



Joint WHO-OFFLU technical teleconference to discuss human–animal interface aspects of the current influenza A (H1N1) situation

Meeting Summary
4 May 2009 (Geneva)

Background

Since the start of the current influenza A (H1N1) epidemic in humans, WHO has been coordinating the global response to the event, both operationally and scientifically. The OIE–FAO Network of Expertise on Animal Influenza (OFFLU), which is sponsored jointly by the World Organisation for Animal Health (OIE) and the Food and Agriculture Organization (FAO), has responded quickly to the current global situation by expanding to include swine influenza expertise. They have posted on their website¹ a request to laboratories around the world that may be holding information on swine influenza to share that information with the international scientific community, especially in light of the current public health concerns. WHO and OFFLU have been collaborating on avian influenza H5N1 for several years, and have now expanded their collaboration to address this new event.

Many laboratories and institutions around the world have long been working on various aspects of swine influenza, and some networks already exist. These networks and laboratories could benefit from building stronger relationships and additional linkages, particularly those between animal health expertise organized within OFFLU and human influenza expertise organized under the WHO Global Influenza Programme.

This joint teleconference was convened to bring together a variety of experts from the various human and animal health influenza networks to address immediate questions about the influenza A (H1N1) virus that is currently circulating in humans. The discussion focused on human–animal interface aspects of the virus and the event. Invited participants included representatives from WHO HQ and regional offices, OFFLU, OIE, FAO, WHO Collaborating Centres and H5 reference laboratories, OFFLU laboratories (including additional animal health institutions providing expertise on swine influenza virus), other public health laboratories and institutions working on influenza, representatives from governmental health departments, and members of the WHO GOARN (Global Outbreak Alert and Response Network) (as observers). During the teleconference, 52 telephone lines were used.

Summary of the technical discussions

Swine influenza is not presently an OIE-listed disease, so historical information on the global veterinary epidemiology of this disease is incomplete; however, some information is available. Classical H1 swine influenza viruses (SIVs) were first detected in North America in the 1930s. Reassortment of genes from swine, avian, and human viruses have occurred periodically, and triple swine, avian, and human H1N1, H1N2, and H3N2 reassortant viruses have been circulating in swine since at least 1998, especially in North America. These viruses have also been detected in some

¹ <http://www.offlu.net/OFFLU%20Site/offlu-29Apr.pdf>

Asian swine populations. There have been sporadic (2-3 per year) incidents of transmission of triple-reassortant swine viruses and other SIVs to humans (e.g. H1N1, H1N2), but no previously reported sustained human-to-human transmission.

The currently circulating A/California/4/2009-like H1N1 virus appears to be a further reassortant of the triple-reassortant swine viruses mentioned above (with the haemagglutinin (HA) derived from the classical H1 swine virus), except that both the neuraminidase (NA) and matrix (M) genes of the original triple-reassortant have now been replaced by genes from viruses whose closest relatives, based on available data, are swine viruses that were isolated in Europe and Asia (see figure, Schematic Representation of the Probable Reassortment Events Resulting in the A/California/4/2009-like H1N1 Influenza Virus). However, it is possible that these Eurasian viruses did not directly contribute these genes, and that one or more common progenitors, as yet unidentified, existed. The gene composition of this virus, in addition to historical data, clearly indicates that SIVs are very prone to reassorting with other SIVs, as well as with avian and human influenza viruses.

