

“...whoever wishes to pursue the science of medicine must first investigate the seasons of the year and what occurs in them.”

Hippocrates, 4th Century B.C.

Climate, Oceans, Microbiomes, and Cholera

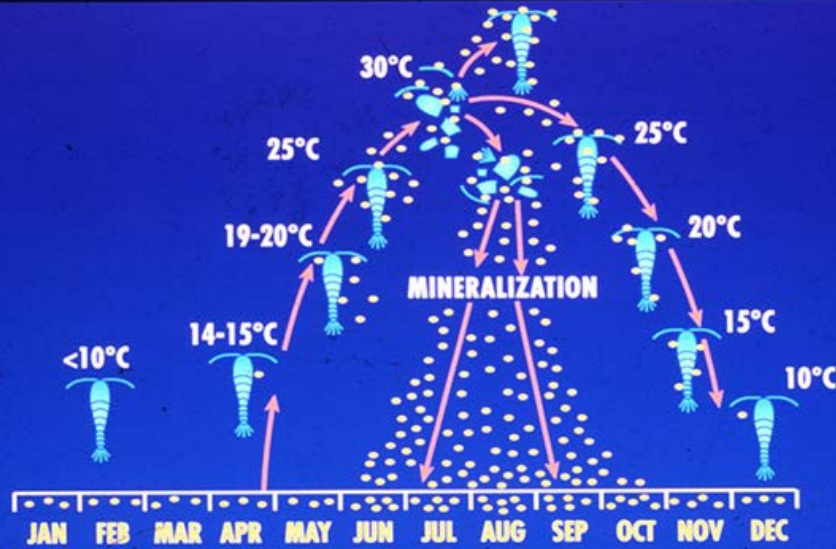
**National Science Board
Vannevar Bush Award
May 9, 2017**

Rita R. Colwell, Ph.D., D.Sc.

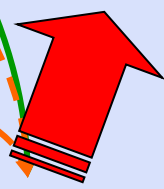
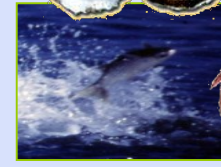
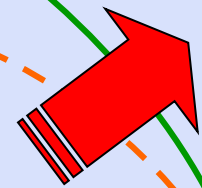
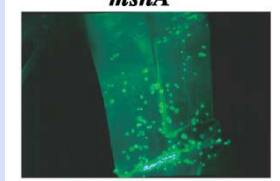
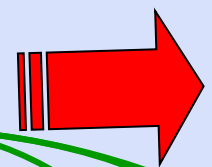
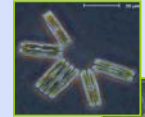
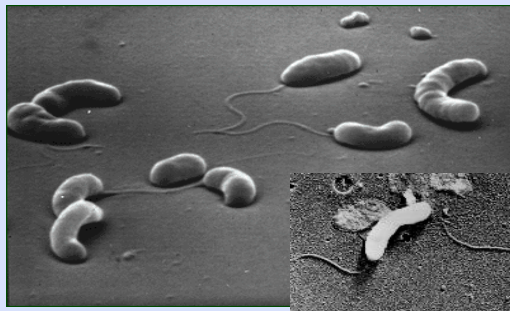
**Distinguished University Professor
University of Maryland, College Park
and**

**Johns Hopkins University Bloomberg
School of Public Health**

VIBRIO CHOLERAE – COPEPOD ANNUAL CYCLE IN THE ENVIRONMENT



Model for the Transmission of Vibrio Cholerae from the Environment to Humans



Chronology of cholera and satellites

Colwell (1996)

Colwell (1996)

