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Precision public health method identifies clusters of respiratory disease in Uganda

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A study led by researchers at Center for Infection and Immunity (CII) at Columbia University's Mailman School of Public Health and the Department of Medicine at the Columbia University Irving Medical Center reports on the use of a genetic sequencing method to identify viral pathogens behind unexplained respiratory illnesses in Uganda over a five-year period. The method, called VirCapSeq-VERT and developed at CII, identified nine clusters of infections, including one potentially related to tourism from the U.K.

The study is published in *Clinical Infectious Diseases*, a journal of the Infectious Diseases Society of America, and is accompanied by an editorial by Hans H. Hirsch, MD, an expert in infectious diseases and viral diagnostics at the University of Basel, Switzerland.

Columbia researchers joined with colleagues at the Uganda Virus Research Institute in Entebbe, Uganda, to identify 2,901 patients with unexplained, influenza-negative severe acute respiratory infections (SARI) through a network of eight hospitals in Uganda between 2010 and 2015. The researchers' analysis of genetic material from nasal and throat swabs yielded information on viral pathogens in 82 percent of the samples, the most common of which was human rhinovirus. They uncovered nine infectious clusters, as well as information about where the clusters were more likely to occur: in urban areas and during rainy seasons. Within these clusters, they found a previously unrecognized outbreak of measles-associated SARI potentially linked to tourism from the U.K., as well a cluster associated with a novel picobirnavirus related to swine and dromedary viruses.

"The discovery potential of deep sequencing of this U.S.-Ugandan study," Hirsch writes in his editorial, "is... highlighted impressively by the identification of picobirnavirus in two cases as well as measles as the cause of SARI clusters in 18 cases... Remarkably, five cases... could be traced back to an unvaccinated tourist from England and an outbreak in Manchester, U.K., in 2011." Hirsch goes on to assert that the "state of the art" test "not only sets standards for resource-rich industrial settings, but provides... another proof-of-concept of feasibility and impact of innovative joint projects and partnerships between advanced research groups and dedicated institutions in the resource-limited countries."

Co-first author Rafal Tokarz, Ph.D., a research scientist at CII, says traditional public health surveillance systems of the kind used by low- and middle-income countries often fail to detect or control outbreaks of infectious disease. "Precision sequencing can improve on these systems by capturing detailed information on at-risk populations while rapidly identifying any new pathogens," he says. "However, continued testing is necessary to assess feasibility of using these methods to conduct real-time public health surveillance."

"What we are talking about is precision public health—integrating genomics, big data, and spatial analyses to identify vulnerable populations and areas where high-impact infections emerge and using these insights to deploy resources precisely and efficiently," says co-first author Matthew J. Cummings, MD, a postdoctoral fellow in the Division of Pulmonary, Allergy, and Critical Care Medicine at Columbia University Irving Medical Center. "One-size-fits-all public health solutions are just as obsolete as one-size-fits-all approaches to cancer therapy."

"Every year, acute lower respiratory infections are responsible for nearly

3 million annual deaths worldwide, predominantly in children and the elderly," says W. Ian Lipkin, MD, co-author, director of CII, and the John Snow Professor of Epidemiology at the Columbia Mailman School. "In addition, outbreaks of associated with novel viruses like avian flu, MERS, and SARS, along with periodic outbreaks caused by vaccine-preventable viruses such as measles, threaten global health security. VirCapSeq-VERT will be an important tool in the identification and containment of outbreaks."

Provided by Columbia University's Mailman School of Public Health

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