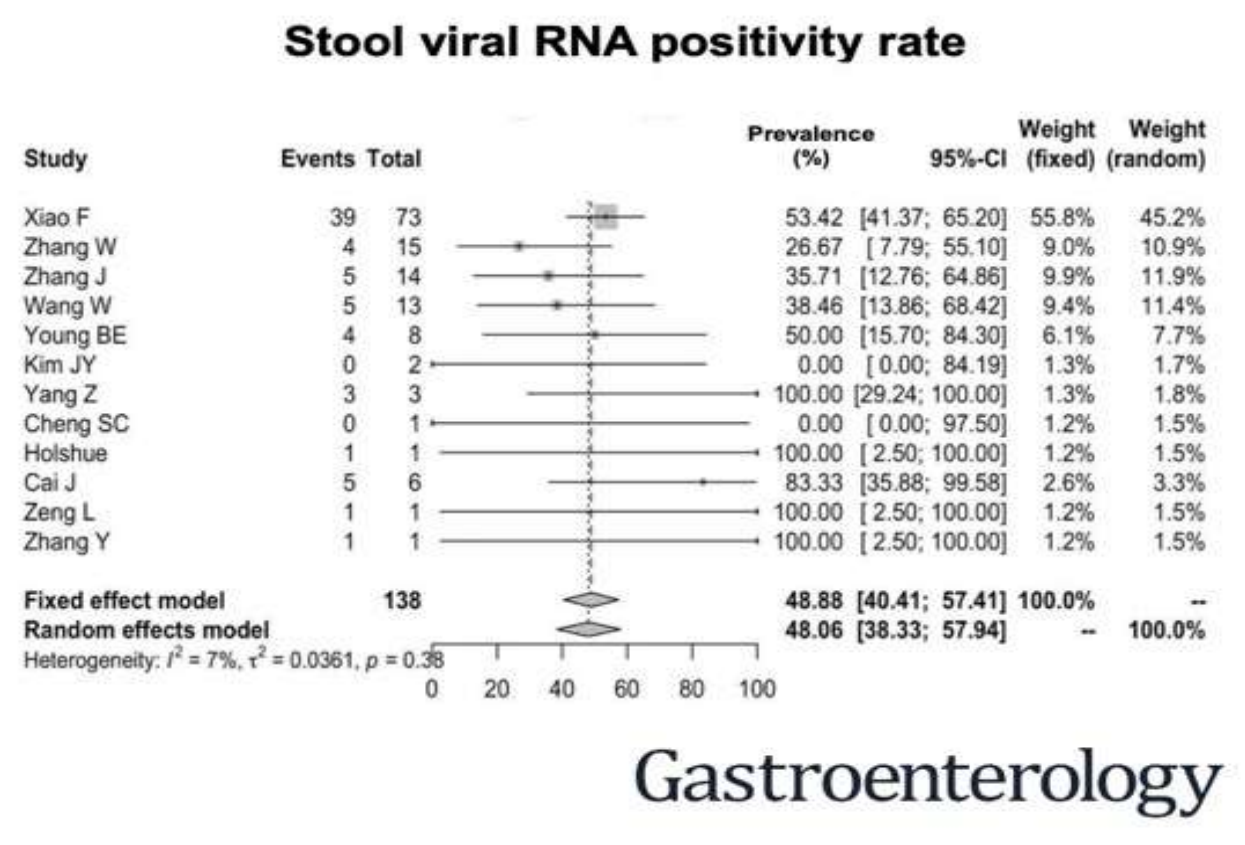


https://www.sciencemag.org/news/2020/04/how-does-coronavirus-kill-clinicians-trace-ferocious-rampage-through-body-brain-toes

Identification of Bacteria and Viruses Present in Respiratory Samples in which SARS-CoV-2 has been Detected