GPM
2014

OCO-2
2014

Landsat 8 (USGS)
2013

Aqua
2002

Terra
1999

Landsat 7 (USGS)
1999

RapidSCAT (ISS)
2014

CATS (ISS)
2015

Suomi NPP
2011

OSTM/Jason-2
2008

Aura
2004

SMAP
2015

DISCOVER (NOAA)
2015

Jason-3
2016

CALIPSO
2006

CloudSat
2006

SORCE
2003

GRACE (2)
2002

EO-1
2000

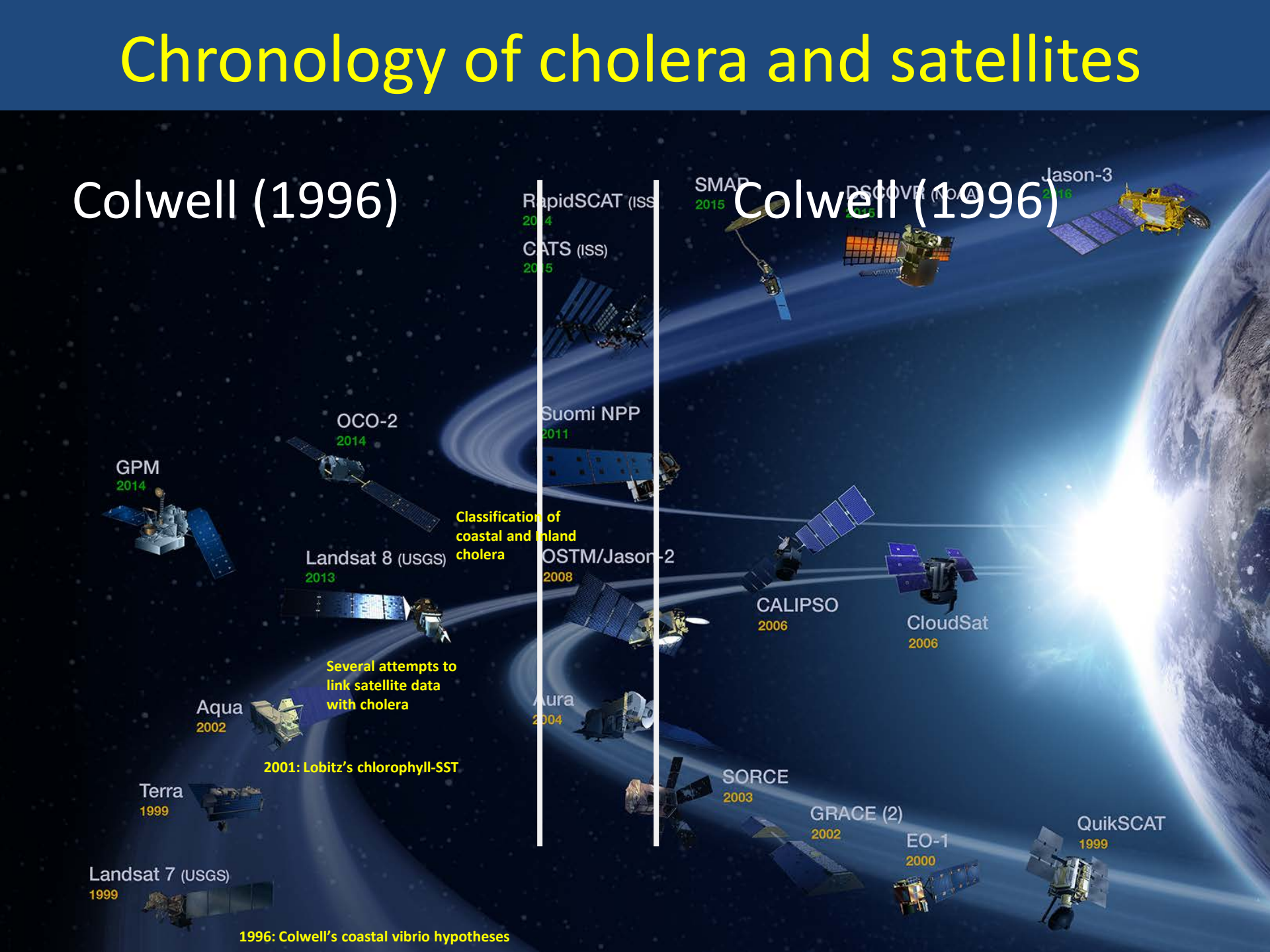
QuikSCAT
1999

Classification of coastal and inland cholera

Several attempts to link satellite data with cholera

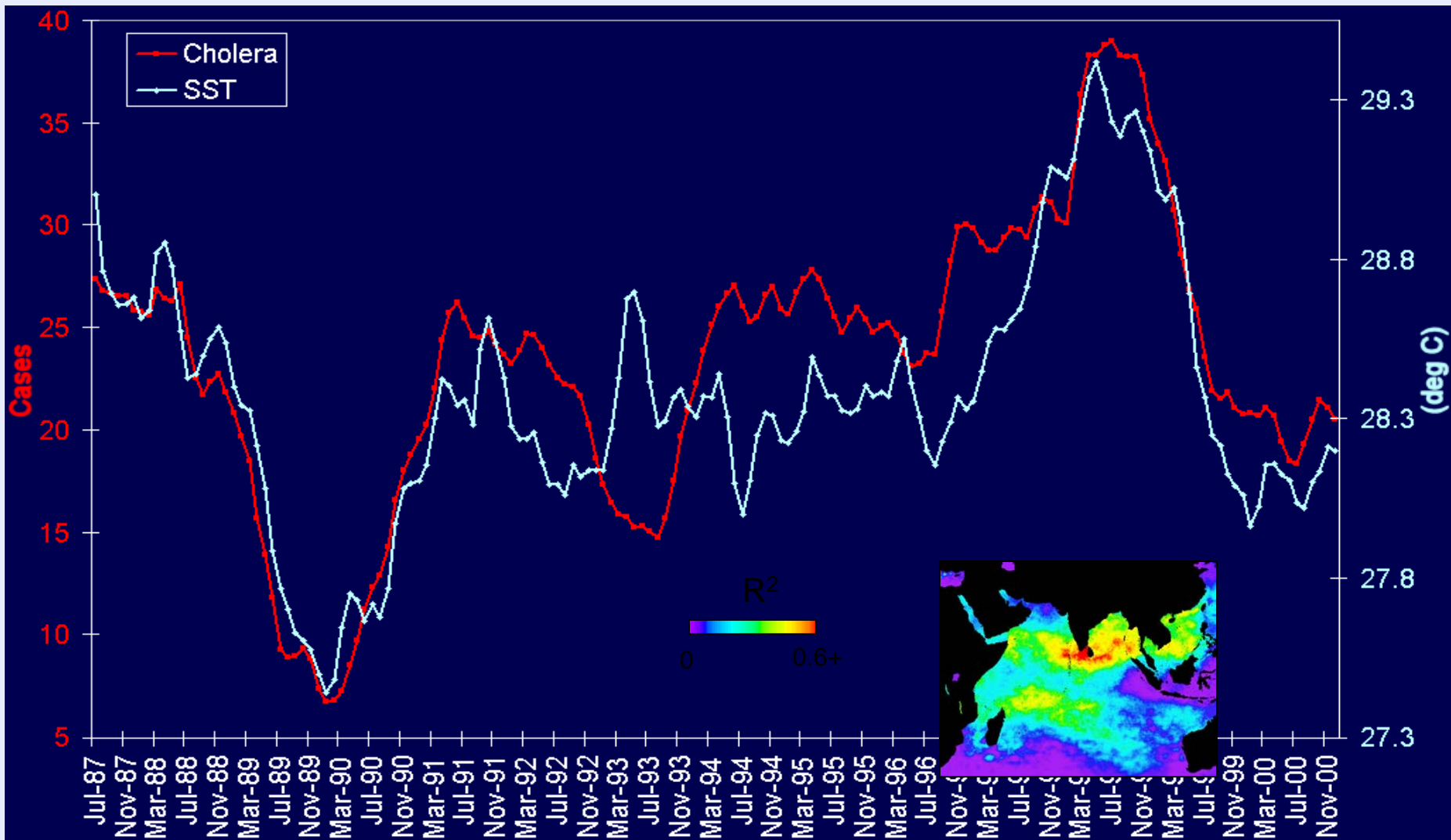
2001: Lobitz's chlorophyll-SST

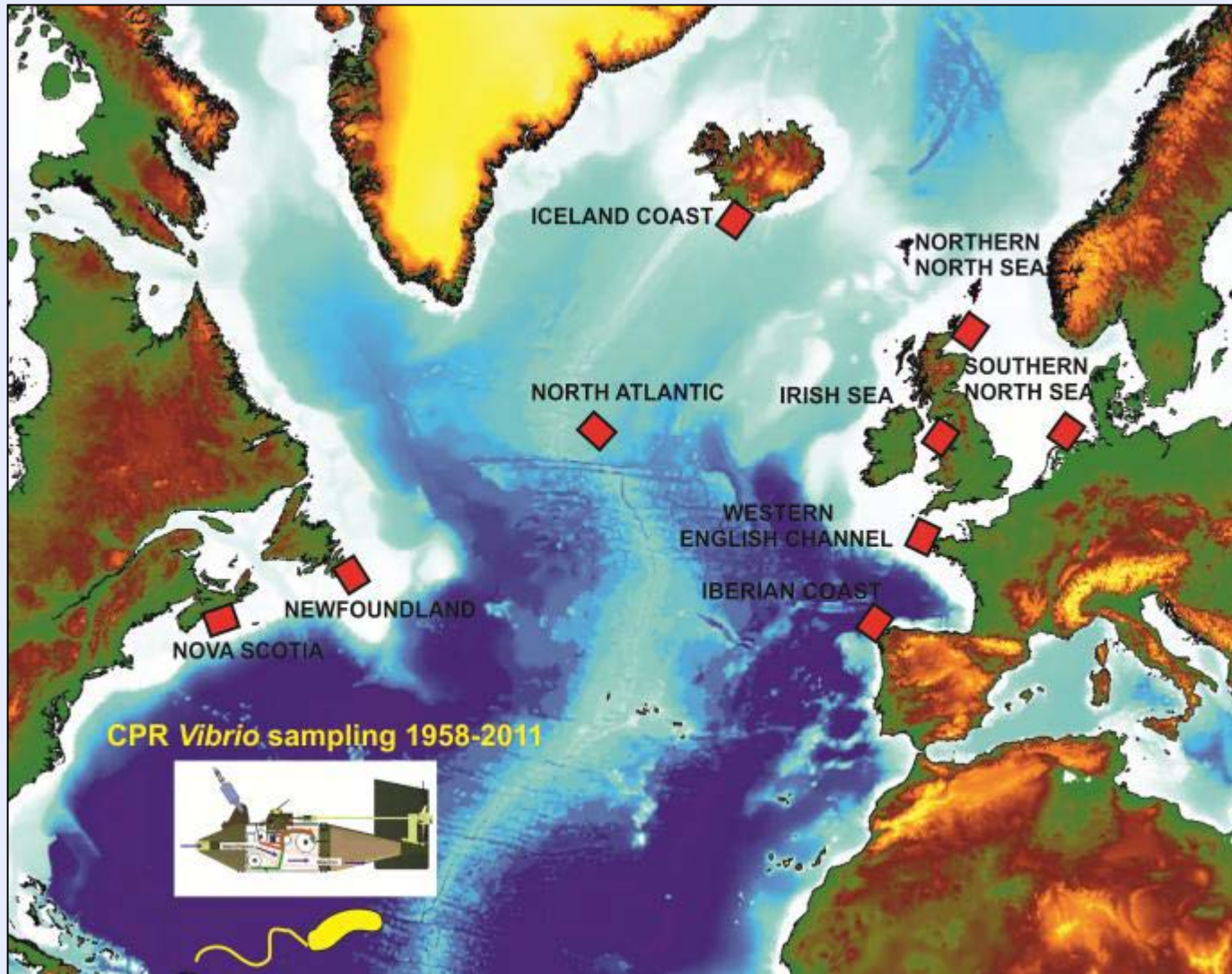
1996: Colwell's coastal vibrio hypotheses



