UK Research council concludes H10N8 influenza not likely an epidemic risk

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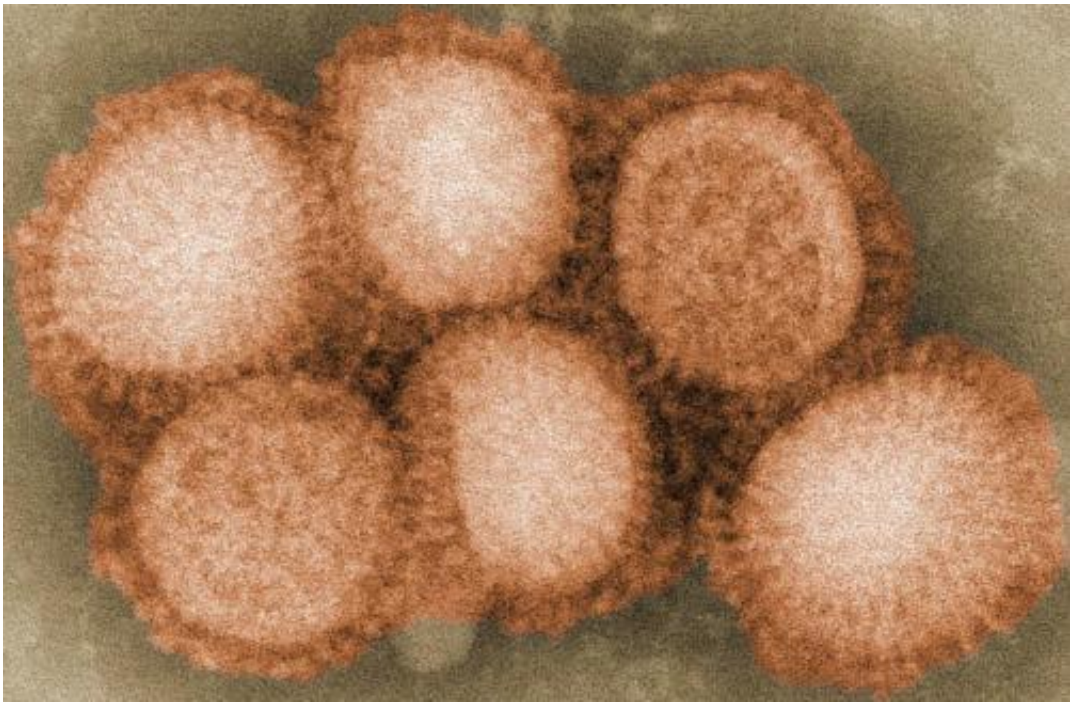

H1N1 virus. Credit: C. S. Goldsmith and A. Balish, CDC

(Medical Xpress)—Scientists with the UK's Medical Research Council (part of the National Institute for Medical Research) have concluded that the H10N8 influenza virus is not likely to pose an epidemic risk. In their paper published in the journal *Nature*, the team outlines their study of the avian flu variant and why they believe it's not likely to infect a lot of people.

Bird flu variants get their names from the most significant proteins involved in their transmission: hemagglutinin and neuraminidase (H and N)—they reside on the surface of the virus and interact with proteins covering host cells and in some cases (when the infection is successful) the cells themselves. To date, there have been just three known cases of people being infected with H10N8, two of which died. Despite the apparent lethalness of H10N8, the researchers in Britain don't believe it poses much of a threat, because close study of the virus has revealed that it prefers birds, to humans.

Reducing its threat potential is its lack of an ability to spread from human to human—to get it a person must come into direct contact with an infected bird (or its feces) most likely a chicken, as is believed to have been the case with the people who are known to have been infected by it. In analyzing the hemagglutinin protein the research team found that there is sufficient binding ability to allow for infection in humans, but it is 150 times stronger in birds. They believe that proteins in the human airway are strong enough to block an attack, preventing the virus from interacting with underlying cells. This is why, they conclude, human infections thus far have been rare events—they all occurred in China, where people interact closely with chickens.

The team also notes that the H10 hemagglutinin structure is similar to the H1N1 and H7 viruses, both of which caused epidemics—the main difference they note, is the clear preference to infecting avian receptors. For that reason, the researchers suggest that H10N8 should be carefully monitored to note immediately if mutations occur that give it a greater preference for infecting human hosts. In the meantime, they suggest efforts to combat influenza in general focus more on other more easily spread variants.

More information: Receptor binding by H10 influenza viruses, *Nature* (2014) DOI: 10.1038/nature13443

Abstract

H10N8 follows H7N9 and H5N1 as the latest in a line of avian influenza viruses that cause serious disease in humans and have become a threat to public health. Since December 2013, three human cases of H10N8 infection have been reported, two of whom are known to have died. To gather evidence relating to the epidemic potential of H10 we have determined the structure of the haemagglutinin of a previously isolated avian H10 virus and we present here results relating especially to its receptor-binding properties, as these are likely to be major determinants of virus transmissibility. Our results show, first, that the H10 virus possesses high avidity for human receptors and second, from the crystal structure of the complex formed by avian H10 haemagglutinin with human receptor, it is clear that the conformation of the bound receptor has characteristics of both the 1918 H1N1 pandemic virus and the human H7 viruses isolated from patients in 2013. We conclude that avian H10N8 virus has sufficient avidity for human receptors to account for its infection of humans but that its preference for avian receptors should make avian-receptor-rich human airway mucins an effective block to widespread infection. In terms of surveillance, particular attention will be paid to the detection of mutations in the receptor-binding site of the H10 haemagglutinin that decrease its avidity for avian receptor, and could enable it to be more readily transmitted between humans.