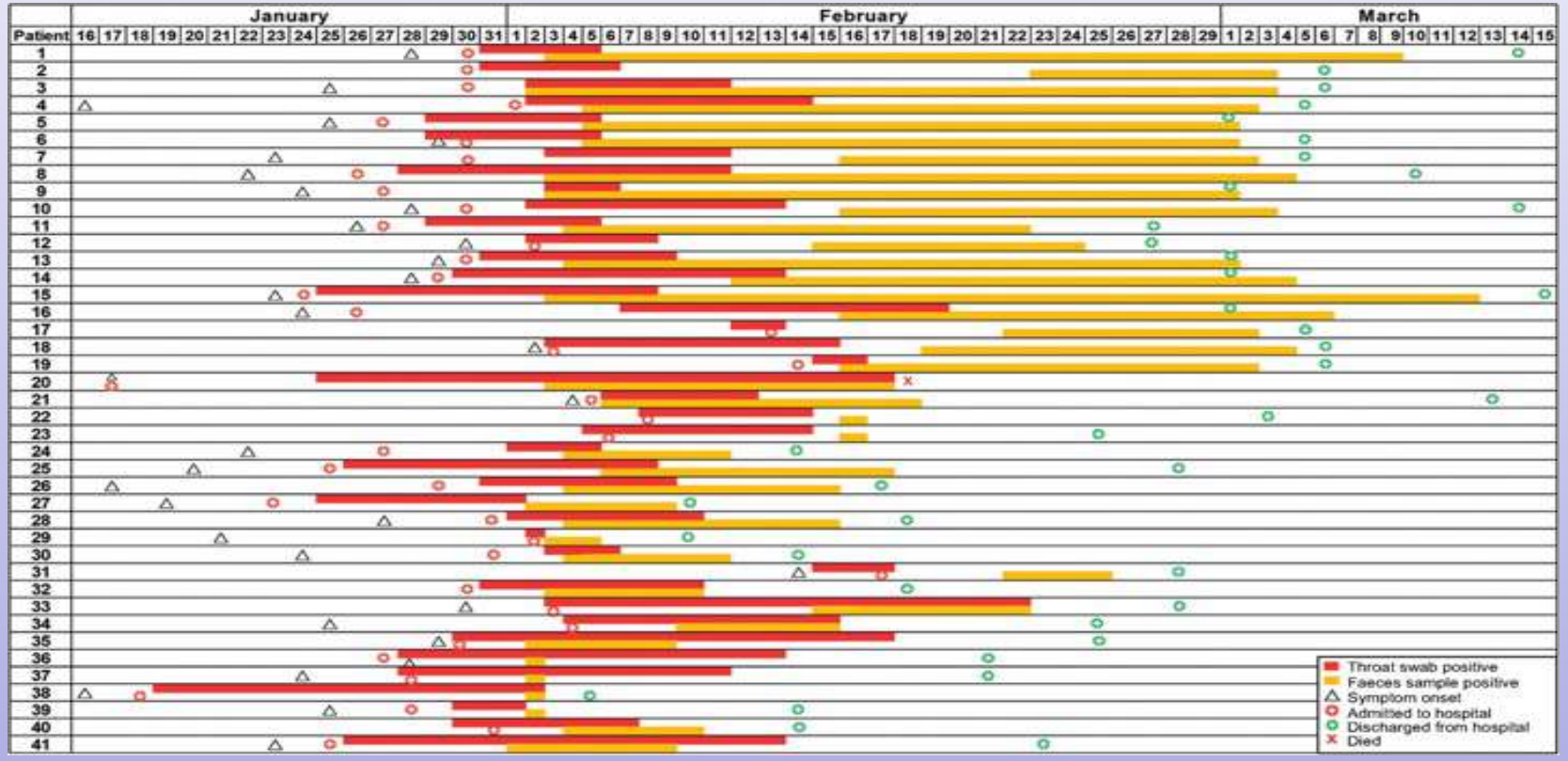


SARS Cov-2 viral RNA has been detected in 48.1% of stool samples



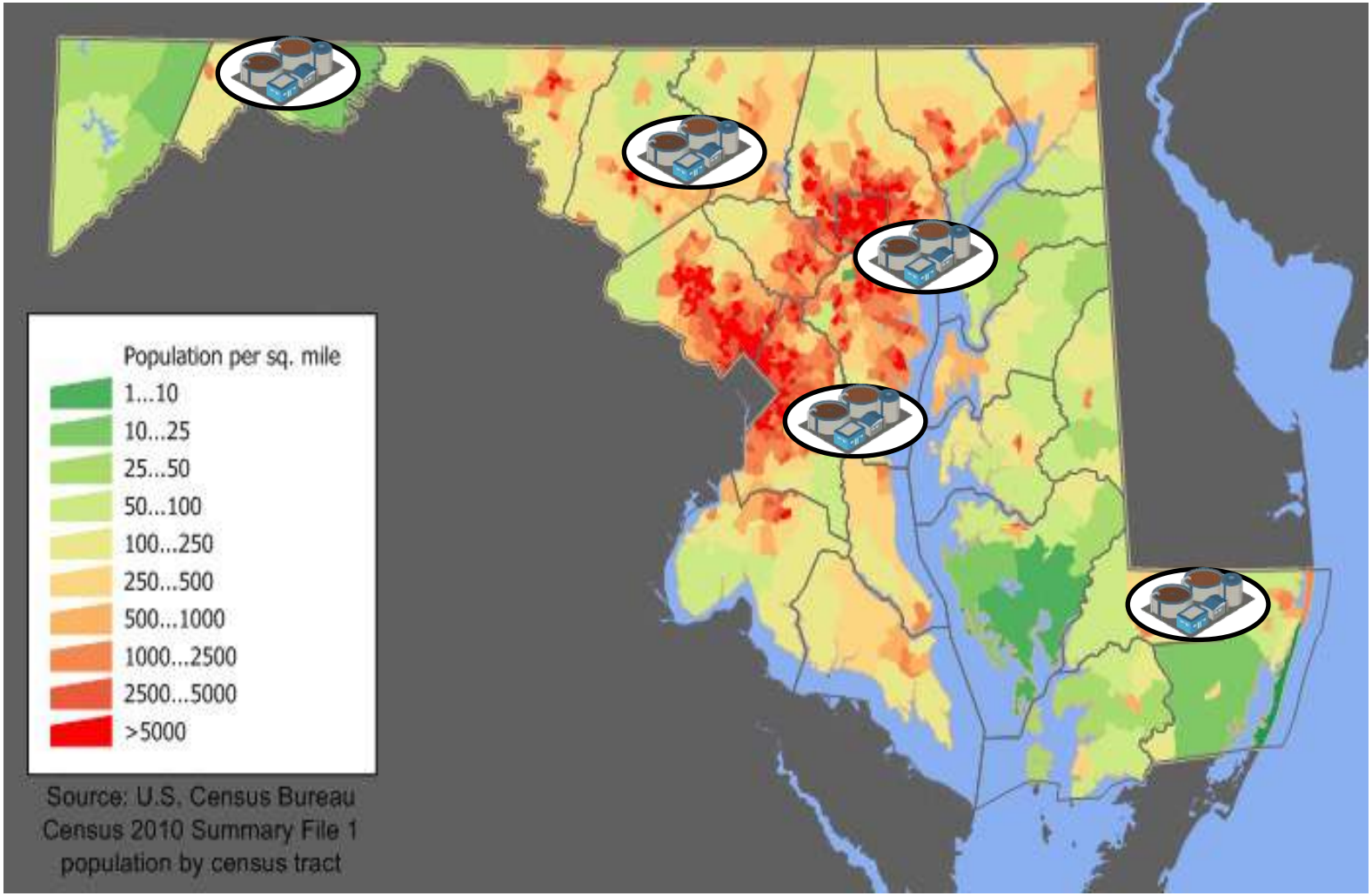
Cheung et al., (2020). Gastrointestinal Manifestations of SARS-CoV-2 Infection and Virus Load in Fecal Samples from the Hong Kong Cohort and Systematic Review and Meta-analysis. Gastroenterology. Pre-Proof

Positive Stool Samples Detected After Respiratory Sample Tested Negative During Recovery