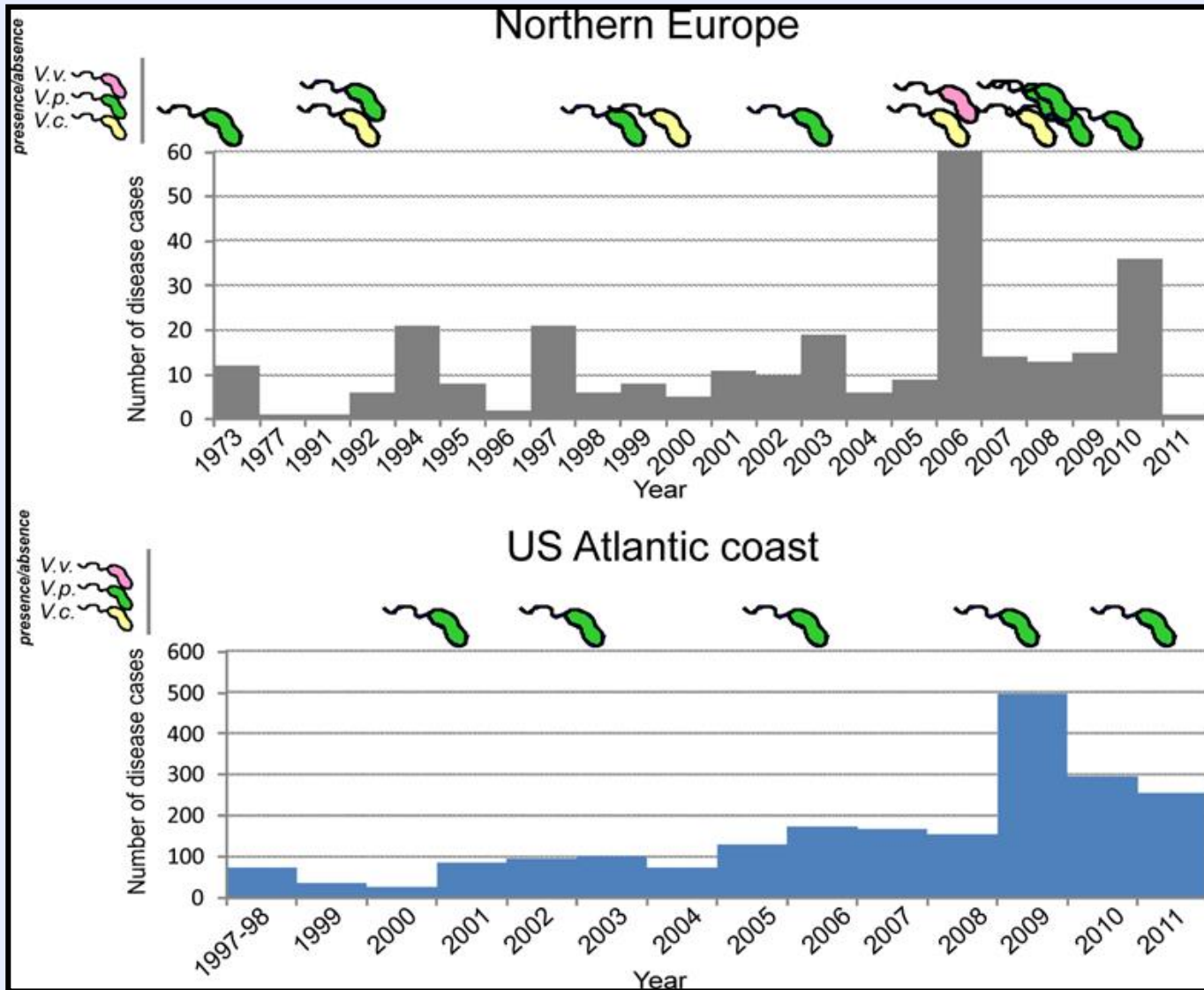
Cholera and SST in the Indian Ocean

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



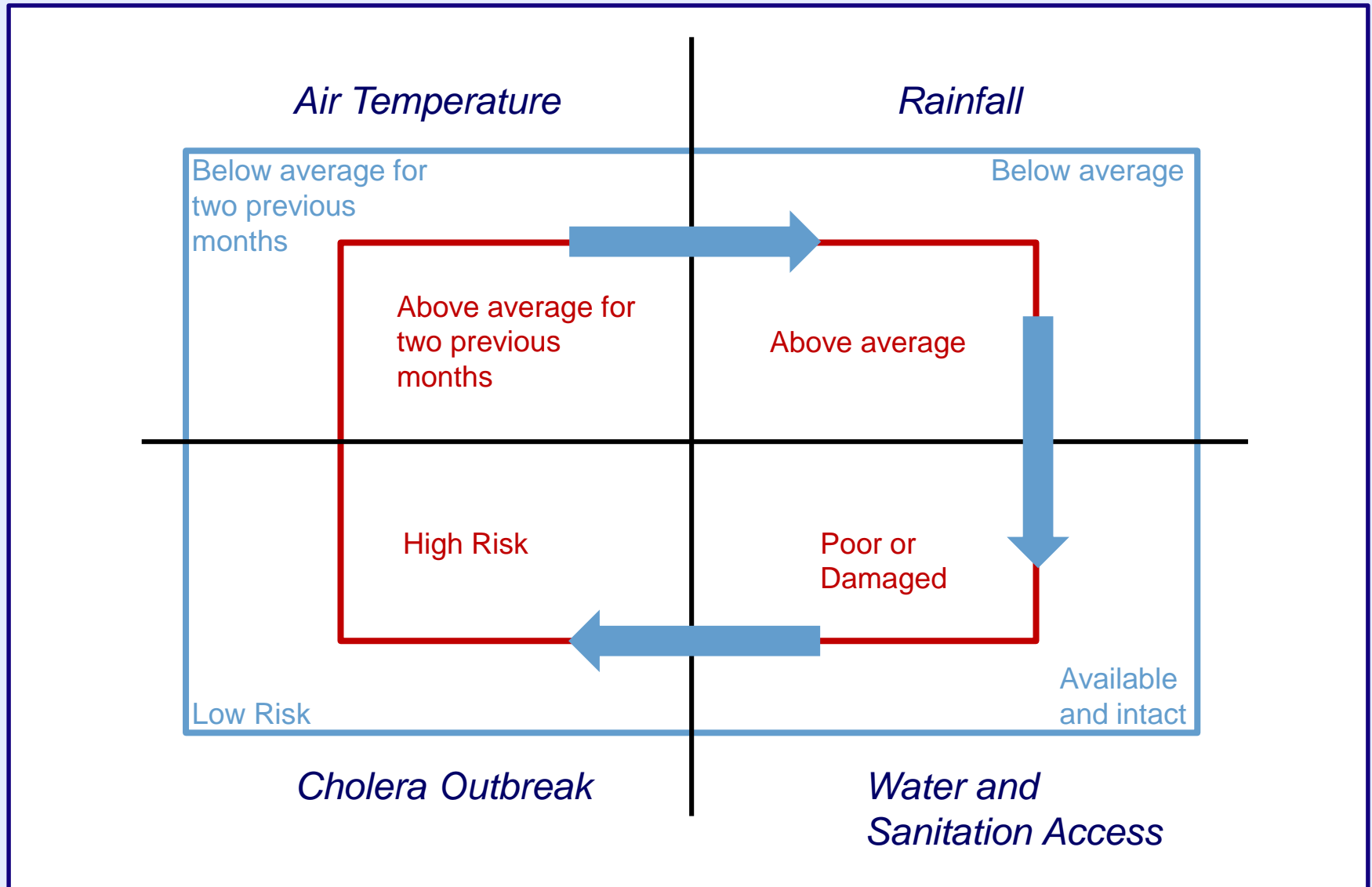


Vezzulli et al. Proc. Natl. Acad. Sci. USA 2016 113 (34)
E5062-E5071 doi:10.1073/pnas.1609157113



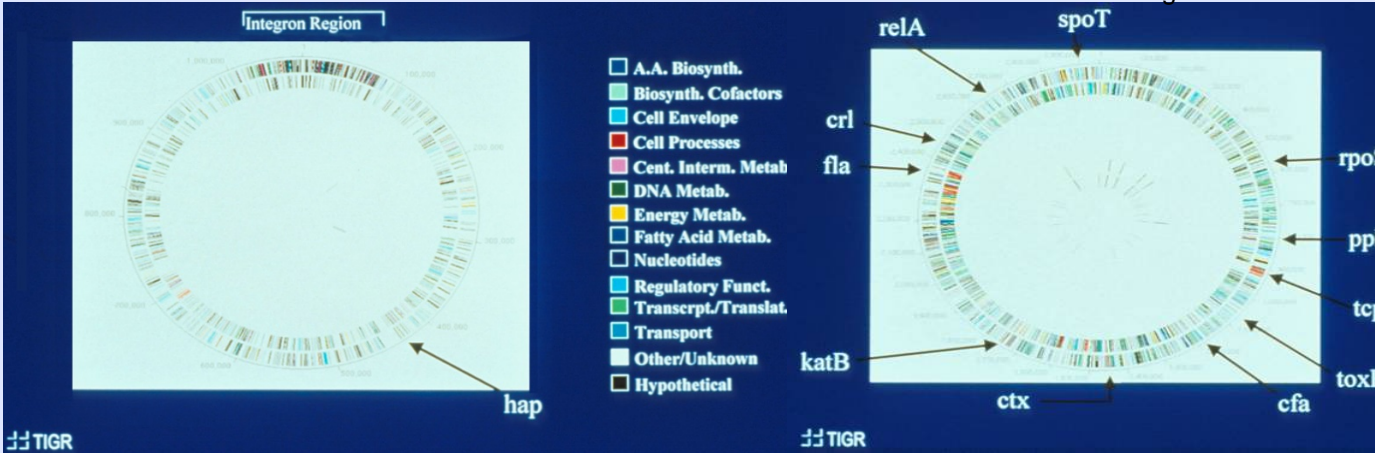
Vezzulli et al. Proc. Natl. Acad. Sci. USA 2016 113 (34)
E5062-E5071 doi:10.1073/pnas.1609157113

