

Suspected spillover of A/H1N1 (2009) from humans to swine in Ghana: Current status of molecular surveillance

Content

The emergence of the A/H1N1 (2009) human pandemic influenza virus that had its origin in pigs caused the most influenza pandemic. This has refocused the world's attention on the possible emergence of zoonotic influenza viruses from pigs. While the human population is in the post-pandemic era with A/H1N1 (2009) now being an endemic seasonal influenza virus, the virus, then referred to as H1N1pdm, has spilled back in pigs in Europe, Asia, and America. Very little information is available from sub-Saharan Africa. We aimed to assess the possible circulation of H1N1pdm in pigs in Ghana. A total of 1200 nasal swabs was collected from 75 pig herds apparent healthy under intensive care in the Ashanti region in two seasons from 2016 -2017. RNA was extracted from all samples and RT-qPCR targeting a conserved region of the influenza A virus (IAV) matrix gene performed. Positive samples were tested for five HA and three NA subtypes, respectively, including H1N1pdm by subtype-specific RT-qPCR. IAV was detected in 2% (12/600) and 0.8% (5/600) of rain and dry season samples, respectively. The overall incidence of IAV was 1.4% (17/1200). All M gene-positive samples also tested positive for H1N1pdm.

Our results confirm the circulation of influenza A H1N1pdm in pigs in Ghana. Virus isolation and full genome sequencing have been initiated to clarify the origin of these viruses as possible spillover infections from humans. Regular swine surveillance is required to provide timely information on possible endemic H1N1pdm infections in swine, and the putative generation of reassortant viruses with pandemic potentials that may emerge from pigs.

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