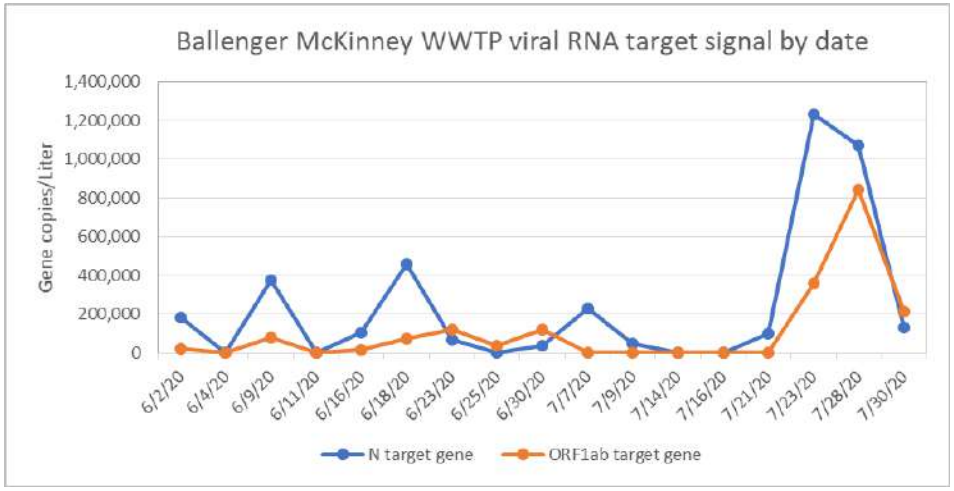


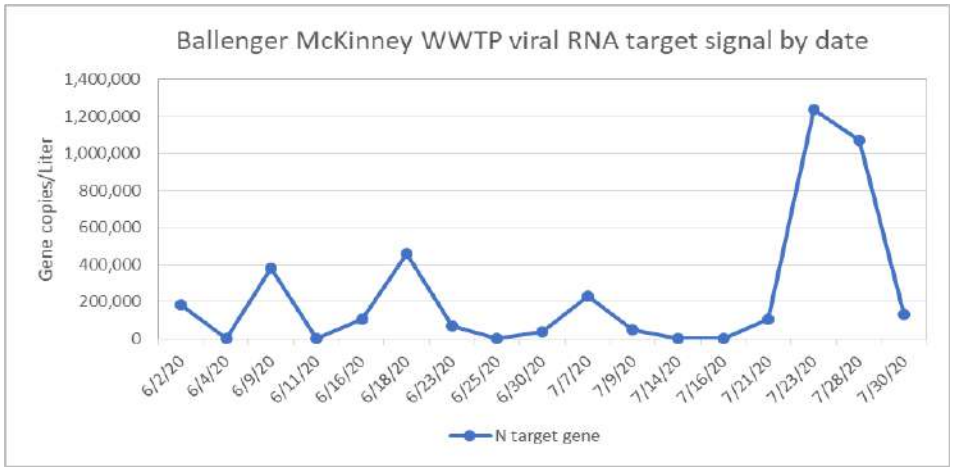
Wu Y, Guo C, Tang L, et al. Prolonged presence of SARS-CoV-2 viral RNA in faecal samples. 2020 *The lancet Gastroenterology – hepatology. Volume 5, Issue 5, 434 - 435*

