

Researchers find two distinct strains in 2010 Haitian cholera outbreak

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A new study by an international team of scientists led by researchers from the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine, the Center for Bioinformatics and Computational Biology at the University of Maryland, College Park, and CosmosIDTM Inc., College Park, have found two distinct strains of cholera bacteria may have contributed to the 2010 Haitian cholera outbreak. The team published its results June 18, 2012 in the *Proceedings of the National Academy of Sciences (PNAS)*.

The researchers say that the findings of their study, which involved the largest number of isolates sequenced and studied from a single outbreak of [cholera](#), show the critical need for an up-to-date, public genomic database of the strains of *Vibrio cholerae* bacteria that cause outbreaks of the disease around the world. Such a database could play an important role in efforts to prevent or respond to cholera outbreaks, say scientists in a team co-led by Claire Fraser, Ph.D., an international leader in genomics and director of the Institute for Genome Sciences at the University of Maryland School of Medicine, and Rita R. Colwell, Ph.D., an internationally recognized expert in cholera and Distinguished University Professor at the Center for Bioinformatics and Computational Biology, University of Maryland, College Park.

"The complete sequencing and phylogenomic analysis of multiple isolates from a single infectious disease outbreak has shown that there is significant genomic diversity among the cholera bacteria," says Dr. Fraser. "The results of the study speak to a critical need for an up-to-

date, curated and publicly available reference genomic database reflecting the species global phylogenetic diversity.

Dr. Colwell emphasizes that "in light of the diversity we have found, such a database would benefit investigations of future cholera epidemics and provide a more accurate risk assessment for public health response."

The team included academic, government, and industry scientists. The project was funded through the University of Maryland School of Medicine Institute for Genome Sciences' Genome Sequencing Center for Infectious Disease contract from the National Institute of Allergy and Infectious Diseases, part of the National Institutes of Health, and a Department of Homeland Security contract with CosmosID, Inc.

Spearheading the work along with Dr. Fraser and Dr. Colwell were Mark Eppinger, Ph.D., a research associate at the Institute for Genome Sciences, Nur Hasan, Thomas Cebula, Ph.D., at CosmosID™ Inc., and Jacques Ravel, Ph.D., associate professor at the University of Maryland School of Medicine and associate director for genomics at the Institute for [Genome Sciences](#), and Seon Young Choi, Ph.D., and Huai Li, Ph.D., at CosmosID™ Inc., and the University of Maryland, College Park. Large scale sequencing technology was used to study the genomic diversity of the Haitian isolates of cholera and the unique microevolutionary aspects of the Haitian [cholera outbreak](#) that began in 2010.

Cholera is a disease endemic in developing countries and the causative agent, *V. cholerae*, is naturally occurring in estuaries and river systems worldwide. The 2010 cholera outbreak in Haiti generated international interest because of its intensity and sudden appearance throughout the country. In this study, the genomic diversity of Haitian isolates was examined on a genome wide scale to determine both the complexity of the species and the relationship of isolates from Haiti to isolates from

concurrent and past epidemics of cholera elsewhere in the world.

"This project is an example of the kind of interdisciplinary, collaborative academic relationship that our outstanding scientists have with those at our sister campus in College Park," says E. Albert Reece, M.D., Ph.D., M.B.A., vice president for medical affairs at the University of Maryland and the John Z. and Akiko K. Bowers Distinguished Professor and dean of the University of Maryland School of Medicine. "We hope that more similarly groundbreaking scientific discoveries will arise from collaborations between the two schools in many areas of science and medicine."

Jayanth Banavar, Ph.D., dean of the College of Computer, Math and Natural Sciences (CMNS), University of Maryland, College Park, emphasizes "the splendid collaborative effort between the scientific teams of the two campuses of the University of Maryland and CosmosID, Inc. to achieve this important public health contribution."

More information: "Genomic diversity of 2010 Haitian cholera outbreak strains," by Nur A. Hasan et al. *PNAS*, 2012.

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