

PUBLIC HEALTHWORKER SAFETY

Title: Genetic and antigenic characterization of 2008 H1 swine influenza viruses from the United States - **NPB #08-031**

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Scientific Abstract

Prior to the introduction of the 2009 pandemic H1N1 virus from humans into pigs, four phylogenetic clusters of the hemagglutinin (HA) gene from H1 swine influenza viruses (SIV) could be found in U.S. SIV. Viruses from the classical H1N1 SIV lineage evolved over time to form α -, β -, and γ -clusters. SIV with HA genes most similar to human seasonal H1 viruses emerged in 2003 to form the δ -cluster. All four HA cluster gene types can be found with neuraminidase genes of either N1 or N2 subtype. Limited sequence information was available regarding the 6 genes that make up the triple reassortant internal gene (TRIG) cassette in contemporary H1 SIV. In addition, information regarding the antigenic relatedness of the H1 viruses and diagnostic reagent updates was lacking due to the dynamic and variable nature of H1 SIV. We characterized 12 H1 isolates from 2008 by sequencing and phylogenetic analysis of all eight gene segments and by serologic cross-reactivity in the hemagglutination inhibition (HI) assay. Based on genetic analysis, each of the four previously described phylogenetic clusters of H1 SIV were represented in the 2008 panel. Additionally, it was demonstrated that the δ -cluster HA diverged into sub-clusters δ -1 and δ -2. Serologic cross-reactivity paired with antigenic cartography demonstrated that the phylogenetic clusters are also divergent antigenically. The genes composing the TRIG were all North American in lineage. Genetic diversity was demonstrated in all gene segments, but most notably in the HA gene. Gene segments from the 2009 pandemic H1N1 formed clusters separate from North American swine lineage viruses, suggesting this virus was not present in U.S. pigs prior to 2009. The HA variability has important implications for diagnostic testing as well as vaccine development.

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