COVID-19 tracking in wastewater



Results from Frederick, Maryland sites, 2020





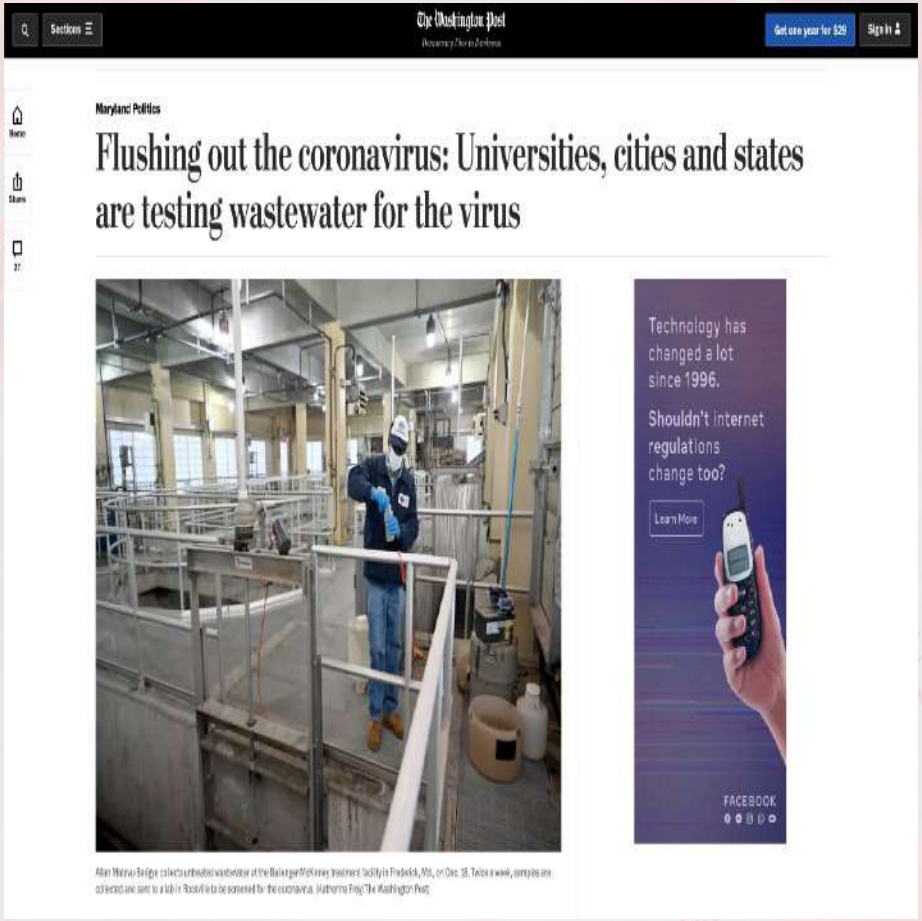
COSMOSID® Unlocking The Microbiome

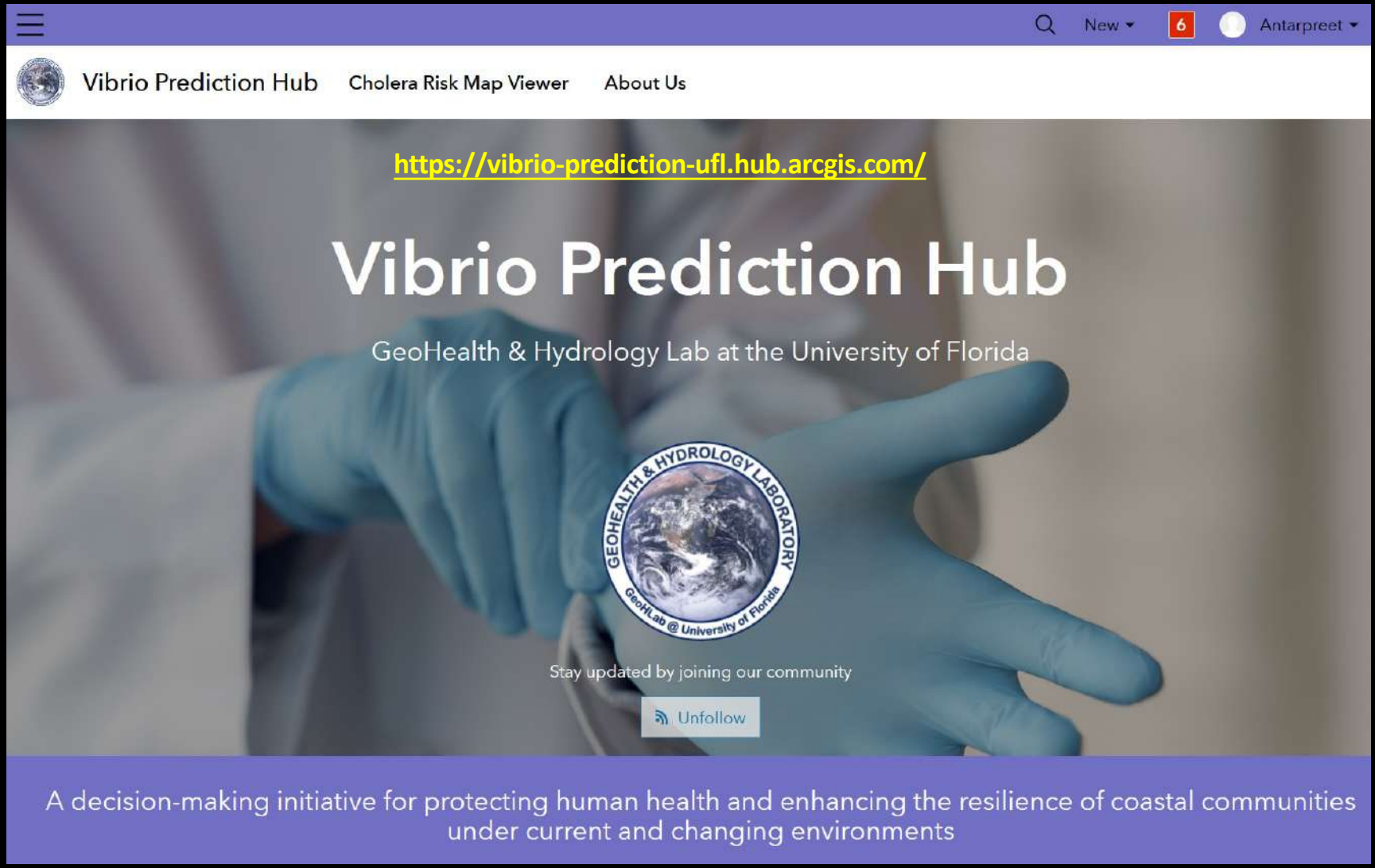
JOHNS HOPKINS UNIVERSITY

UNIVERSITY OF MARYLAND 18 56

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




New
6
Antarpreet
Vibrio Prediction Hub
Cholera Risk Map Viewer
About Us
https://vibrio-prediction-ufl.hub.arcgis.com/
Vibrio Prediction Hub
GeoHealth & Hydrology Lab at the University of Florida
GEOHEALTH & HYDROLOGY LABORATORY
GeoHiLab @ University of Florida
Stay updated by joining our community
Unfollow
A decision-making initiative for protecting human health and enhancing the resilience of coastal communities under current and changing environments

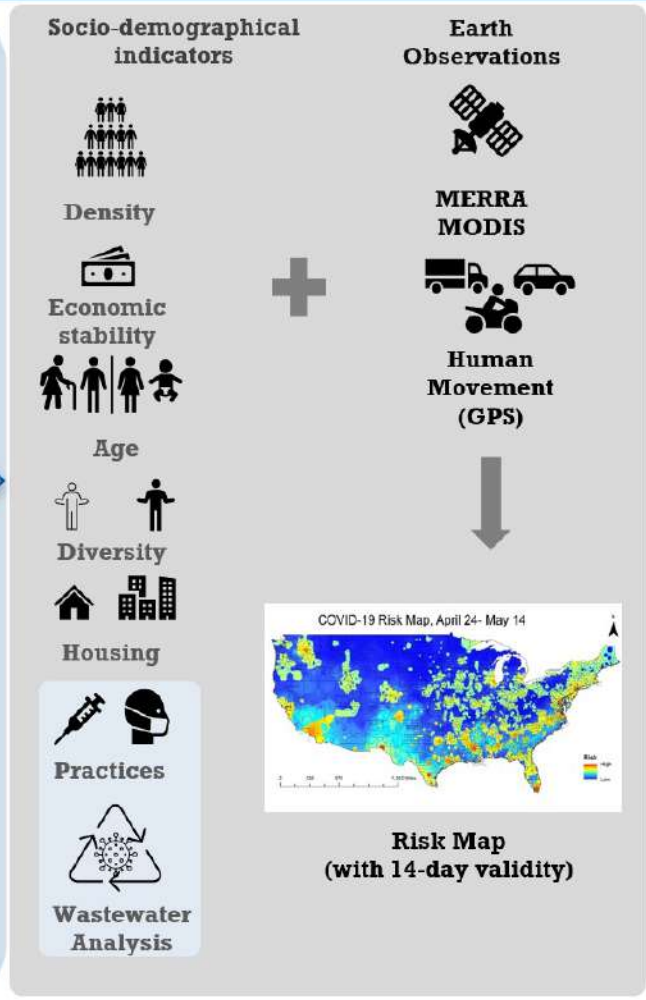
SARS-CoV-2 (COVID-19)

