Researchers discover a way to detect new viruses

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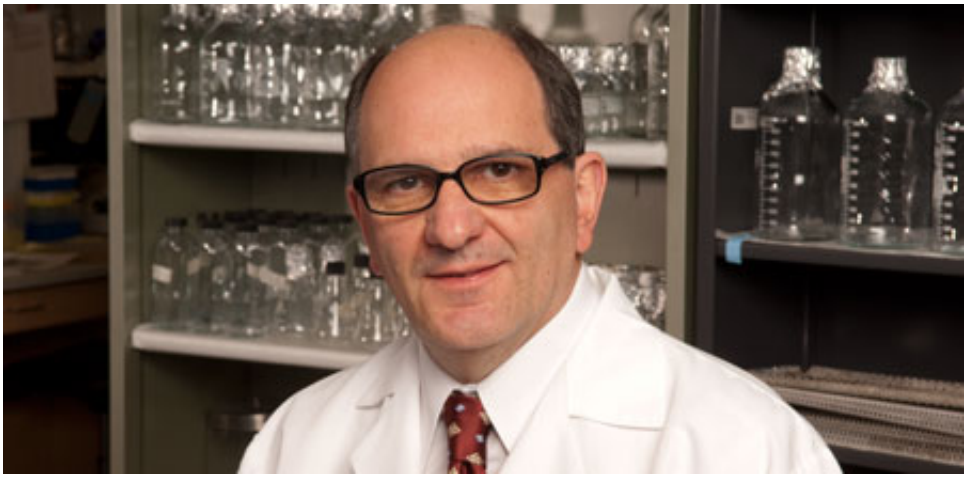

Adrian Di Bisceglie, M.D., is chairman of the department of internal medicine at Saint Louis University

(Phys.org) —In research published in *Biochemical and Biophysical Research Communications*, Saint Louis University researchers describe a technology that can detect new, previously unknown viruses. The technique offers the potential to screen patients for viruses even when doctors have not identified a particular virus as the likely source of an infection.

In the new approach, scientists use blood serum as a biological source to categorize and discover viruses.

Taking advantage of the complete deciphering of the human genome, SLU researchers used a next-generation sequencing (NGS) approach called transcriptome subtraction. With this process, the research team subtracted the entire human genetic sequence from the genetic material in the blood they were examining. By studying what remained, they were able to identify viral genetic material in the blood.

"We have discovered a technology that allows us to detect new viruses," said Adrian Di Bisceglie, M.D., chairman of the department of internal medicine at Saint Louis University. "We isolate DNA and RNA, amplify the amount of genetic material present in the blood, do ultra-deep sequencing and use an algorithm to search for matches for every known piece of genetic code, both human and for microbes.

"Once we remove the known portions, we're ultimately left with new viruses."

When doctors suspect that a patient has a viral infection, it can be difficult to determine which virus is the culprit.

One way to test for the presence of a virus is to grow it in the lab from a biological sample, like tissue or blood, from the patient. However, that approach won't work if tissue isn't available, if there is no logical starting place for deciding which viruses to screen for (such as knowing that a patient was exposed to a particular virus), or in a "hit and run" viral infection, in which case there is a narrow time frame for tissue sampling.

Another option is to search for viral genetic material in the body.

There are several methods that use this approach (such as immune based-library screening, mass spectrometry and microarray), but the most useful is next-generation sequencing.

After sorting out the human genetic material from the viral material, the research team compared the viral material against database libraries of known viruses. This identifies any known viruses in the blood.

After this second subtraction, researchers examined the remaining, unidentified material, and sorted out bacteria, phages, and viruses, among other material, based on specific protein signatures that mark each type of microorganism. The discovered, previously unknown viruses remain candidates for further investigation.

Key to the research team's success was the discovery of how to amplify the genetic material in the blood, says study researcher Xiaofeng Fan, M.D., associate professor of internal medicine at Saint Louis University.

In the past, blood serum wasn't used to its full potential because RNA degrades too quickly, leaving too little material to study. The amplification process used by the research team eliminated this problem.

The approach that the research team developed has the potential for immediate application in clinical situations concerning an unknown viral infection, like, for example, the recent outbreak of a SARS-like virus in Saudi Arabia.

In addition to offering a way to discover new viruses and test for known viruses in ill patients, this new technology could provide a valuable approach for those in the biodefense field looking for a way to quickly spot existing bio-threats.

Di Bisceglie says this technique will contribute to our understanding of the many viruses that live in the human body.

"Just as the human microbiome project is chronicling the bacteria that live and co-exist in every person, we also are studying the human virome

to know more about the viruses that live in all of us. We believe not all are harmful and some may even be beneficial," Di Bisceglie said.

Saint Louis University has applied for patent protection of this technology and will now actively pursue its commercialization.

"Dr. Di Bisceglie is a recognized world leader in virology and we expect scientific companies and commercial enterprises in this field to have strong interest in the new technique," said Graeme Thomas, director of SLU's office of technology management.

More information: www.sciencedirect.com/science/ … ii/S0006291X13009601

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