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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Novel Natural Recombinant H5N5 Influenza Virus from Ducks in Central China

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We reported the complete genome sequence of an H5N5 avian influenza virus (AIV) that was first isolated from duck in central China in 2010. Genomic sequence and phylogenetic analyses showed that this virus was a recombinant between H5N1 AIV circulated in southeastern Asia and an N5 subtype influenza virus. These data are beneficial for investigating the epidemiology and ecology of AIVs in central China.

Avian influenza A virus (AIV) is a single-strained negative-sense RNA virus belonging to the family *Orthomyxoviridae* (6). On the basis of the surface hemagglutinin (HA) and neuraminidase (NA) glycoproteins, the AIVs are divided into 17 HA subtypes and 9 NA subtypes (5). Theoretically, there are 153 subtypes of AIV. However, the H5N5-subtype virus was rarely isolated. At present, only four H5N5 subtype AIVs were submitted to the NCBI database, including two American isolates and two eastern China isolates (2, 4).

In this study, an H5N5 strain, named A/Duck/HuBei/03/2010(H5N5) (03/H5N5), was first isolated from duck in central China in 2010. The complete genome of the virus was amplified and sequenced with an ABI 3730 genetic analyzer. The results indicated that the full lengths of each segment (PB2, PB1, PA, HA, NP, NA, M, and NS) were 2,341, 2,341, 2,233, 1,776, 1,565, 1,467, 1,027, and 875 nucleotides, respectively. The eight genes encoded the following proteins, followed by the deduced amino acid lengths: PB2, 759; PB1, 757; PB1-F2: 91; PA, 716; HA, 567; NP, 498; NA, 472; M1, 252; M2, 97; NS1, 225; and NS2, 121. The deduced amino acids at the cleavage site of the HA protein were SPLRERRRKR ↓ GLF, with the characteristic of potential highly pathogenic property (1, 3). An analysis of potential N-glycosylation sites of the surface proteins indicated that the strain possessed nine potential N-glycosylation sites (positions 10, 11, 23, 154, 165, 193, 286, 483, and 542) in the HA protein and six (positions 25, 31, 44, 61, 121, and 378) in the NA protein.

Compared with the eastern China H5N5 isolate [(A/duck/eastern China/008/2008(H5N5)], the homologies of the PB2, PB1, PA, HA, NP, NA, M, and NS genes of 03/H5N5 were 94.4%, 89.8%, 95.3%, 97.4%, 91.8%, 92.0%, 98.7%, and 97.6%, respectively. Phylogenetic analysis revealed that the PB2, PA, HA, NP, NA, M, and NS genes of this virus originated from H5N1 AIV and showed a high homology with the virus A/wild duck/Hunan/021/2005 (H5N1). Meanwhile, all six of these genes were closely related to the viruses isolated from infected people, A/China/GD01/2006 and A/Anhui/2/2005, which belonged to clade 2.3.4 and still circulated in southeastern Asia. However, the NA and PB1 genes were highly homologous with the swine H10N5 strain isolated in our lab (GenBank accession numbers JX500445 and JX500441). Notably, the NA and PB1 genes of the 03/H5N5 virus showed very high homology with A/chicken/Hubei/119/1983(H10/N5) and A/chicken/Hubei/wk/1997(H5N1), respectively, which were isolated in 1997 and 1983 in the same region of central China, indicating that the PB1 and NA genes had existed early and still circulated and even underwent further reassortment with different subtypes of AIV in central China.

Therefore, continuing influenza virus surveillance in poultry is beneficial for understanding the ecology and evolution properties of AIVs in central China.

Nucleotide sequence accession numbers. The genome sequences of A/Duck/HuBei/03/2010(H5N5) have been deposited in GenBank under accession numbers JX878680 to JX878687.

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