Development of prediction algorithm

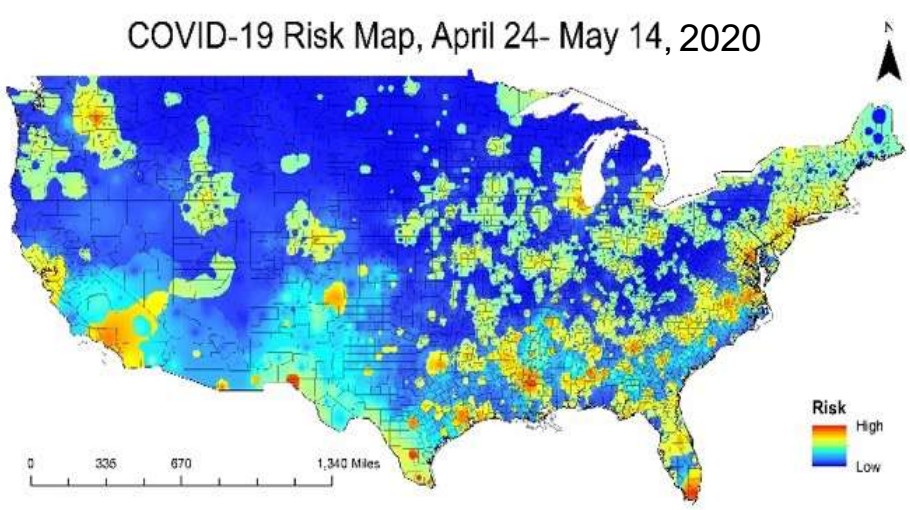
In-house cholera prediction algorithm was modified for COVID-19
Algorithm is based on geographically weighted raster probabilistic dose-response assimilation technique

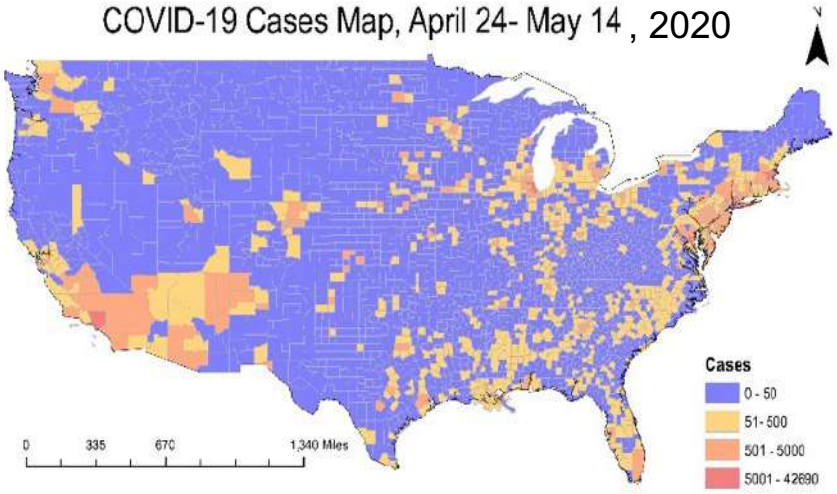
(Email ajutla@ufl.edu and moiz.usmani@ufl.edu for details)

