

Complete Genome Sequence of an Avian-Like H4N8 Swine Influenza Virus Discovered in Southern China

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We report here the complete genomic sequence of an avian-like H4N8 swine influenza virus containing an H5N1 avian influenza virus segment from swine in southern China. Phylogenetic analyses of the sequences of all eight viral RNA segments demonstrated that these are wholly avian influenza viruses of the Asia lineage. To our knowledge, this is the first report of interspecies transmission of an avian H4N8 influenza virus to domestic pigs under natural conditions.

Influenza A virus can infect various hosts, including migratory waterfowl, resident birds, horses, swine, dogs, sea mammals, and humans. Among these species, swine serve as an important component of the human-animal interface and play an important role in influenza evolution and ecology (2). Although pigs can be simultaneously infected with avian influenza viruses and human influenza viruses, the viruses can exchange genes and produce new variants, which suggests that pigs have become mixing vessels for influenza viruses (3). However, in nature, interspecies transmission of avian viruses to pigs is not often documented (1).

In October 2011, an avian-like H4N8 swine influenza virus was isolated from a commercial pig farm during an outbreak of severe respiratory diseases in pigs in Guangdong Province, Southern China. The strain had hemagglutination (HA) activity, and the HA titers ranged from 128 to 256. Subsequently, nucleotide sequences of the eight viral genes were amplified through reverse transcriptase PCR (RT-PCR). The amplified products were purified and cloned into the pMD18-T vector (TaKaRa) and sequenced with an ABI 3730 XL genome sequencer. Sequences were assembled and manually edited to produce the final genome sequence. The strain was identified as subtype H4N8.

The results showed that the virus was avian-like H4N8 swine influenza virus, whose HA gene had the highest homology with that of A/avian/Japan/8K10185/2008(H4N6) (99%) and whose NA gene had the highest homology with that of A/chicken/Guangxi/2117/2010(H3N8) (98%). The NP gene was phylogenetically close to those in H5N1 avian influenza viruses. Accordingly, the nomenclature for this isolate was A/swine/Guangdong/K4/2011(H4N8). Phylogenetic analyses of the sequences of all eight viral RNA segments demonstrated that these are wholly avian influenza viruses of the Asia lineage. The nucleotide sequence identity between each segment of A/swine/Guangdong/K4/2011(H4N8) and its potential progenitor identified in the public database varied from 97% to 99%. Finding an NP gene fragment ostensibly of avian influenza (H5N1) virus in this strain implies that subtype H5N1 viruses may be able to contribute genes to virus pathogenic processes in pigs in Southern China.

The amino acid sequence at the cleavage site in the HA molecule is PEKASR/GLF, indicating that it is a low-pathogenicity

avian influenza virus. Analysis of potential N-glycosylation sites of HA protein showed that this virus has four potential N-glycosylation sites at positions 18, 34, 178, and 310. This virus has Q226 and G228 (H3 numbering) in the receptor-binding site in the HA protein, which preferentially bind to an avian-origin receptor. The analysis of PB2 protein showed that it has 627E and 701D, with no substitutions.

In the past decades, many influenza pandemic strains were reported to emerge in Southern China. This is the first report of avian-like H4N8 swine influenza virus containing an H5N1 avian influenza virus segment in Southern China. This finding further confirms that this area is critical for the emergence of novel influenza A viruses.

Nucleotide sequence accession numbers. The GenBank accession numbers of A/Swine/Guangdong/K4/2011(H4N8) are JX151007 to JX151014.

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