

# THE ORIGIN OF THE RECENT SWINE INFLUENZA A(H1N1) VIRUS INFECTING HUMANS

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Preliminary analysis of the genome of the new H1N1 influenza A virus responsible for the current pandemic indicates that all genetic segments are related closest to those of common swine influenza viruses.

A new H1N1 influenza A virus has been identified in Mexico, and has spread rapidly to other regions around the world. The World Health Organization in collaboration with many other national and international agencies is working efficiently to evaluate, diagnose and implement measures to contain the spread of this virus. Among the many efforts is the timely release of the genomic sequences from different viral isolates [1]. This is allowing thousands of scientists to participate in the endeavour.

There have been some questions raised about the origin of the new strain. Influenza A is a single stranded RNA virus with eight different segments. When two viruses co-infect the same cell, new viruses can be produced that contain segments from both parental strains.

By using sequences collected in public databases, we can identify the closest relatives of the new strain found in Mexico, and construct clusters and phylogenetic trees. Sequence alignment and similarity, cluster analyses by principal component analysis and phylogenetic tree all point to similar results.

Our preliminary analyses show that the closest relatives to this new strain are found in swine, and occasionally in turkeys. Six segments of the virus are related to swine viruses from North America and the other two (NA and M) from swine viruses isolated in Europe/Asia. The closest clusters (for the HA segment) in the NCBI data base are North America swine influenza A(H1N2) and H3N2s. The closest relatives of the neuraminidase (NA) gene of the new virus, are influenza A isolates from 1992. As more data becomes accessible, the evolution of this gene could be clarified.

The North American ancestors are related to the multiple reassortants, H1N2 and H3N2 swine viruses isolated in North America since 1998 [2,3]. In particular, the swine H3N2 isolates from 1998 were a triple reassortment of human, swine and avian origin.

Therefore, this preliminary analysis suggests at least two swine ancestors to the current H1N1, one of them related to the triple reassortant viruses isolated in North America in 1998. So far, the new strain has not been reported in pigs. It is not clear if this is due to insufficient surveillance of the swine population, or if this virus has been generated in a very recent reassortment event.

### References

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