Theoretical framework for predicting cholera outbreaks in epidemic regions



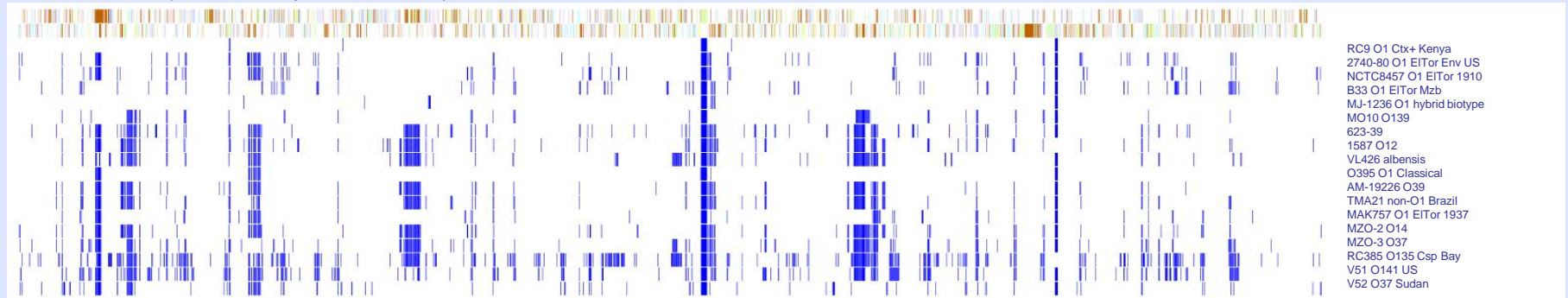
Vibrio cholerae

Sequenced and published in 2000

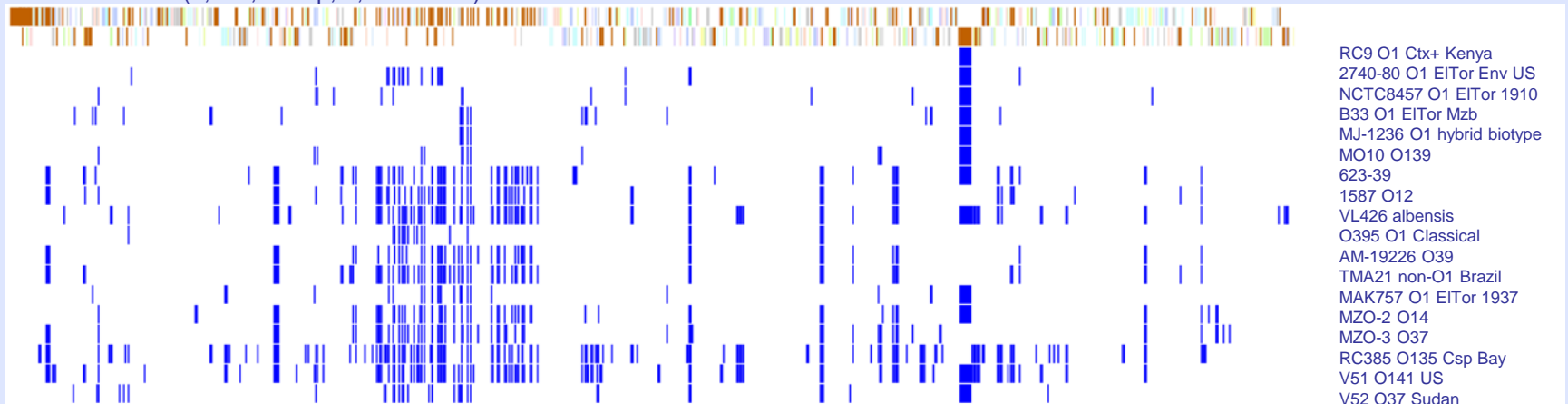


Source: The Institute for Genomic Research

Chromosome I (2,961,149 bp, 2,742 ORFs)



Chromosome II (1,072,315 bp, 1,093 ORFs)



Missing ORFs in *V. cholerae* strains (Reference: N16961; cutoff = 70% DNA similarity)

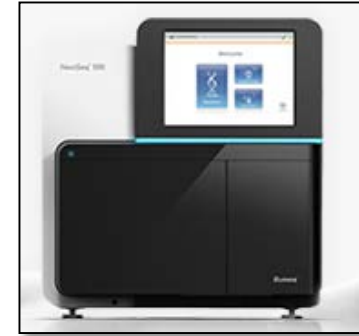
Microbes



Extracted DNA



DNA Sequencing

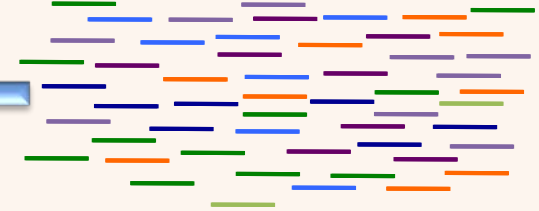
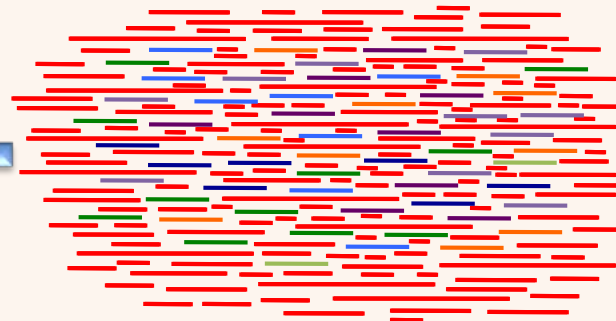
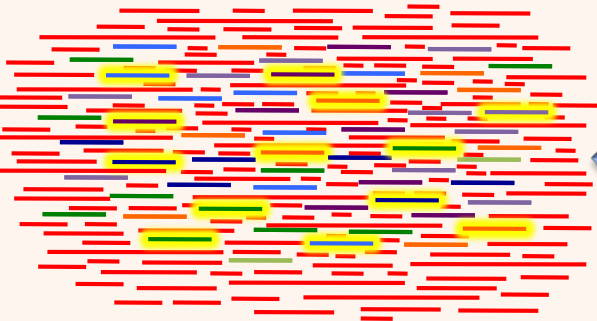


RESEARCH & TESTING LAB:
SEQUENCING SERVICE

GENIUS®: Probabilistic Matching

GENEBOOK® Library

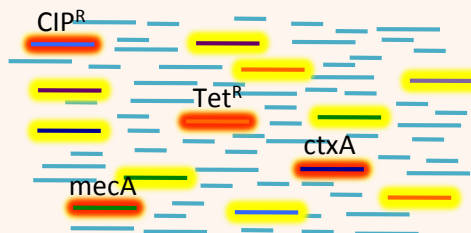
Raw Sequence Reads



Identified Bacteria



GENEBOOK® Antibiotic Resistance & Virulence Factor Library



Applications:

- Pathogen detection for health and wellness;
- food safety and probiotics
- biothreat and public health surveillance;
- forensic and scientific investigation

