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Content on this page was developed during the 2009-2010 H1N1 pandemic and *has not been updated.*

- **The H1N1 virus that caused that pandemic is now a regular human flu virus and continues to circulate seasonally worldwide.**
- **The English language content on this website is being archived for *historic and reference purposes only*.**
- **For current, updated information on seasonal flu, including information about H1N1, see the CDC Seasonal Flu website (http://www.cdc.gov/flu/) .**

Origin of 2009 H1N1 Flu (Swine Flu): Questions and Answers

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Where did the 2009 H1N1 flu virus come from?

The 2009 H1N1 influenza virus (referred to as “swine flu” early on) was first detected in people in the United States in April 2009. This virus was originally referred to as “swine flu” because laboratory testing showed that its gene segments were similar to influenza viruses that were most recently identified in and known to circulate among pigs. CDC believes that this virus resulted from reassortment, a process through which two or more influenza viruses can swap genetic information by infecting a single human or animal host. When reassortment does occur, the virus that emerges will have some gene segments from each of the infecting parent viruses and may have different characteristics than either of the parental viruses, just as children may exhibit unique characteristics that are like both of their parents. In this case, the reassortment appears most likely to have occurred between influenza viruses circulating in North American pig herds and among Eurasian pig herds. Reassortment of influenza viruses can result in abrupt, major changes in influenza viruses, also known as “antigenic shift.” When shift happens, most people have little or no protection against the new influenza virus that results. For more information, see “How the Flu Virus can Shift: Drift for Shift.” (/flu/about/viruses/change.htm)

Why does CDC think this?

There are three primary reasons why experts from CDC and other public health research institutions around the world think 2009 H1N1 influenza resulted from reassortment of influenza viruses that occur naturally among pigs.

Reason One

The different gene segments of the 2009 H1N1 influenza virus are traceable to influenza viruses found in pigs. All influenza viruses have eight genes. Six of the eight genes found within the 2009 H1N1 influenza virus are associated with influenza viruses that regularly cause illness in pigs in North America. The remaining two genes of the 2009 H1N1 flu virus are associated with influenza viruses that previously were only known to be circulating among pigs from Eurasia.[1, 2 (#12)] The mixing of live pigs from Eurasia and North America through international trade or other means could have created the circumstances necessary for influenza viruses from North American and Eurasian pigs to mix. In fact, a 2009 study in Nature demonstrated that reassortant influenza viruses with genes from North American and Eurasian pigs were found in samples collected from pigs in Hong Kong as early as 2004.[2 (#12)] *

*The reassortant influenza viruses found in Hong Kong from 2004 are different from the 2009 H1N1 influenza viruses that have caused human illness around the world today, but these viruses serve as an example of how reassortment can occur naturally among influenza viruses found in Eurasian and North American pigs.

Reason Two

Evidence suggests that the 2009 H1N1 influenza virus has existed and evolved in nature for some time prior to being detected in humans. There are laboratory techniques available for looking at how and at what speed influenza viruses evolve and change. This is related to a concept known as “molecular evolution.” Evolution refers to small changes in influenza viruses that happen continually over time. Generally speaking, influenza viruses generate mutations by passing from one animal to another animal for several years and through virus replication in the animal host. These mutations are represented by changes in the nucleotides and amino acids found within influenza viruses. These small changes occur at a relatively stable rate in all influenza viruses. As a result, scientists can compare the number of mutations found within a new influenza virus with older, related influenza viruses to estimate the amount of time that it may have taken for one strain to evolve into a new strain of influenza virus. Researchers at CDC used this molecular evolution method to determine that the 2009 H1N1 influenza virus likely evolved in nature – perhaps through circulation in an unknown animal host – for a number of years before being detected. At this time, CDC continues to monitor the 2009 H1N1 influenza virus for changes. Research so far suggests that the 2009 H1N1 influenza virus is changing at a normal rate as compared to other influenza viruses.

Reason Three

The 2009 H1N1 influenza virus does not have the adaptations that are typical of influenza viruses grown or created in laboratories. For example, the standard method of growing influenza virus in laboratories involves injecting the virus into fertilized chicken eggs. The 2009 H1N1 influenza virus lacks the properties associated with growth in eggs.

Have viruses similar to the 2009 H1N1 virus been seen before?