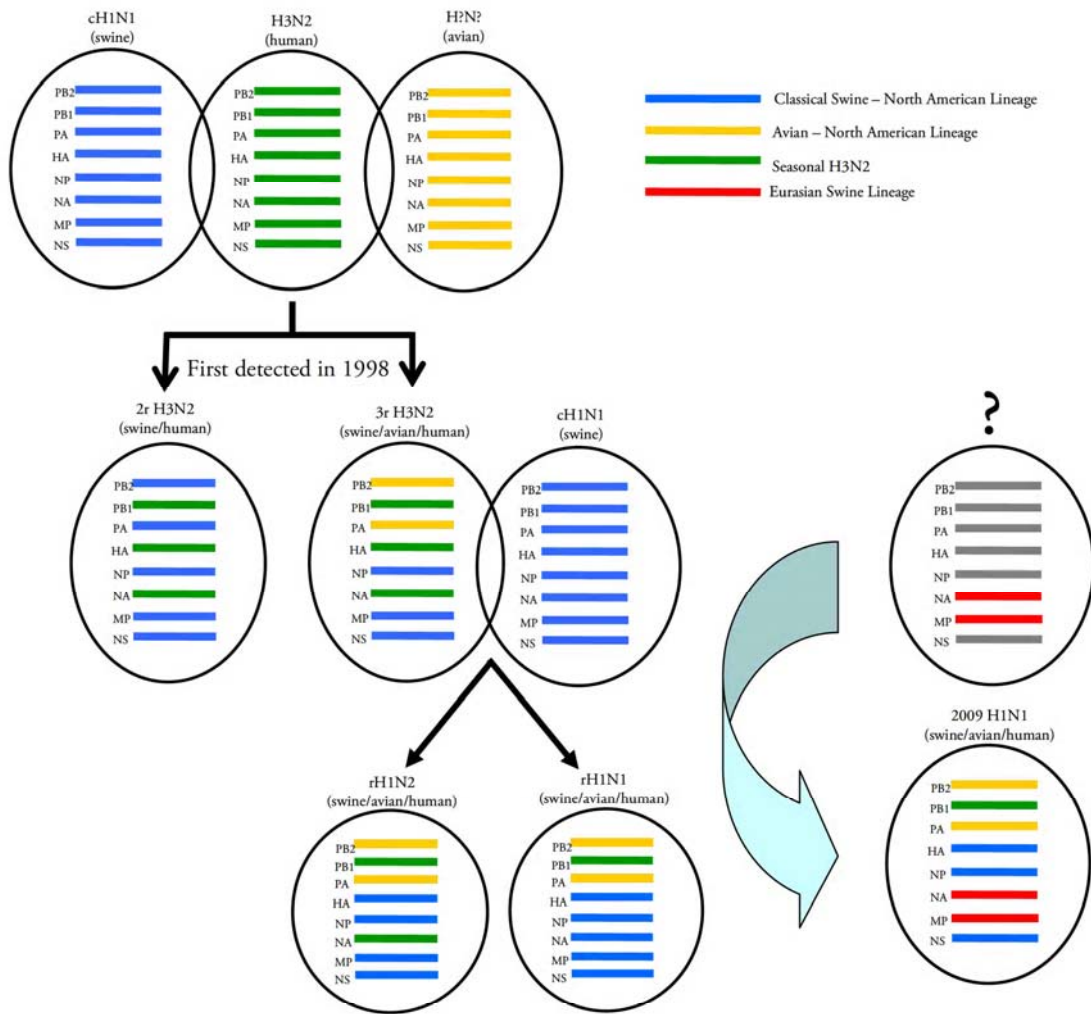


Figure: Schematic Representation of the Probable Reassortment Events Resulting in the A/California/4/09-like H1N1 Influenza Virus (prepared by Centers for Disease Control (CDC) Atlanta, Georgia, USA for the Joint WHO-OFFLU technical teleconference to discuss human-animal interface aspects of the current influenza A (H1N1) situation, 4 May, 2009)

When compared with genes from other viruses for which information is available, the closest genetic relatives of each of the genes of the currently circulating virus are gene segments from other swine viruses, but these relationships remain relatively distant. This is probably due to the large gaps in the historical global animal influenza surveillance data. It is possible that the donors of the genes that now comprise the A/California/4/2009-like virus have circulated without being detected, isolated, sequenced, and/or relevant data being put into the public domain. The lack of historical data and insufficient geographical coverage of data from swine populations globally limit the ability to draw conclusions about where and when this virus emerged.

Although there are on average about 40 amino-acid differences in the HA protein between the H1N1 triple-reassortant swine virus most recently detected in a human before this event and the currently circulating virus, preliminary data show some cross-reactivity between the currently circulating H1N1 virus and North American triple-reassortant swine H1N1 viruses. In contrast, the HA of the

circulating virus differs, both antigenically and genetically, from the HA of currently circulating human seasonal H1N1 viruses.

So far, the viruses isolated from humans during the course of this epidemic have been homogeneous, with a maximum of only 5 amino-acid differences among them. Based on current knowledge, there is no known molecular evidence of genetic changes to this virus that would explain its transmissibility among people. Also, none of the human pathogenicity motifs described in previous pandemic viruses nor those from the zoonotic avian influenza H5N1 are present. The gene segments remain most similar to swine consensus sequences, with no known molecular markers or motifs present in this virus that would allow predictions to be made about its potential to infect or cause disease in other animal species. Because the genes of this virus are most closely related to those of known swine viruses, it would be expected to be transmissible also among swine. Some data show that certain SIVs are transmissible in turkeys under certain conditions. Work to quantify transmissibility to other species (including poultry) is scheduled to start this month.

An update on the situation on the swine farm in Alberta, Canada, that is currently experiencing an outbreak of a similar virus was presented by representatives of the national animal and public health authorities. Ongoing epidemiological investigations of the human and animal situation continue.

Conclusions and next steps

Participants agreed that it is crucial to increase structured influenza disease surveillance in humans, swine, and other potentially susceptible species (such as turkeys), and to ensure close monitoring of the circulating influenza viruses to allow identification of potentially concerning future mutation and reassortment events, including reassortment with human seasonal viruses. Similarly, assessment of all available historical information on influenza viruses previously circulating in swine and other species would allow hypotheses on the origin of this virus to be strengthened. To this end, OFFLU has already requested any laboratories or other institutions who might have such information to put it into the public domain. It was suggested that the private swine production sector may have some important data and might be invited to participate in further discussions.

There was some concern expressed that this virus could be transmissible among and within several different species. Transmission studies are required to assess the transmissibility as well as pathogenicity in various species. Some of these studies (in swine, Japanese quail, domestic ducks, chickens and turkeys) have already been initiated.

It was agreed that additional joint teleconferences will be set up to discuss other relevant issues at the human–animal interface, as needed, starting with a discussion of surveillance and diagnostics.