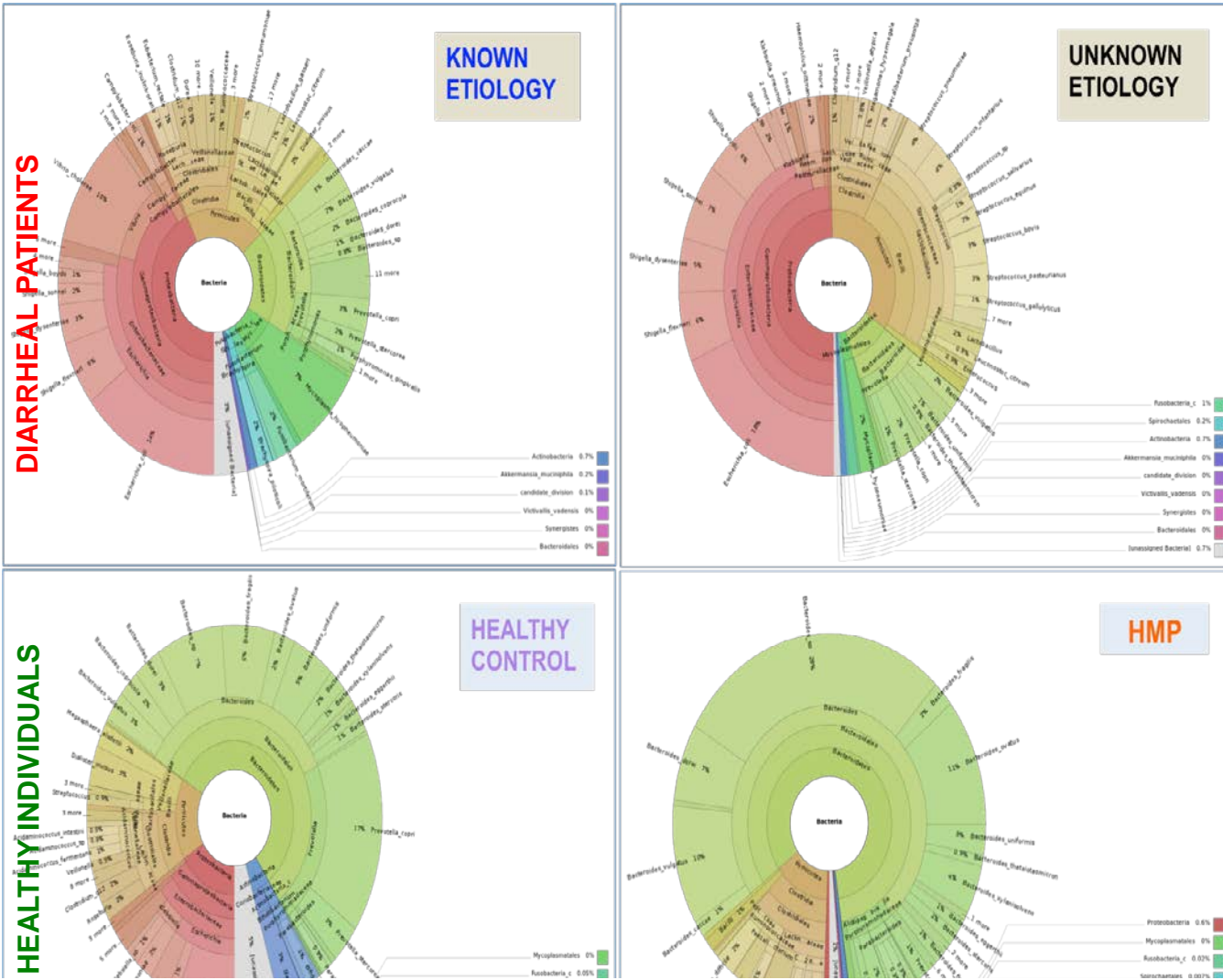
COSMOSID GENIUS® ANALYSIS SERVICE

National Institute of Cholera and Enteric Disease Kolkata, India



www.niced.org.ind

Microbiomes of Diarrheal Subjects Compared to Healthy



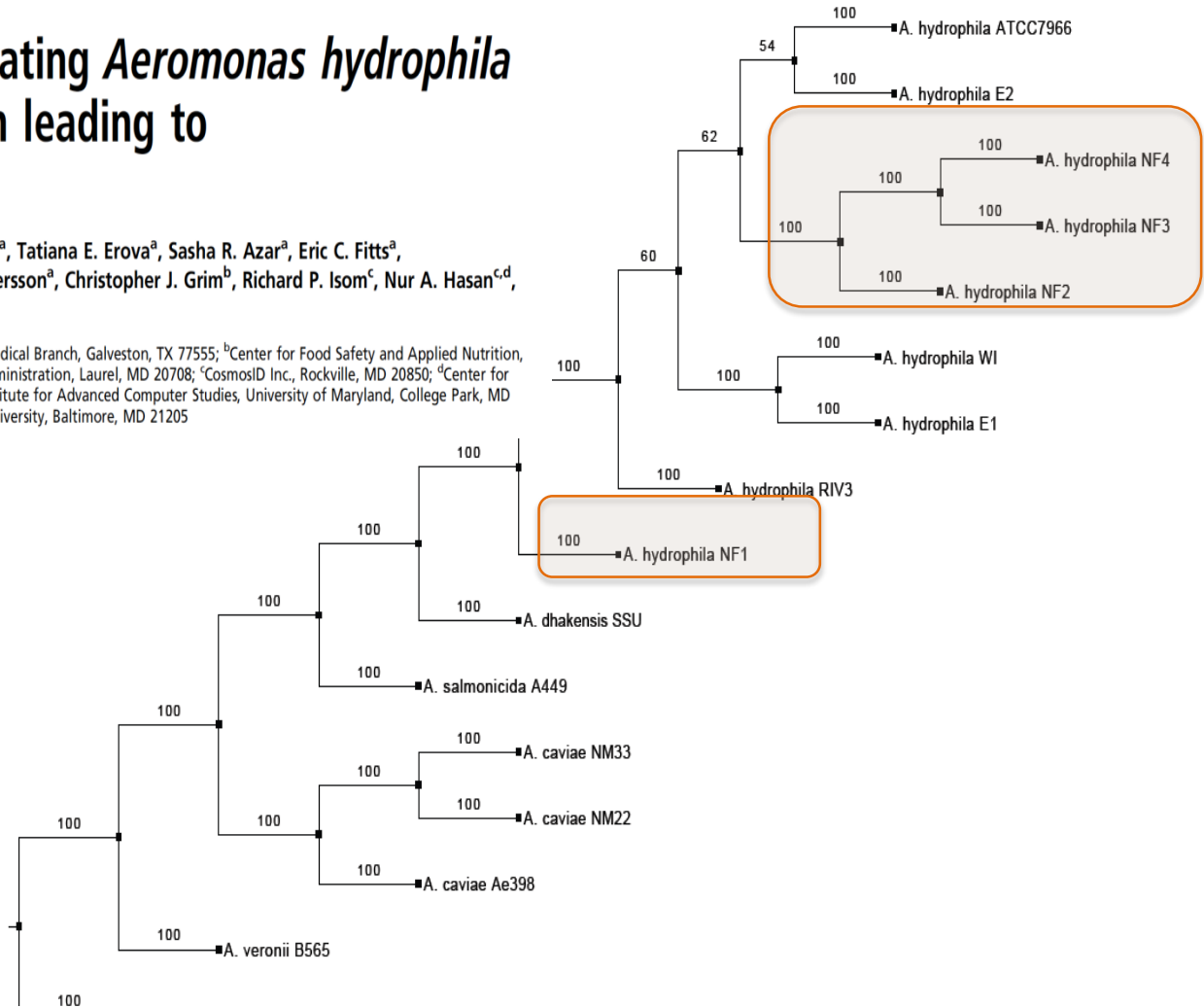
Proteobacteria
Firmicutes
Bacteroidetes

Polymicrobial Infection: Necrotizing Fasciitis

Cross-talk among flesh-eating *Aeromonas hydrophila* strains in mixed infection leading to necrotizing fasciitis

