

Influenza in swine and the novel H1N1 virus

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The challenge with writing an article for publication in August about a disease outbreak in June is trying not to make any predictions that will be too far off the mark. To be on the safe side, I can start with a quick synopsis up to this point (i.e. June 2009). A novel influenza A virus (H1N1) was first detected in Mexico and the United States in March and April, 2009, and confirmed by laboratory testing at Centers for Disease Control (CDC) on April 15th, 2009. Canada's National Microbiology Laboratory in Winnipeg was also involved in the early work to decode the genetic makeup of the H1N1 virus. This analysis showed that the virus was composed of genetic components of swine, avian and human influenza viruses. Currently, there are thousands of confirmed cases in the world, with continued spread in the human population. In contrast, although given the moniker of "swine flu" initially, there has been only one report of the infection in pigs, and that was attributed to contact with a farm worker who became ill after returning from Mexico. However, that case and recent experimental infections show that this virus can infect pigs. The experimental infection study revealed a mild clinical disease with similar transmission rates as other swine influenza viruses. The relatively short virus shedding period, seemingly restricted to the nasopharyngeal route, is consistent with the following statement that was issued jointly by the Food and Agriculture Organization of the United Nations (FAO), the World Organization for Animal Health (OIE), the World Health Organization (WHO) and the World Trade Organization.

"In light of the spread of influenza A/H1N1, and the rising concerns about the possibility of this virus being found in pigs and the safety of pork and pork products, we stress that pork and pork products, handled in accordance with good hygienic practices recommended by the WHO, FAO, Codex Alimentarius Commission and the OIE, will not be a source of infection."

However, official recommendations do not always hold sway in public perception and international trade. The Alberta hog producer whose animals were infected by the H1N1 virus ended up culling his herd because despite the safety of pork products, he could not find a market for his hogs.

From our diagnostic lab perspective, there have been between 7 and 25 cases of swine influenza per year at PDS in the four previous years. In 2009, as of May 1st, 12 samples were tested for the virus, with 4 positive results. Three of the samples were typed; two were H1 and one was H3. In the preceding 4 months (Feb to June) about 10% of serum samples had antibodies to swine influenza using either the H1N1 (20 of 212 samples) or H3N2 (33 of 237 samples) ELISA tests. The National Centre for Foreign Animal Diseases (NCFAD) Laboratory in Winnipeg has provided PDS with reagents for a PCR test that will detect the novel H1N1 virus.

For a quick review of the key points of influenza viruses, I retrieved the following information from "*A Concise Review of Veterinary Virology*", Carter GR and Wise DJ, eds., International Veterinary Information Service, Ithaca, NY (www.ivis.org):

Influenza viruses have a genome that is segmented (7 to 8 segments) rather than consisting of a single piece of RNA. The segmented genome facilitates genetic reassortment, which accounts for antigenic shifts. In reassortment, entire segments

of RNA are exchanged between two viruses infecting the same host, each of which codes for a single protein. As a result of co-infection by two viruses, a third one may arise. Point mutations in the RNA genome account for antigenic drifts that are often associated with epidemics. In either case, the changes frequently occur in the hemmagglutinin (HA) and neuraminidase (NA) proteins. The HA is an envelope antigen that is responsible for the attachment of the virion to cell surface receptors (neuraminic acid, sialic acid). If blocked by antibody, attachment of the virus to a susceptible cell is prevented; thus it is very important in protective immunity mediated by neutralizing antibody. A hemagglutination-inhibition titer of 1/40 is considered to be protective. NA is an envelope protein whose enzymatic activity results in the liquefaction of mucus thus contributing to viral spread. Specific antibody slows down the spread of virus. The HA and NA antigens determine subtypes of the virus.

The internal proteins consist mainly of nucleocapsid protein (NC), some matrix proteins (M1) and three polymerases (PA, PB1 and PB2). The proteins NC and M1 determine type specificity. (A, B, C). Viruses of veterinary importance are type A influenza viruses, which cause equine, swine, and avian influenza.

Influenza viruses are designated as follows: type/place/time of isolation/H and N content. Therefore, the virus: A/Bangkok/3/79 (H3N2) denotes, respectively, type A, isolated in Bangkok, local laboratory designate of number 3, first isolated in 1979, and envelope antigens of H3N2.

The novel H1N1 strain is a good example of how influenza viruses can change. From: *Influenza in Swine and the A/H1N1-2009 – A Historical Perspective*, May 27, 2009—Harry Snelson AASV e-Letter online: [<http://www.aasv.org/news>]:

Classical H1 (cH1N1) swine influenza viruses (SIV) were first identified in North America in the 1930s. The virus remained genetically stable until the 1998 emergence in swine of a triple-reassortant virus, H3N2, comprised of genes of swine, avian and human origin. The H3N2 virus then combined with the cH1N1 endemic in the swine population to form two reassortant viruses comprised of human, avian and swine genes, rH1N2 and rH1N1. To this point, all of the genetic components were derived from influenza viruses of North American lineage or seasonal human viruses.

In 2009, a new variant, A/H1N1-2009, was detected in the human population. This novel H1N1 contains avian genes (PB2 & PA), human genes (PB1) and swine genes (HA, NP & NS) of North American lineage. Notably, however, it also contains neuraminidase and matrix protein genes (NA & MP) of Eurasian swine origin which have never been identified previously in North America.

FAO has put together an educational animation describing the reassortment process for which can be viewed at:

http://www.fao.org/ag/againfo/programmes/en/empres/AH1N1/download/influenza_ah1n1_origins.swf.

One would assume that as the infection becomes more common in the human population, it is only a matter of time before it becomes transferred to swine. Therefore continued vigilance on detecting swine influenza, as well as any changes in the makeup of the virus, will be important as this outbreak unfolds.

References:

Since this is a new and evolving situation, this article has relied on information obtained from the websites of Centers for Disease Control (<http://www.cdc.gov/h1n1flu/>), the Public Health Agency of Canada (<http://www.phac-aspc.gc.ca/index-eng.php>), and the International Society for Infectious Diseases - ProMED-mail (<http://www.promedmail.org>).