

Emerging Health Threats Forum

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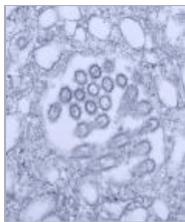
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Detecting new flu viruses faster

Lab technique that singled out the 'swine flu' virus could speed up detection, study suggests



Colorized transmission electron micrograph showing novel H1N1 virus virions in tissue sample.

Image credit: CDC/C. Goldsmith and D. Rollin

When two children caught the flu in California in March of 2009, standard diagnostic tests failed to match the virus with strains of human influenza known to circulate regularly in the country. But US health officials didn't know for sure whether they had a new flu virus on their hands until two weeks later, after the Centers of Disease Control and Prevention (CDC) sent samples of the virus to one of their reference labs, San Diego's Naval Health Research Center.

At the Center, David Metzgar and colleagues used an experimental laboratory technique and confirmed that the virus isolated from the first patient, a 10-year-old boy, was like no other seen before in humans, and had a zoonotic origin.

In a paper published online in the *Journal of Clinical Microbiology*, the team describes how the novel H1N1 virus was detected with the method, called T5000 Universal Biosensor. When they tested how well it performs against standard PCR methods, they found it could spot a greater proportion of viruses and identified at least 99% of them accurately.

It also did this faster than PCR methods. Although the system can't identify a virus definitively, it can show lab scientists whether they're dealing with a strain not seen before within six hours — suggesting that if approved for clinical use, it could buy precious time in the response to infections with other as yet-unknown strains of flu.

Noting that the 2009 pandemic was caused by an unfamiliar strain, rather than H5N1, the authors argue that developing methods for detecting specific strains is "futile".

"We need universal influenza virus diagnostics that can detect and characterize all known strains of influenza, and also... previously unrecognized strains," they write. "In the course of the emergence of the 2009 pandemic H1N1 influenza, the T5000 demonstrated that capability in a very compelling real-world situation."

The technique was designed to amplify genetic fragments from any virus using PCR. These results are then combined with mass spectrometry to generate information about evolutionary features of a virus, in order to identify the group to which it belongs.

When the system fails to find an exact match to a particular strain, it brings up genetic segments that correspond to those picked up from viruses in the sample. On testing the samples that arrived from the CDC back in April, the authors found segments that belonged to strains other than those known to be circulating among people, and saw a mixed pattern that pointed to a novel reassortant virus.

Because only one DNA fragment was produced for each genetic segment, the researchers knew that they were dealing with a single strain rather than co-infection — which pointed to a reassorted virus "for which different segments ultimately arose from different sources". Eventually they matched genetic segments to strains of the swine-origin H2N2 virus and the avian-origin H3N2 virus.

Metzgar and colleagues say T5000 could be used in diagnostic labs to speed up the detection of influenza because it can detect both known and unfamiliar viruses, and can tell apart novel strains from co-infections. This promises to cut delays between emergence of a new virus and public health response.

Metzgar and another one of the authors, Darcie Baynes, are employed by Abbott, the company that developed the system.

Reference and link

1. Metzgar D, Baynes D, Myers CA, Kammerer P, Unabia M, Faix DJ, *et al.* Initial identification and characterization of an emerging zoonotic influenza virus prior to pandemic spread. *J Clin Microbiol* 2010. doi: [10.1128/JCM.01336-10](https://doi.org/10.1128/JCM.01336-10)

[CDC information](#) on 2009 H1N1 flu

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