

DNA testing could prove valuable tool for identifying viral infections, including MERS

Genetic testing has been the driving force of the personalized medicine revolution, allowing physicians to identify gene mutations earlier than ever before and helping to usher in a new era of preventative medicine. While genetic testing has helped with early identification of genetic mutations, new research suggests that it might also be a valuable tool in testing for viral infections.

A team of Duke University researchers, led by Dr. Aimee Zaas, has developed a blood test that analyzes genetic information in the immune system to determine whether an infection is caused by a virus or bacteria. The test, which looks for the genetic signature of activity in the 30 genes that are activated when a viral infection hits, acts as a snapshot of what the genes are doing at the time the test is administered.

[According to the study](#), “improved ways to diagnose acute respiratory viral infections could decrease inappropriate antibacterial use and serve as a vital triage mechanism in the event of a potential viral pandemic.”

Zaas and her team first published a preliminary real-world test of the study last week in [Science Translational Medicine](#). The study focused on 102 patients with a fever. Of those 102, 28 had a viral infection, 39 had a bacterial infection and 35 were healthy patients used for the control group. The test accurately identified 25 of the 28 viral infections and correctly ruled out non-viral infections at an impressive rate of 94 percent, nearly twice as accurate as [traditional methods](#).

Additionally, the test delivers results in as little as 12 hours, which is a dramatic improvement over current testing methods, which can take several days or more. The slow turnaround time of current tests often leads doctors to prescribe antibiotics using trial and error when the nature of the infection is unclear, since time is of the essence when treating these types of infections.

DNA testing for viral infections would allow for quicker diagnosis, thereby allowing doctors to prescribe suitable treatments to patients and avoid unnecessary administration of antibiotics, which could be detrimental to public health.

“One of the big global threats at the moment is the emergence of bacterial resistance, and that is largely driven by overuse of antibiotics,” said Dr. Chris Woods, co-senior author of the study. “A tool that enables us to accurately identify viral infections could curb the indiscriminate use of antibiotics and reduce the development of resistant pathogens.”

While this test needs to be evaluated further before it can be used widely, early results show that this type of highly accurate DNA testing could be a valuable tool in fighting against viral infections. It could be particularly useful in preparing for complicated new viruses, such as Middle East Respiratory Syndrome (MERS), a potentially fatal respiratory virus first identified in Saudi Arabia last year.

Since MERS was first identified, researchers have used DNA sequencing to gain some insight into the mysterious virus. New research, [published in The Lancet](#), revealed that MERS may be transmitted by

jumping repeatedly from animals to humans and that transmissions between humans are much more complex than first thought.

For the study, researchers, led by Dr. Matthew Cotten, conducted 21 sequences of the virus from infected patients in Saudi Arabia. By analyzing and comparing these genome sequences, the researchers were able to reconstruct the evolution and determine a possible origin of the virus.

Since first diagnosed in early 2012, MERS has infected more than 100 people globally and is responsible for at least 52 deaths, most of which were in Saudi Arabia and neighboring countries. The respiratory virus is clinically similar to severe acute respiratory syndrome (SARS), a 2002 outbreak of which infected more than 8,000 people worldwide with a fatality rate of nearly 10 percent. Like SARS, MERS causes infected patients to first develop a cough and fever, which then leads quickly to pneumonia and kidney failure.

The Cotten-led study suggests that a common ancestor host acted as the original animal source of the virus, which then passed from animals to humans several times in different locations. According to the study authors, “the genetic diversity in the Al-Hasa (Saudi Arabia) cluster suggests that the hospital outbreak might have had more than one virus introduction.”

Researchers are currently investigating potential sources of the virus, known as animal reservoirs, which may carry the virus without showing signs of illness. While it is still unknown which species might be responsible for transmitting the virus to humans, [molecular investigation of a number of different animals](#), including visibly ill camels and goats that reportedly had contact with infected MERS patients, has led researchers to believe that bats are likely the animal reservoir responsible for the first transmission to humans.

As scientists continue to investigate MERS and other viruses, relatively new genetic testing tools should prove valuable for the quick and accurate identification of viral infections and for gaining critical insights into the way these viruses operate.

Additional Resources:

- “DNA test for viral infections ‘highly accurate’,” BioNews
- “[MERS at one: The deadly virus drizzle](#),” National Geographic
- “[New test aims to better detect viral infections](#),” Bloomberg Businessweek
- “[Saudi efforts to stop MERS virus faulted](#),” Wall Street Journal