Since April of 2009, the novel swine-origin influenza A (H1N1) virus (S-OIV) has rapidly spread across the globe. The World Health Organization declared the outbreak a global pandemic in June. The new S-OIV has a unique genome composition and contains genes derived from avian, human, and swine influenza viruses. It has been reported that the new S-OIV may have emerged from the reassortment of previous reported triple-reassortant swine influenza viruses and Eurasian avian-like swine lineages. Human infections with swine influenza A viruses had been reported in the past. Although the infections occurred sporadically, some cases were fatal.

In this study, phylogenetic analysis of human H1N1 viruses was carried out to characterize the similarity and differences between the new S-OIV and previously reported human H1N1 viruses. Human H1N1 virus protein sequences were downloaded from NCBI influenza virus sequence database. The data consists of all samples of H1N1 viruses in human hosts deposited in Genbank before Sept. 2009. Phylogenetic trees for the viruses were inferred using the neighbor-joining method, with genetic distances calculated based on mPAM.

The results of this study reveal relationships among the new S-OIV and the previously reported human H1N1 viruses. The phylogenetic trees based the sequences of four proteins (PB2, PA, NP, NA) present three clearly visible clusters of H1N1 viruses. In the tree based on NA (Fig. 1), 59 samples of S-OIV were clustered together in the second cluster along with five cases in 1976, a 2005 Iowa case, a 1998 Wisconsin case and a few isolated cases in 1988 and 1991. The results from other six proteins (PB2, PA, HA, NA, NS1, NS2) also indicate the new S-OIV is closely related to the Fort Dix swine flu outbreak happened in 1976 also. As reported in the journal Nature (June 25, 2009), the common ancestor of S-OIV and the closest related swine viruses existed between about 10 and 20 years ago. However, the Fort Dix swine flu virus existed over 30 years ago. The results suggest that although some zoonotic influenza virus infections occur occasionally, they can potentially evolve into strains that causes pandemic.

Figure 1. Genetic relationships among human H1N1 viruses (NA)