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Outbreaks of influenza of swine and human origin in mink (*Neovison vison*)

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Influenza A virus infections in farmed mink, that are associated with respiratory disease, have occasionally been reported from mink producing countries. The viruses isolated have mainly been of avian or swine origin. Infections in mink with seasonal human influenza viruses have been inferred mainly from antibody detections. In 2009, the first outbreak with Influenza A virus was recognized in Danish farmed mink. The virus was a novel reassortant H3N2 virus. The HA and NA genes were most closely related to the 2005/06 human seasonal influenza virus and the internal genes were of contemporary swine influenza virus origin. All the infected farms received feed from the same feed producer. The feed contained fresh swine offal and the outbreak was therefore suspected to be feed-borne.Since 2009, Influenza A viruses have been detected in farmed mink in Denmark almost every year. Outbreaks are typically associated with sneezing, pneumonia and haemolytic E. coli infections. Characteristic is also bleeding from the nose. The mortality varies but is normally between three to five per cent in the affected farms.

The aim of this study was to elucidate the origin of influenza A viruses detected in Danish farmed mink in recent years by genetic and phylogenetic analyses of influenza A virus genes.The results showed that the viruses involved were either closely related to contemporary swine influenza viruses (avian-like H1N2 or H1N1) or to H1N1pdm09. The 2009 H3N2 virus has not been detected since 2009. The avian-like HA swine H1N1 and H1N2 viruses have never been detected in humans in Denmark, but are the most prevalent subtypes detected in the Danish swine herds with respiratory disease. Thus feed content of swine origin is a likely source of these viruses in mink.

The H1N1pdm09 viruses have been circulating in Danish swine since 2010 and the same subtype is now considered seasonal influenza virus in humans, rather than being “pandemic”.Genetic analyses showed that some of the H1N1pdm09 viruses found in mink had a higher level of identity to H1N1pdm09 strains detected in humans than in swine. This suggests that these viruses were transmitted directly from humans to mink.