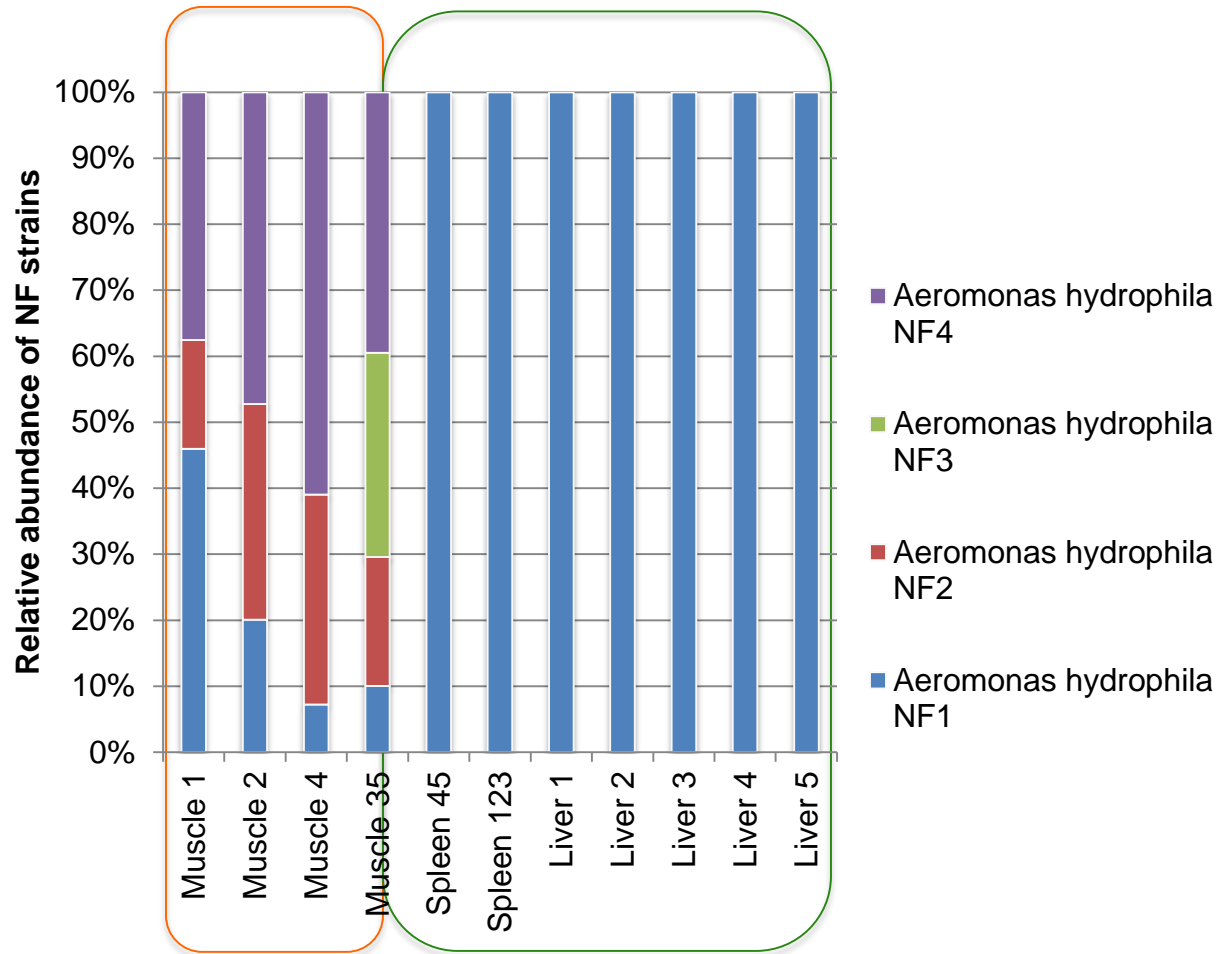
Duraisamy Ponnusamy^{a,1}, Elena V. Kozlova^{a,1}, Jian Sha^a, Tatiana E. Erova^a, Sasha R. Azar^a, Eric C. Fitts^a, Michelle L. Kirtley^a, Bethany L. Tiner^a, Jourdan A. Andersson^a, Christopher J. Grim^b, Richard P. Isom^c, Nur A. Hasan^{c,d}, Rita R. Colwell^{c,d,e,2}, and Ashok K. Chopra^{a,2}

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Neighbor-joining tree using 2,514 conserved full length predicted proteins

Strain level ID shows selective dissemination



Relative distribution of four *Aeromonas hydrophila* strains NF1, 2, 3, and 4 into different metagenomic datasets derived from muscle, spleen and liver samples

Summary

Disease state patients often have multiple pathogenic organisms

Advances in microbial genomics and **identification to strain level** allow for better understanding of polymicrobial infections

Metagenomics can be used to explore biofilm/patient interactions in hospital settings

Metagenomic analysis for these studies was done with CosmosID and our curated database of >65,000 genomes, please contact me if you are interested in working together, or try it yourself:

