Health & Medicine

With New Diagnostic Test, Viruses Have Nowhere to Hide

By
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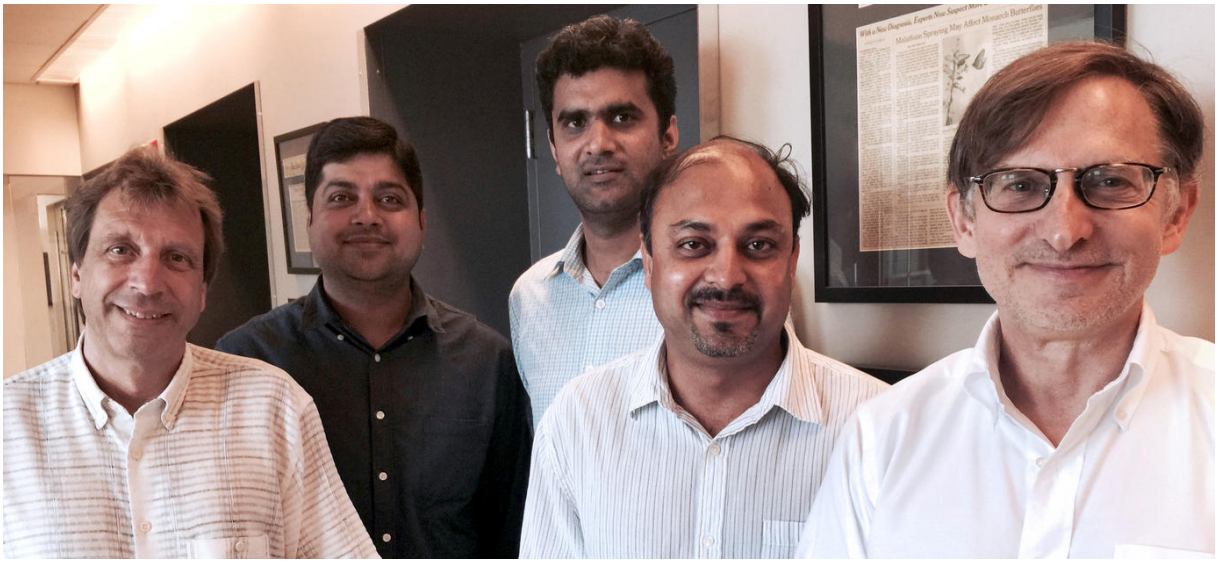
A team of virologists led by Mailman School epidemiologist W. Ian Lipkin have developed a diagnostic tool that they say could dramatically speed up the detection and treatment of a wide range of infectious diseases, from common influenza to Dengue fever. The new technology, which the scientists described in a recent issue of the journal *mBio*, is capable of detecting any of the approximately one thousand viruses known to infect humans and other vertebrates. This is a major advance, Lipkin and his colleagues say, because the viral diagnostic techniques that currently exist are each designed to spot only a narrow class of viruses.

“Today, if you go into a hospital with a serious viral infection, physicians must guess whether to test you for, say, a rhinovirus, coronavirus, papillomavirus, or any of hundreds of other specific types of viruses,” Lipkin says. “If the initial tests come back negative, they have to guess again and run more tests. This is a time-consuming and expensive process, and it can lead to dangerous delays in treatment.”

The system that Lipkin and his colleagues at the Mailman School’s Center for Infection and Immunity developed, which they call the Virome-Capture-Sequencing Platform for Vertebrate Viruses, or VirCapSeq-VERT, employs state-of-the-art genetic technology. When a patient’s blood or tissue sample is broken down into its constituent nucleic acids, a magnetic process will pull out DNA or RNA sequences that match those in a library of viral genetic signatures. Scientists can then perform a full genetic analysis on the viruses discovered in a patient’s sample.



From left: Thomas Briese, Nischay Mishra, Arvind Kumar, Amit Kapoor, and W. Ian Lipkin. Photo by Tim Paul.

“We’ve basically figured out how to perform the gold standard of microbial detection, which is genetic-sequencing analysis, across all vertebrate viral taxa at once,” says Thomas Briese, an associate professor of clinical epidemiology and the lead author of the *mBio* paper. “The trick was devising a way to fit the genetic fingerprints of all the viruses into a probe library. We solved this by breaking down the one thousand viral genomes into millions of pieces and then constructing our library using the minimum number of genetic pieces you need to reliably identify those viruses.”

The scientists say they are currently in conversation with several diagnostic laboratories interested in using the VirCapSeq-VERT. In the meantime, they are planning to adapt the system to also test for bacteria.

“We believe that if hospitals and diagnostic laboratories around the world were equipped with the VirCapSeq-VERT,” says Lipkin, “it could be a game changer for medical care and for public health.”

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