Climate, Oceans, Microbiomes, and Cholera

National Science Board
Vannevar Bush Award
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University of Maryland, College Park
and
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“...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.
Model for the Transmission of Vibrio Cholerae from the Environment to Humans
Chronology of cholera and satellites

Colwell (1996)

1996: Colwell’s coastal vibrio hypotheses

2001: Lobitz’s chlorophyll-SST

Several attempts to link satellite data with cholera

Classification of coastal and inland cholera

1996: Colwell’s coastal vibrio hypotheses
Cholera and SST in the Indian Ocean

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

Lobitz et al., 2000, PNAS Vol. 97, No. 4 pp. 1438-1443
Theoretical framework for predicting cholera outbreaks in epidemic regions

<table>
<thead>
<tr>
<th>Air Temperature</th>
<th>Rainfall</th>
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<tbody>
<tr>
<td>Below average for two previous months</td>
<td>Below average</td>
</tr>
<tr>
<td>Above average for two previous months</td>
<td>Above average</td>
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<table>
<thead>
<tr>
<th>Cholera Outbreak</th>
<th>Water and Sanitation Access</th>
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<tbody>
<tr>
<td>Low Risk</td>
<td>Available and intact</td>
</tr>
<tr>
<td>High Risk</td>
<td>Poor or Damaged</td>
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*Vibrio cholerae*
Sequenced and published in 2000

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)

GENIUS®: Probabilistic Matching

GENEBOOK® Library

Raw Sequence Reads

Applications:
- Pathogen detection for health and wellness;
- Food safety and probiotics;
- Biothreat and public health surveillance;
- Forensic and scientific investigation
Diarrheal Disease Study

National Institute of Cholera and Enteric Disease
Kolkata, India

www.niced.org.ind
Microbiomes of Diarrheal Subjects Compared to Healthy

DIARRHEAL PATIENTS

KNOWN ETIOLOGY

UNKNOWN ETIOLOGY

HEALTHY INDIVIDUALS

HEALTHY CONTROL

Proteobacteria
Firmicutes
Bacteroidetes
Polymicrobial Infection: Necrotizing Fasciitis

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

Duraisamy Ponnusamy¹, Elena V. Kozlova², Jian Sha¹, Tatiana E. Erova³, Sasha R. Azar⁴, Eric C. Fitte³, Michelle L. Kirtley², Bethany L. Tiner³, Jourdan A. Andersson⁵, Christopher J. Grim⁴, Richard P. Isom⁶, Nur A. Hasan⁷, Rita R. Colwell⁸,⁶,⁷, and Ashok K. Chopra²,⁸

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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
Orange County Water District Study
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 *Acanthamobea polyphaga* based on observed frequency of DNA sequences identified. Parasite sequences were not found in the RO-biofilms.
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

Anwar Huq, Professor
University of Maryland, College Park, MD

Antarpreet Jutla, Assistant Professor,
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Morgantown, WV

Dr. Nur Hasan
Vice-President, Research and Development
CosmosID, Inc.
College Park, MD

Dr. Seon Young Choi,
Bioinformatic Scientist,
CosmosID Inc.
College Park, MD
Safe water is a global challenge