

# Complete Genome Sequence of an H5N2 Avian Influenza Virus Isolated from a Parrot in Southern China

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**We report the complete genome sequence of an H5N2 avian influenza virus (AIV) that was first isolated from a parrot in Guangdong in southern China in 2004. Genomic sequence and phylogenetic analyses showed that it was highly homologous with the North American H5N2 viruses and all eight genes of this virus belonged to the North American gene lineage. These data will help in the investigation of the epidemiology and host range of AIVs in southern China.**

Influenza A viruses (AIVs) are zoonotic agents recognized as a continuing threat to both veterinary and human public health (2). All AIVs are further divided on the basis of their hemagglutinin (HA) and neuraminidase (NA) glycoproteins (7). Among the HA subtypes, the H5-encoding AIVs are of particular interest because of their high pathogenicity in poultry (9, 10). In 1983, highly pathogenic avian influenza (HPAI) H5N2 virus occurred in commercial poultry in Pennsylvania with devastating effects on the poultry industry (6). HPAI H5N2 viruses also occurred in central Mexico during 1994 and 1995 and in Italy during 1997 and 1998 (1, 3). More recently, HPAI H5N2 viruses occurred in South Africa and Taiwan in 2012 (<http://www.oie.int/>). The Pennsylvania 1983 and Mexican 1994-1995 outbreaks clearly demonstrate the emergence of HPAI H5N2 virus from low-pathogenicity precursor H5N2 AIVs (3, 6). In this regard, emphasis should be placed on the extensive epidemiological surveillance of H5N2 AIVs to prevent an HPAI pandemic.

Here we report the complete genomic sequence of an H5N2 strain, designated A/Parrot/Guangdong/258/2004 (H5N2), that was isolated from a parrot in Guangdong in southern China in 2004. Psittacine birds are susceptible to AIVs, but naturally acquired disease is rare (4, 5, 8).

To investigate the molecular characteristics of this virus and understand its origin, we completely sequenced its genome with an ABI 3730 genetic analyzer. The complete genome of the strain consists of eight segments of negative-sense single-stranded RNA molecules, including PB2, PB1, PA, HA, NP, NA, M, and NS. The full lengths of the segments are 2,341, 2,341, 2,233, 1,767, 1,565, 1,467, 1,027, and 890 nucleotides, respectively. The eight genes encode proteins with the following amino acid lengths: PB2, 759; PB1, 757; PA, 716; HA, 564; NP, 498; NA, 469; M1, 252; M2, 80; NS1, 230; NS2, 121. The amino acid sequence at the cleavage site of the HA molecule is RETRGLF, which is characteristic of low-pathogenicity AIVs. The strain possesses seven potential N-glycosylation sites (at positions 26, 27, 39, 181, 302, 496, and 555) in the HA protein and five (at positions 61, 69, 86, 146, and 234) in the NA protein. The strain has Q226 and G228 (H3 numbering) in the receptor-binding site of the HA protein, which shows that it is an avian-origin influenza virus.

The homologies of the HA and NA gene nucleotide sequences with those of the A/chukar/MN/14591-7/1998 (H5N2) and A/pheasant/NJ/9804565/1998 (H5N2) viruses, respectively, were both 99.7%. The homologies of the PB2, PB1, NP, and NS gene

nucleotide sequences with those of the A/pheasant/NJ/1355/98 (H5N2) virus were above 99%. The homology of the PA gene nucleotide sequence with that of the A/pheasant/NJ/9804568/1998 (H5N2) virus was up to 99.9%. However, the homology of the M gene nucleotide sequence with that of the A/duck/Eastern China/06/2000 (H5N2) virus was 99.3%. Phylogenetic analysis demonstrated that all eight genes of this virus belong to the North American gene lineage.

These data will help in the investigation of the epidemiology and host range of AIVs in southern China.

**Nucleotide sequence accession numbers.** The genome sequences of the virus described here have been deposited in GenBank under accession numbers [JQ990145](#) to [JQ990152](#).

## ACKNOWLEDGMENTS

This work was supported by grants from the Natural Science Foundation of Guangdong Province (10251064201000004, 10151064201000021), the National Natural Science Foundation of China (31172343), the Science and Technology Projects of Guangdong Province (2010B020307005), the Earmarked Fund for Modern Agro-Industry Technology Research System (nycytx-42-G3-03), and the High-Level Talents in University Project of Guangdong Province.

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Received 12 May 2012 Accepted 16 May 2012

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doi:10.1128/JVI.01189-12

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