Complete Genome Sequence of an H10N5 Avian Influenza Virus Isolated from Pigs in Central China

Nan Wang,^{a,b} Wei Zou,^a Ying Yang,^a Xuebo Guo,^a Yafeng Hua,^a Qiang Zhang,^a Zongzheng Zhao,^a and Meilin Jin^a

Unit of Animal Infectious Disease, National State Key Laboratory of Agricultural Microbiology, Huazhong Agricultural University, Wuhan, People's Republic of China,^a and Laboratory of Animal Infectious Disease, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, People's Republic of China^b

An avian H10N5 influenza virus, A/swine/Hubei/10/2008/H10N5, was isolated from pigs in the Hubei Province of central China. Homology and phylogenetic analyses of all eight gene segments demonstrated that the strain was wholly of avian origin and closely homologous to the Eurasian lineage avian influenza virus. To our knowledge, this is the first report of interspecies transmission of an avian H10N5 influenza virus to domestic pigs under natural conditions.

Influenza A viruses belong to the *Orthomyxoviridae* family. So far, 16 hemagglutinin (HA) and 9 neuraminidase (NA) subtypes have been identified in mammals and birds (6, 8). Few H10N5 influenza viruses have been reported to have been isolated, especially from mammals. The first H10 mammal influenza virus was reported to have been isolated from mink in Sweden in 1984 (2, 4). In 2004, the H10 influenza virus infection of two infants in Egypt was reported (10). A H10N7 subtype influenza virus (A/Sydney/2/2010) had also caused infection of poultry abattoir workers in Sydney in 2010. To our knowledge, this is the first report of H10N5 influenza virus in pigs.

Samples were collected from pigs in slaughterhouses, homogenized, and injected into 10-day-old chicken embryos. An avian influenza virus was isolated and named A/swine/Hubei/10/2008/H10N5 (SW/HB/10).

The complete genome of the virus consists of eight segments, including PB2, PB1, PA, HA, NP, NA, M, and NS. The full lengths of each segment are 2,341, 2,341, 2,233, 1,728, 1,585, 1,523, 1,027, and 889 nucleotides, respectively. The eight genes encode the following proteins, with the indicated amino acid lengths: PB2, 759; PB1, 757; PA, 716; HA, 561; NP, 498; NA, 472; M1, 252; M2, 80; NS1, 230; and NS2, 121. SW/HB/10 contained the entire PB1-F2 open reading frame (ORF) of 90 residues and the PA-X ORF of 232 residues. The isolate contained the amino acid sequence IIQGR/GLF at the cleavage site in the HA protein, suggesting that this virus might be a low-pathogenicity virus. Analysis of potential *N*-glycosylation sites (PGS) of the surface proteins indicated that six PGS (positions 12, 29, 236, 290, 406, and 478) (H3 numbering) were conserved in the HA protein of most H10 strains, while the PGS at residue 236 was lost in SW/HB/10, and six PGS were conserved (positions 46, 52, 65, 82, 142, and 399) in the NA protein. SW/HB/10 had histidine, glutamate, glutamine, and QGS at amino acid positions (H10 numbering) 177, 184, 216, and 226 to 228 of the HA protein, which favors binding of sialic acid α -2,3-galactose (3, 5). SW/HB/10 possessed a mutation, D701N, of the PB2 protein, which may be the key factor leading to interspecies transmission (1, 7, 9).

The HA segment of SW/HB/10 was most closely related to the gene of A/duck/Hong Kong/768/97/H10N3. The HA genes of SW/HB/10 and mink/1984-like virus belong to the same group (early Eurasian lineage). The NA and M genes of SW/

HB/10 had the highest degree of identity with A/chicken/Hubei/119/1983/H10N5. They both fell into the Eurasian lineage group. The six internal genes were closely related to that of A/Tree sparrow/Henan/3/2004/H5N1 isolated from terrestrial birds (a nonsusceptible host of influenza virus) and belonged to the Eurasian avian lineage.

The presence of the H10N5 influenza virus in pigs enriches the genotype diversity of swine influenza viruses. These data in our study are useful for analyses of interspecies transmission of avian influenza virus and reassortants of influenza virus in pigs.

Nucleotide sequence accession numbers. The genome sequences of A/swine/Hubei/10/2008/H10N5 have been deposited in GenBank under accession numbers [JX500440](#) to [JX500447](#).

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Address correspondence to Meilin Jin, jml8328@126.com.

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