app.cosmosid.com

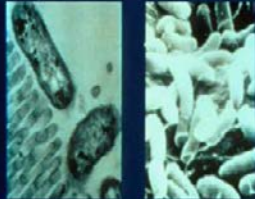


A Simple, Sustainable
Method for
Reducing Cholera

A Simple Solution for Cholera Prevention: Sari Filtration

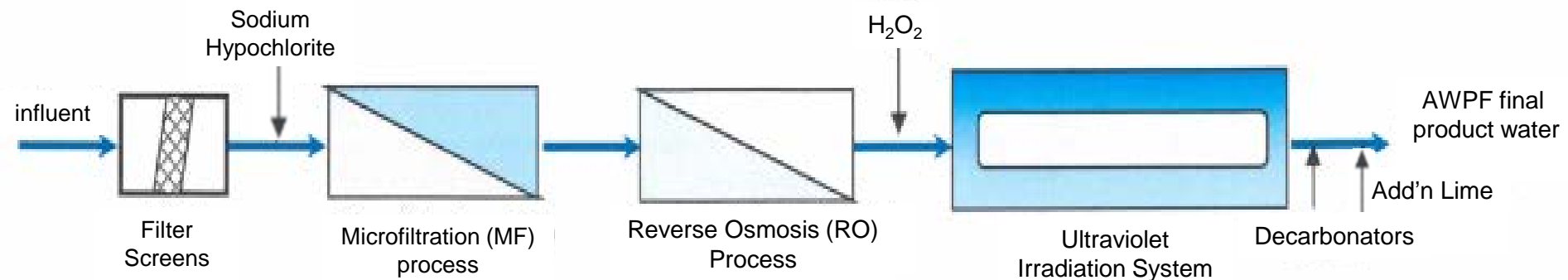


Vibrio cholerae

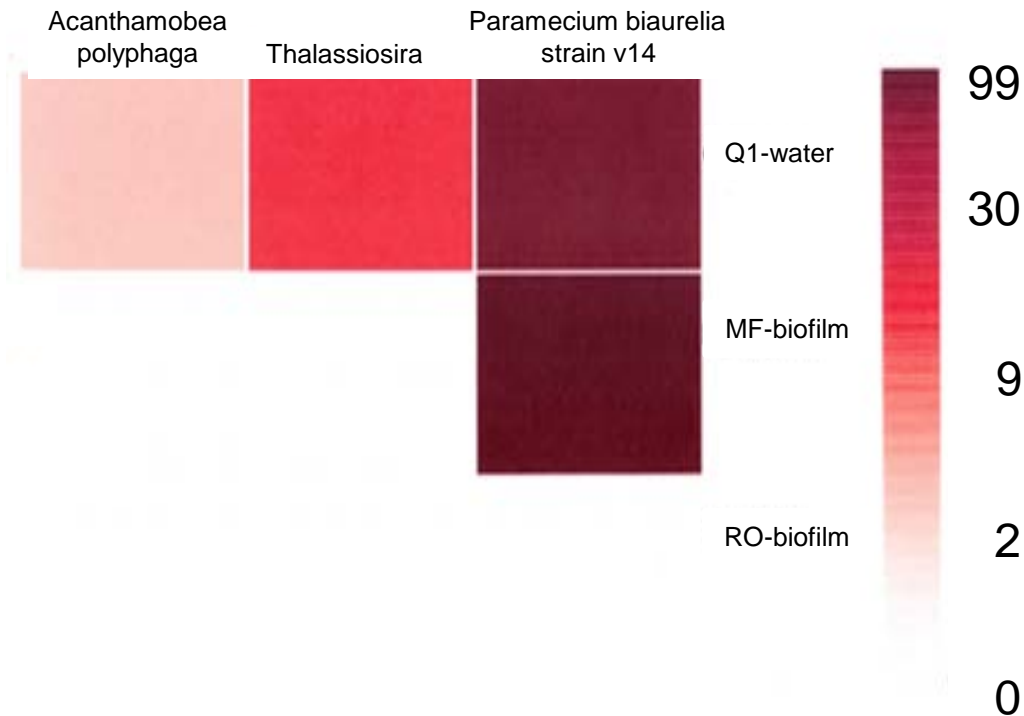


Orange County Water District Study

Metagenomics and Public Health

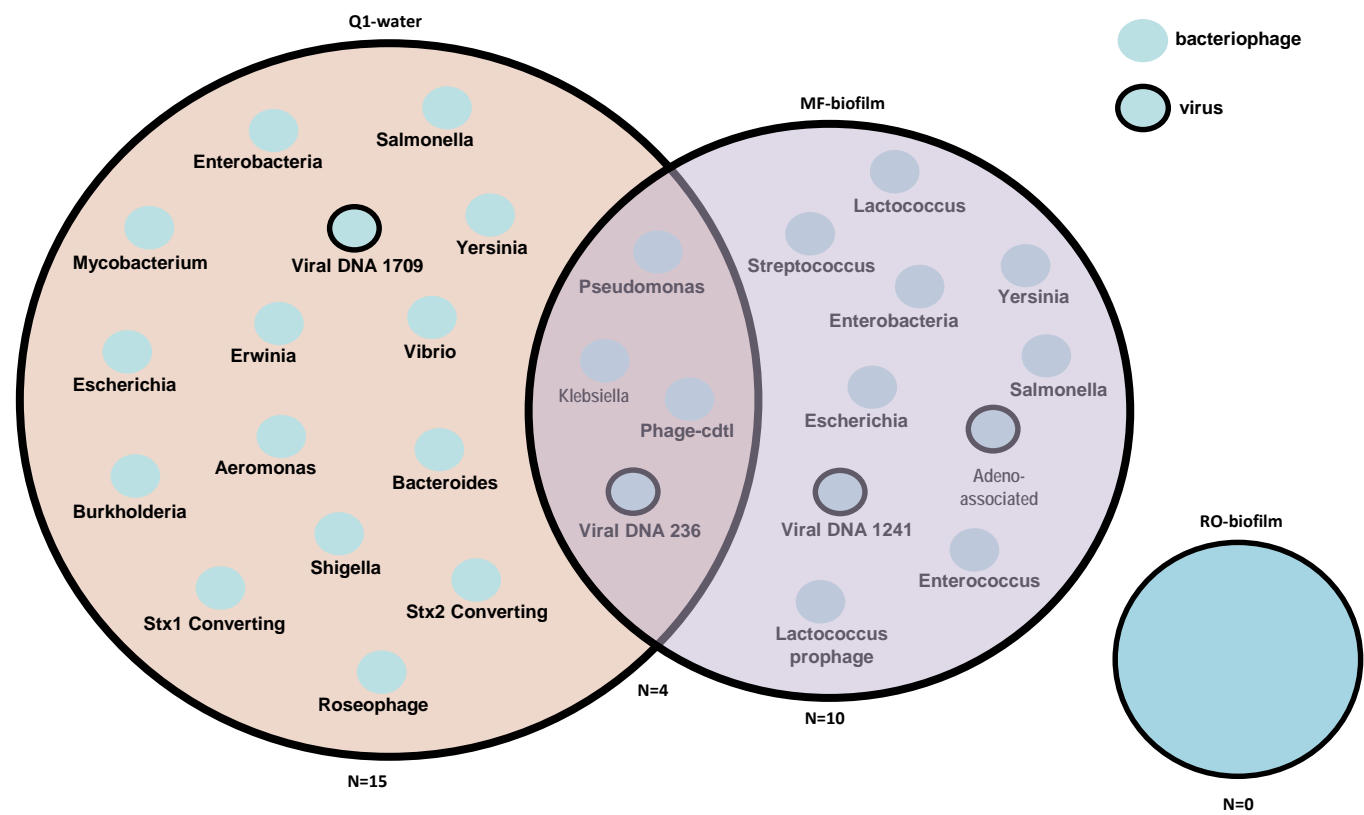


The influent, secondary treated municipal wastewater of the AWPF treatment train is purified by a three-step process: microfiltration, reverse osmosis, and ultraviolet (UV) light with hydrogen peroxide. Initially the wastewater is screened at 4mm Sodium hypochlorite as disinfectant is added prior to microfiltration. Hydrogen peroxide (H₂O₂) is added before UV treatment. The decarbonators remove CO₂ and raise the pH; addition of lime further stabilizes the purified water.



Relative abundance and diversity of parasite DNA in MF-biofilm and Q1-water. The approximate relative abundance heat map was simplified, using the GENIUS bioinformatics algorithm and curated databases. The 99 relative abundance corresponds to sequences classified as *Paramecium biaurelia* strain v14, *Thalassiosira*, and *Acanthamoeba polyphaga* based on observed frequency of DNA sequences identified. Parasite sequences were not found in the RO-biofilms.

Comparison of virus and bacteriophage DNA sequences



Virus and bacteriophage DNA sequences comparison demonstrate the presence of bacteriophages and virus DNA in the membrane filter (MF)-biofilm and in the influent water, Q1. Note, the absence of bacteriophages and DNA viruses in the reverse osmosis (RO)-biofilm. Presence and absences of sequences (partial or complete) related to bacteriophage and viruses in MF-biofilm were compared to the Q1 water.



“When one tugs at a single thing in nature, he finds it hitched to the rest of the universe.”

**John Muir
(1838-1914)**

Collaborators and Colleagues



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Safe water is a global challenge



Courtesy of GB Nair, NICED, Kolkata, India