https://covid-ufl.hub.arcgis.com/apps/covid-19-risk-map/explore

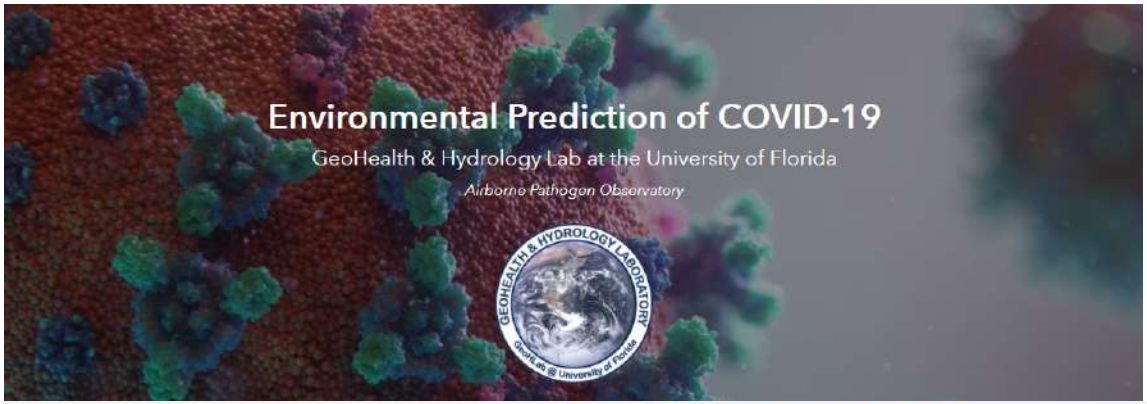


Prediction of coronavirus risk

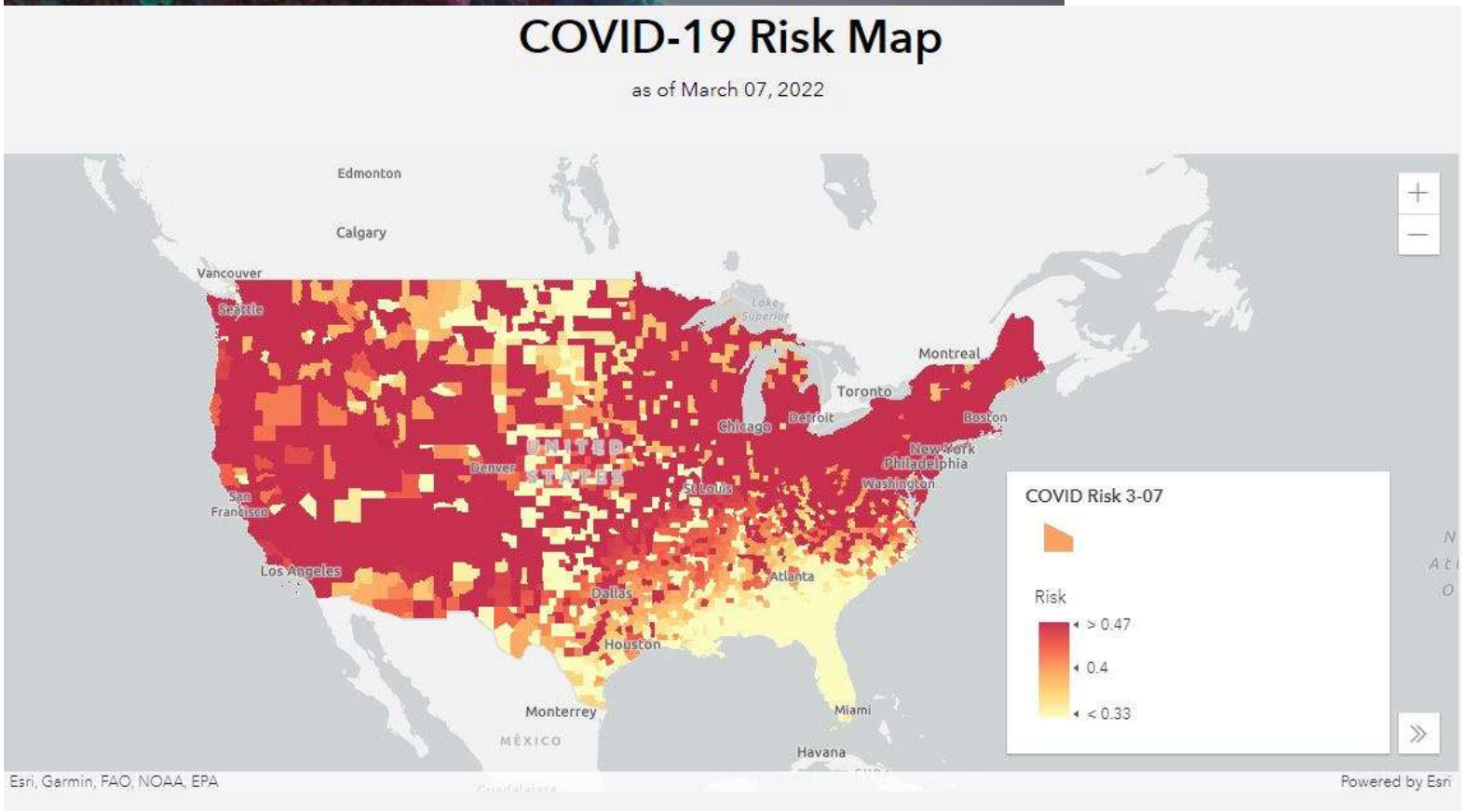




Left panel: **Prediction** made on April 24th 2020 and valid until May 14th, 2020.
Right panel: **Actual number** of COVID19 cases during those three weeks: a heuristic prediction model developed in GeoHLab

