RESEARCH ABSTRACT

SWINE HEALTH

Title: Genetic assessment of VDL SIV isolate pool for evidence of the swine flu strain reported to be infecting people and development of a high-throughput differential test for the novel strain
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Scientific Abstract

A novel H1N1 influenza virus (now referred to as "2009 pandemic H1N1") emerged and infected human in Mexico and caused widespread clinical disease in US and other countries. The novel virus is a reassortant between North American lineage and Eurasian lineage of swine influenza viruses (SIVs) which has not been reported in human and swine populations throughout the world previously. Although human-to-human transmission was the main mode, the potential and perception that pigs might have been the initial source of the novel strain (hereafter, 'pH1N1') had significantly negative impact on both domestic and export markets of U.S. pigs and pork products. Although preliminary tests indicated otherwise, uncertainty existed as to whether or not the novel strain had been circulating undetected in the US swine population. Therefore, retrospective and proactive surveillance for the new virus was necessary to address this concern.

First, archived H1N1 SIV isolates (n=118) and clinical specimens from 55 H1N1-positive cases submitted from Iowa and surrounding major swine producing states to the Iowa State University Veterinary Diagnostic Laboratory during 2008 and the first quarter of 2009 were selected, sequenced and analyzed for HA, NA and M genes in comparison to those of the novel H1N1. Second, the effort was made to develop an M gene-based PCR assay in a multiplex format for rapid differentiation of pH1N1 from endemic SIVs which have been circulated in US swine population since the novel virus contains the unique M gene (i.e., Eurasian lineage) as compared to endemic SIVs (North American lineage).

Sequence analyses for HA, NA and M genes revealed no pH1N1 among the 118 archived H1N1 SIV isolates and H1N1-positive clinical specimens. The vast majority of the virus isolates were classified into one of β, γ, and δ clusters based on their HA sequences. To our surprise, M gene showed a high degree of variability and the degree of homology was related to year of submission. As a differential PCR assay was successfully developed for detecting and differentiating pH1N1 from endemic SIVs, specimens collected from 165 animals after emergence of pH1N1 in humans were tested by the assay. In contrast to the observation on the archived isolates/samples, 5 animals (2 porcine, 2 feline and 1 canine) were determined to be positive for

pH1N1 (i.e., EA matrix) while 6 animals were positive for endemic (NA matrix) influenza A virus (5 porcine and 1 feline).

In conclusion, evidence that the novel H1N1 virus was circulating undetected in US swine population prior to its emergence in human is lacking. Furthermore transmission of novel H1N1 strain from affected humans to pigs was apparent, suggesting that good biosecurity measure and farm personnel management should be practiced when an influenza epidemic due to a new strain occurs in humans. Continuous monitoring of swine herds for emergence of a novel strain may be necessary as reassortment between pH1N1 and endemic SIVs is expected.