

# Major mid-century influenza epidemics caused by novel hybrid viruses

February 29 2008

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Reassortment of the influenza A virus occurs frequently throughout its evolutionary history, according to a new study published February 29 in the open-access journal *PLoS Pathogens*.

Researchers at Pennsylvania State University and the National Institute of Health used an evolutionary analysis of influenza viruses sampled from 1918 – 2005 to investigate the influenza viruses that cause seasonal epidemics in humans, particularly those where mortality was unusually high.

Specifically, the researchers found that the severe influenza epidemics of 1947 and 1951 were caused by genetic reassortment events in which two human influenza viruses of the same H1N1 strain exchanged genetic material, producing a new hybrid virus in both cases.

It has been a mystery why unusually severe epidemics of influenza occur from time to time, such as in 1947 and 1951, when illness and mortality rates exceeded standard epidemic levels. The standard model of human influenza virus evolution holds that major influenza pandemics, the largest of which occurred in 1918, are caused by reassortment between human and avian influenza viruses. But seasonal influenza epidemics, which occur each winter in the United States, do not involve the reassortment of genetic material.

These new findings suggest that the evolution of seasonal influenza is more complex than previously thought, and that multiple forms of the

same strain co-circulate and re-assort within a single population, rapidly generating genetically novel viruses with the potential to ignite major epidemics. It is therefore critical that intensive surveillance is undertaken to capture the full extent of influenza genetic diversity that co-circulates at a given time, particularly as an aid to vaccine design.

Citation: Nelson MI, Viboud C, Simonsen L, Bennett RT, Gieseher SB, et al. (2008) Multiple Reassortment Events in the Evolutionary History of H1N1 Influenza A Virus Since 1918. PLoS Pathog 4(2): e1000012. doi:10.1371/journal.ppat.1000012 ([www.plospathogens.org/doi/ppat.1000012](http://www.plospathogens.org/doi/ppat.1000012))

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Citation: Major mid-century influenza epidemics caused by novel hybrid viruses (2008, February 29) retrieved 23 April 2024 from <https://medicalxpress.com/news/2008-02-major-mid-century-influenza-epidemics-hybrid.html>

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