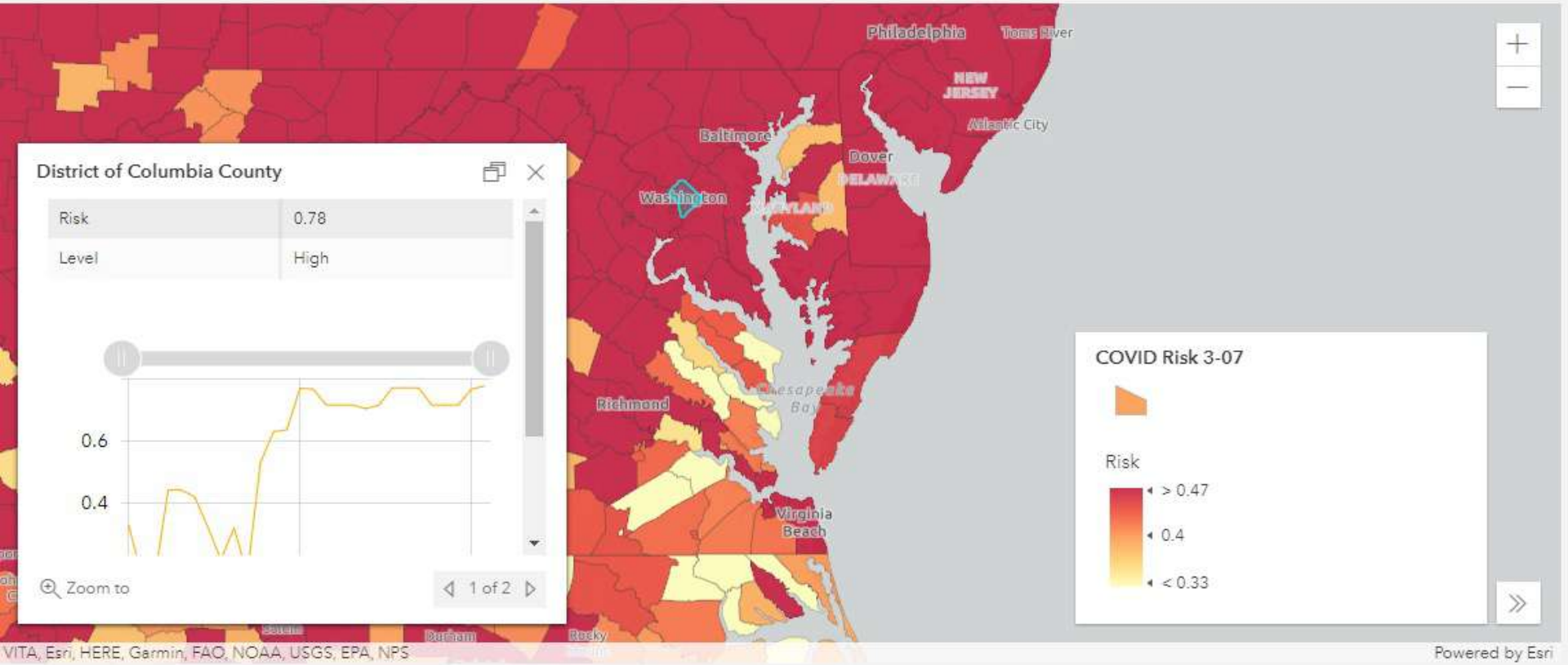


https://covid-ufl.hub.arcgis.com/



COVID-19 Risk Map

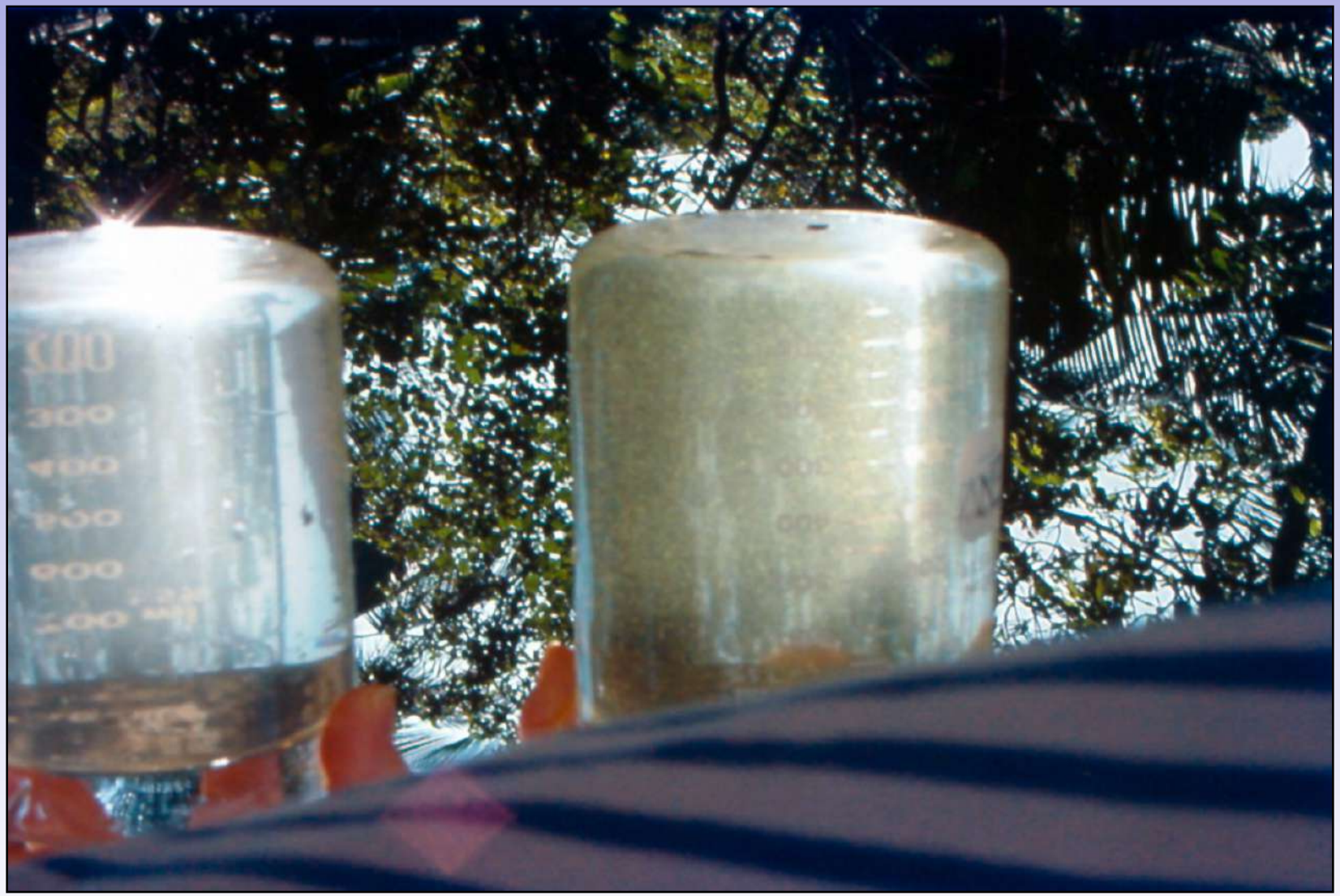
as of March 07, 2022



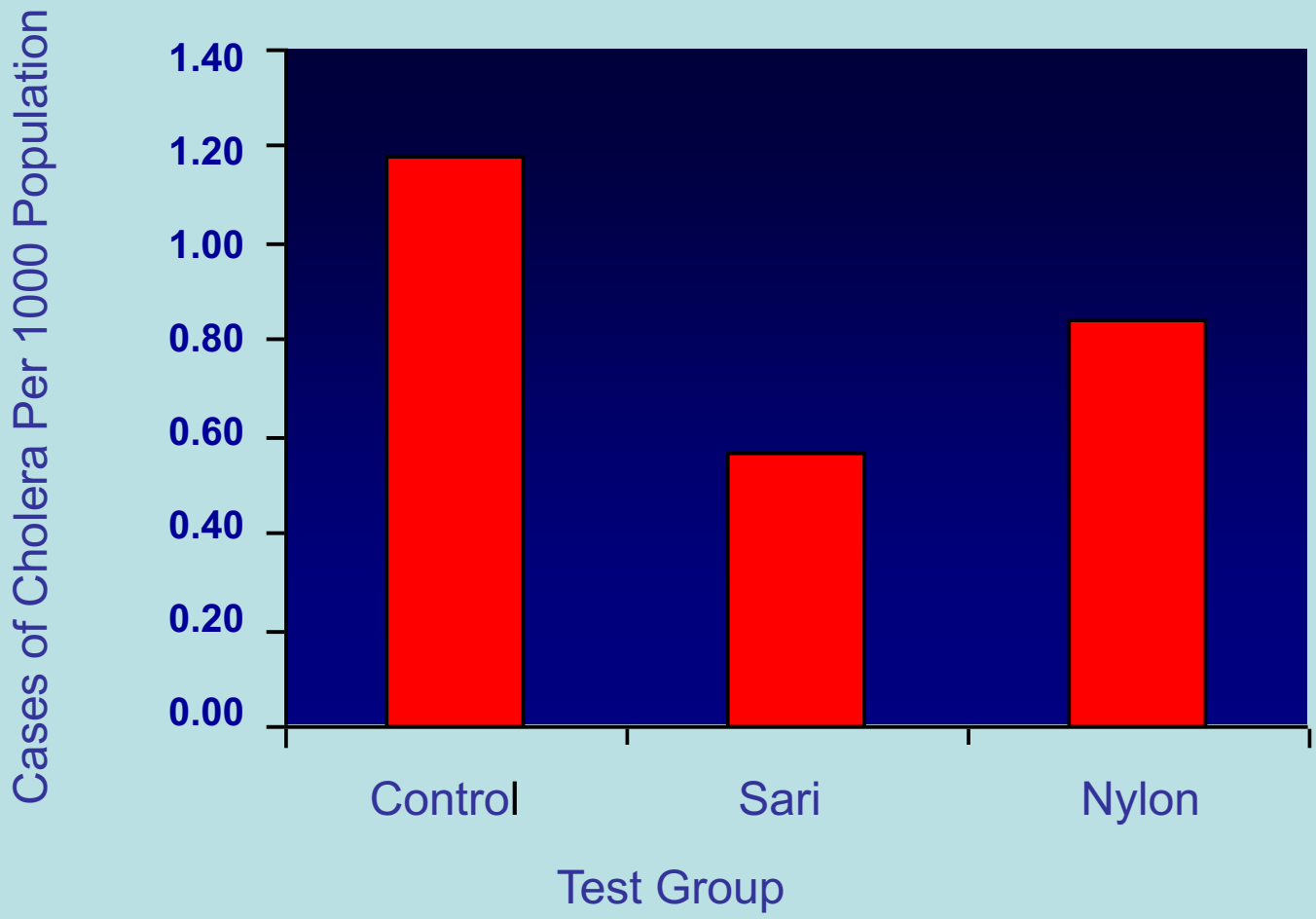
COVID 19 risk on 03/07/2022


A Simple, Sustainable
Method for
Reducing Cholera


Vibrio cholerae



Full Study


Cases of Cholera Per 1000 Population
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
Control
Sari
Nylon
Test Group

Safe water is a global challenge

