

Complete Genome Sequence of a Novel Avian-Like H3N2 Swine Influenza Virus Discovered in Southern China

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We report here the complete genomic sequence of a novel avian-like H3N2 swine influenza virus containing an H5N1 highly pathogenic avian influenza virus segment that was obtained from swine in southern China. Phylogenetic analysis indicated that this virus might originate from domestic aquatic birds. The sequence information provided herein suggests that continuing study is required to determine if this virus can be established in the swine population and pose potential threats to public health.

Pigs are susceptible to both human and avian influenza viruses and have been proposed to be intermediate hosts, or mixing vessels, for a generation of pandemic influenza viruses through reassortment or adaptation to the mammalian host (3). However, in nature, interspecies transmission of avian viruses to pigs is not often documented (2).

In December 2011, an avian-like H3N2 swine influenza virus was isolated from a pig farm with an outbreak of severe respiratory problems in Guangdong Province, southern China. The strain had hemagglutination (HA) activity, and the HA titers ranged from 128 to 256. The HA-positive isolates were further identified as subtype H3N2. Subsequently, nucleotide sequences of the 8 viral genes were amplified through reverse transcription-PCR (RT-PCR). 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 results showed that the virus was avian-like H3N2 swine influenza virus (SIV), whose HA gene and neuraminidase (NA) gene had the highest homologies with those of A/white-backed munia/Hong Kong/4519/2009(H3N2) (95% and 96%, respectively), and the M gene was phylogenetically close to those in H5N1 highly pathogenic avian influenza viruses (HPAIVs). Accordingly, the nomenclature for this isolate was A/swine/Guangdong/L21/2011(H3N2). All eight segments of the phylogenetic analysis showed that this avian-like H3N2 SIV originated from domestic aquatic birds. The nucleotide sequence identity between each segment of A/swine/Guangdong/L21/2011(H3N2) and its potential progenitor identified in the public database varied from 95% to 100%. Finding an M gene fragment ostensibly of highly pathogenic 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 proposed antigenic sites, receptor-binding sites, and potential glycosylation sites were analyzed. Antigenic sites, regions of molecules involved in antibody binding to SIV, have been defined. A/Swine/Guangdong/L21/2011(H3N2) was similar to the A/Chicken/Korea/LMP88/2006(H3N2) isolate because only three amino acid changes were observed at all of the antigenic sites between these two viruses. No amino acid changes at the receptor-binding site were observed when comparing the A/Swine/Guangdong/L21/2011(H3N2) and A/Chicken/Korea/LMP88/2006(H3N2) isolates, suggesting that

the two viruses might have preferential receptor-binding specificity to the NeuAca2,3Gal form rather than the NeuAca2,6Gal form. A/Swine/Guangdong/L21/2011(H3N2) has six potential glycosylation sites (N-X-S/T) at positions 6, 22, 38, 165, 285, and 483, and only one potential glycosylation site change at position 6 was observed out of all of the antigenic sites between these two viruses, whereas the recent isolate, the human-like H3N2 swine influenza virus A/Swine/Guangdong/L9/2010, has 11 potential glycosylation sites.

In the past decades, many influenza pandemic strains were reported to emerge in southern China. Recently, several scientific research teams have achieved some success in isolating influenza A/H5N1 viruses that are transmitted efficiently between mammals (1). This is the first report of avian-like H3N2 SIV containing an H5N1 highly pathogenic avian influenza virus segment in southern China, further confirming 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/L21/2011(H3N2) are JX096501 to JX096508.

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