New England Journal of Medicine Publishes Study on Zika Genomic Sequence Identification by IDbyDNA

Metagenomics Company's Taxonomer identifies disease in first Zika virus-related death in U.S.

San Francisco, Calif., Sept. 28, 2016 – IDbyDNA, a precision medicine company focused on metagenomic approaches for infectious disease identification, today announced publication results in the New England Journal of Medicine that its metagenomics tool, Taxonomer, was used in the identification of Zika virus genomic sequence in the first Zika virus-related death in the continental U.S.

Researchers from the University of Utah, including Dr. Robert Schlaberg, Chief Medical Officer of IDbyDNA and a medical director at ARUP Laboratories, report a rapidly progressive fatal Zika virus infection case. The elderly patient was admitted to the hospital at the end of June, but was not diagnosed with Zika virus infection until after his death, according to Utah health officials. The unidentified Utah resident had traveled to the southwest coast of Mexico where ZIKV transmission has been reported. Taxonomer analysis of the metagenomic Next-Generation Sequencing data of the patient's serum RNA revealed presence of a ZIKV virus strain that shared 99.8 percent of its genome sequence with a strain isolated from a mosquito in Chiapas, Mexico in 2016.

Current diagnostic techniques rely heavily on testing for suspected pathogens, which can be inconclusive and time consuming. Because Taxonomer can test for a very large number of pathogens all at once, a doctor doesn't have to suspect the cause of a patient's infection, but can instead simply ask, "What does my patient have?" In this case, a presumptive diagnosis of dengue shock syndrome was made, but tests were negative. Zika virus was then identified by PCR and Taxonomer analysis.

"The very fast and comprehensive analysis also helped us characterize the viral genome sequence of this fatal infection and to address whether additional infections may have worsened the course of disease," says lead author, Dr. Sankar Swaminathan, the Don Merrill Rees Presidential Endowed Chair and Chief of Infectious Diseases at University of Utah Health Care.

"This study demonstrates the utility of Taxonomer for very rapid and comprehensive identification of known, and novel, pathogen strains, including bacteria, viruses, fungi and others," says IDbyDNA's Dr. Schlaberg. "Through our recent Series A funding, led by ARTIS Ventures, we hope to further accelerate the development of our DNA search technology and plan to expand our offerings to new customers, including health systems, the pharmaceutical industry, and develop the broadest and most accurate DNA search applications available."

In a previous paper published in the Journal of Clinical Microbiology, Schlaberg and his collaborators demonstrated that high-throughput sequencing, in combination with Taxonomer, can reliably detect pathogens in patient samples, and identify previously missed pathogens.

About IDbyDNA

Based in the San Francisco Bay Area, IDbyDNA is developing technologies to enable universal microorganism detection. IDbyDNA's mission is to help doctors and scientists to detect any pathogen in any sample, thereby removing barriers for the adoption of metagenomics in clinical settings, ultimately leading to faster public health responses during infectious disease outbreaks. For more information

about IDbyDNA, please visit http://www.idbydna.com. For Taxonomer, please visit http://www.taxonomer.com.

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