Courtesy of GB Nair, NICED, Kolkata, India

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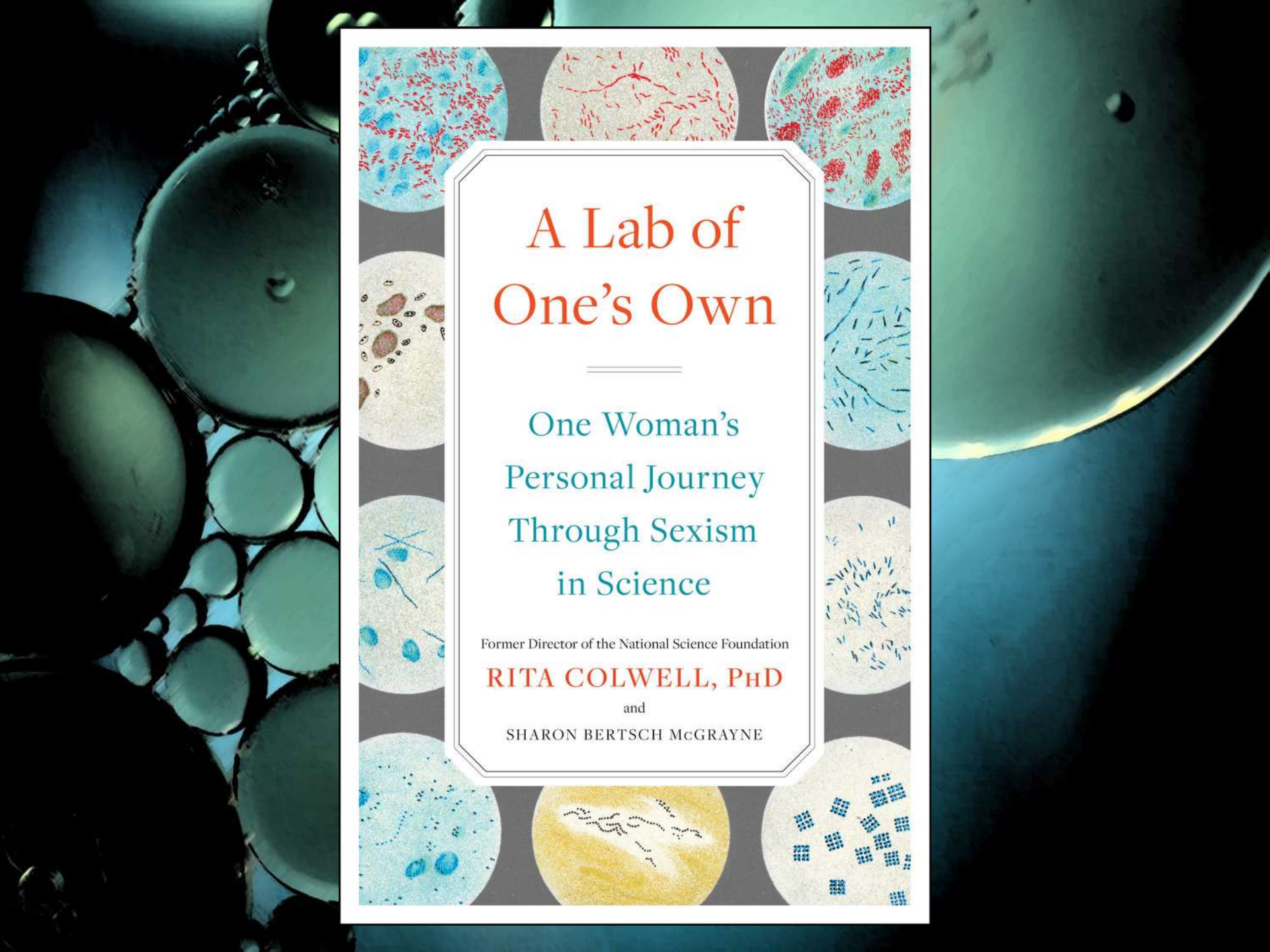
- Linda Zall, Office of the Chief Scientist
- Fred Zimmerman, ISciences, Burlington, VT

“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)


A Lab of One's Own
One Woman's Personal Journey Through Sexism in Science
Former Director of the National Science Foundation
RITA COLWELL, PhD
and
SHARON BERTSCH McGRAYNE