Prior to the discovery of the 2009 H1N1 influenza virus, this particular combination of gene segments from North American and Eurasian swine had never been detected before in a single influenza virus and this new virus is different from the influenza viruses that normally circulate in North American and Eurasian pigs. It is not known when reassortment occurred to create the 2009 H1N1 influenza virus. Testing of the virus suggests that this reassortment event may have occurred years prior to the first reports of 2009 H1N1 influenza infection in people.[1, 2 (#12)] Scientists call 2009 H1N1 influenza a "quadruple reassortant" virus, because although each separate gene segment of the virus has been found in pigs previously, the individual gene segments of the virus originated from humans, birds, North American pigs and Eurasian pigs.

Why does the 2009 H1N1 flu virus have genes from humans, birds, and from pigs on different continents?

Pigs can be infected by influenza viruses found in birds and other animals as well as people. Therefore, pigs represent a mixing vessel in which influenza viruses from different species can swap genes. For example, in a setting where people and animals are in close contact, pigs can be infected by influenza viruses found in pigs, poultry or humans – sometimes at the same time. For at least 80 years, influenza viruses known as “classical swine H1N1” viruses have circulated in North American pigs. However, in the late 1990s, a series of reassortment events occurred between influenza viruses found in pigs, humans and birds. As a result, swine influenza viruses with genes from humans, North American pigs and birds have existed in many parts of the world for around 10 years prior to 2009 H1N1 flu. Mixing of these “triple reassortant North American swine influenza viruses” with Eurasian swine viruses likely resulted in the 2009 H1N1 influenza virus.

Was the 2009 H1N1 flu virus created in a laboratory?

This is very unlikely. Each of the gene segments within the 2009 H1N1 influenza virus have been found in pigs for more than 10 years prior to the beginning of the 2009 H1N1 influenza outbreak.[2] (#12) Pigs have long been considered a possible mixing vessel for influenza viruses that originate within pigs, birds and humans. In addition, a 2009 Nature study showed that reassortment between influenza viruses found in North American and Eurasia pigs had already occurred at least once naturally in the 5 years prior to the identification of 2009 H1N1 flu. Also, the 2009 H1N1 influenza virus does not have adaptations consistent with viruses grown in laboratories. For more information, see reasons 1, 2 and 3 (#Reasons) above.

How often does reassortment of influenza viruses occur?

We know that reassortment occurs frequently in nature. Fortunately, reassortment rarely results in a virus with pandemic potential, though it has done so at least twice in the 20th century. The influenza viruses that caused the 1957 and 1968 pandemics contained a mixture of gene segments from human and avian influenza viruses. What is clear from genetic analysis of the viruses that caused these past pandemics is that reassortment (gene swapping) occurred to produce novel influenza viruses that caused the pandemics. In both of these cases, the new viruses that emerged showed major differences from the parent viruses. However, not all viruses emerge directly from reassortment events. For example, the origins of the 1918 virus are not precisely known, but experts think it is likely that the 1918 virus may have resulted from a bird influenza virus directly infecting humans and pigs at about the same time without reassortment.

What can be done to identify influenza viruses circulating in animals that have pandemic potential?

The emergence of the 2009 H1N1 influenza virus in humans highlights the need for better surveillance of influenza viruses in pigs and other animals. The mixing of influenza genes in pigs can result in the emergence of viruses with pandemic potential in humans. Improved surveillance of influenza in pigs and other animals may help to detect the emergence of influenza viruses with the potential to cause illness and spread among people, possibly resulting in a pandemic. Early detection of such viruses can alert public health officials and aid in pandemic preparedness through the development of appropriate diagnostic tests and influenza vaccine candidate viruses, if necessary.

What scientific studies are available for additional information?

1. “Antigenic and Genetic Characteristics of the Early Isolates of Swine-Origin 2009 A (H1N1) Influenza Viruses Circulating in Humans” by Rebecca J. Garten & C. Todd Davis et al. *Science*. 325: no. 5937, pp. 197-201. (10 July 2009). (http://www.sciencemag.org/cgi/content/full/325/5937/197) (http://www.cdc.gov/Other/disclaimer.html)
2. “Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic” by Gavin J.D. Smith et al. *Nature*. 459, 1122-1125. (25 June 2009). (http://www.nature.com/nature/journal/v459/n7250/abs/nature08182.html) (http://www.cdc.gov/Other/disclaimer.html)

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