

Complete Genome Sequence of a Novel H4N1 Influenza Virus Isolated from a Pig in Central China

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Pigs are proposed to be “mixing vessel” hosts that can produce genetically novel reassortant viruses with pandemic potential. The appearance of any novel influenza viruses among pigs should pose concerns for human health. Here, we report the complete genome sequence of a novel H4N1 influenza virus [A/Swine/HuBei/06/2009(H4N1)] isolated from a pig in Central China in 2009. The genomic sequence analysis indicates that this virus is a wholly avian-original influenza virus. Each gene may come from different avian influenza viruses outside mainland China, suggesting the role of migratory birds in the dispersal of influenza virus.

Influenza A viruses are important pathogens for human and many other species. While all hemagglutinin (HA) and neuraminidase (NA) subtypes of influenza A viruses have been isolated from wild waterfowl (10), only subtypes H1 and H3 have circulated in both human and swine populations (11). Pigs play a key role in human health, as they serve as intermediate hosts and “mixing vessels” for the generation of human pandemic viruses (6). In recent years, pigs have been infected with avian influenza viruses of multiple subtypes, including mainly H5N1 (8) and H9N2 (7). Few H4N6-subtype viruses isolated from pigs were reported (3, 4). The H4N6 virus is one of the most frequently isolated subtypes of viruses from bird species and is deemed to transmit to pigs under natural conditions (1, 5). Since H4 viruses have been reported to infect individuals (5), it is necessary to emphasize the extensive epidemiological surveillance of H4-subtype influenza A viruses in the pig industry.

Cases about H4N1 strains are limited, and only several H4N1 influenza virus strains isolated from waterfowl are registered in GenBank. Here, we report the first documentation of an H4N1 influenza virus from a naturally infected pig and its full genome sequence. This H4N1 influenza virus [A/Swine/HuBei/06/2009(H4N1)] was isolated in 2009 from a pig exhibiting severe respiratory syndrome. The virus was propagated in Madin-Darby canine kidney (MDCK) cells, and the eight genome segments were amplified and sequenced with an Applied Biosystems (ABI) 3730 genome analyzer (2).

Sequence analysis showed that the full lengths of each segment are 2,341 (PB2), 2,341 (PB1), 2,233 (PA), 1,738 (HA), 1,565 (NP), 1,398 (NA), 1,027 (M), and 890 (NS) nucleotides, encoding PB2 (759 amino acids [aa]); PB1 (759 aa), PB1-F2 (91 aa), and N40 (718 aa); PA (716 aa); HA (560 aa); NP (498 aa); NA (469 aa); M1 (252 aa) and M2 (80 aa); and NS1 (230 aa) and NS2 (121 aa), respectively. The phylogenetic analysis showed that all viral genes exhibited avian genotype and shared the highest sequence homologies (98 to 99%) with distinctive duck influenza virus from outside mainland China, indicating transmission of avian influenza viruses to pigs from migratory birds. The deduced amino acid sequence of hemagglutinin possesses the cleavage site with characteristic of low-pathogenicity avian influenza virus (KASR G). It should be noted that the amino acids Q226 and G228 (H3 numbering [9]) are conserved among other avian H4 sequences in GenBank, with an avian-like virus binding preference for SA α 2,3Gal. An analysis of N-glycosylation sites showed that the mature HA and NA proteins possess five (positions 2, 18, 162, 294, and 481) and three (positions 39, 97, and 186) potential N-glycosylation sites, respectively.

The appearance of this novel influenza virus in pigs should be of both veterinary and human public health concern.

Nucleotide sequence accession numbers. The genome sequences of the viruses described here have been deposited in GenBank under accession number [JX878672](#) to [JX878679](#).

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