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“Swine Flu” was circulating undetected, scientists say

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Courtesy Science
and World Science staff

By sequencing the genomes of more than 50 samples of the new A(H1N1) influenza or “Swine Flu” virus, researchers have found that the virus is distantly related to its nearest relatives.

That suggests its genes have been circulating undetected for an extended period, according to scientists, and that in the future pig populations will need to be closely monitored for emerging influenza viruses.

The virus has sickened 11,168 people worldwide and caused 86 deaths, most of them in Mexico, according to the World Health Organization.

Rebecca Garten at the U.S. Centers for Disease Control and Prevention and colleagues sequenced the full or partial genomes of 2009 A(H1N1) viruses isolated in Mexico and the United States.

They investigated the origins of the virus’ eight gene segments and found that the combination of these gene segments has not previously been reported among swine or human influenza viruses. All of the segments originated in avian hosts and then began circulating in pigs at various times in history, from 1918 through to 1998, according to the group.

Six of the eight segments were found to have originated from combined genetic material from human, avian and swine viruses that have been circulating in North America and Asia since about 1998. The other two segments were found to be derived from Eurasian swine viruses.

The sequences for the gene segments did not reveal the signatures of high transmissibility or virulence that have been found in other influenza A viruses, suggesting that other, yet-unknown genetic sequences are responsible for the new virus’ ability to replicate and spread in humans, the scientists reported.

The findings are published in the May 22 issue of the research journal *Science*.

The investigators also took a closer look at the new A(H1N1) virus’ hemagglutinin protein, which is considered responsible for the virus’ ability to bind to and infect its host cell. Test-tube experiments that examined how ferret immune system molecules reacted against this protein suggested the new strain has properties that are similar to those of other swine A(H1N1) viruses but distinct from seasonal human flu. Researchers will need to continue to look for changes in the hemagglutinin protein in the new virus, which may affect the selection of vaccine candidates, the authors said.

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