Full Genome Sequence of a Recombinant H5N1 Influenza Virus from a Condor in Southern China

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In this study, we report the first genomic information on an H5N1 avian influenza virus (AIV) isolated from a condor in Guangdong Province in southern China in 2003. Full genome sequencing and phylogenetic analyses show that it is a recombinant virus containing genome segments derived from the Eurasia and North America gene pools. This will be useful for analyses of the evolution of H5N1 AIV in southern China.

H5N1 highly pathogenic avian influenza (HPAI) is caused by H5N1 influenza A virus, which can result in serious systemic or respiratory diseases in birds. H5N1 avian influenza viruses (AIV) have been reported to be transmitted from wild birds to domestic poultry and various mammalian species (1). In 1996, the H5N1 HPAI virus (A/Goose/Guangdong/1/1996) was first isolated from a sick goose in southern China (2, 9). In 1997, the transmission of H5N1 viruses to humans had caused the deaths of 6 of 18 infected persons in southern China (3, 8). Since 2003, H5N1 HPAI viruses which had developed a high degree antigenic variation began to spread and caused serious outbreaks in more than 60 countries of Asia, Europe, and Africa, not only resulting in the destruction of hundreds of millions of poultry but also causing serious infection and death of humans. Therefore, H5N1 AIVs are zoonotic agents recognized as a continuing threat to both the poultry industry and human public health.

Here, a H5N1 influenza virus (A/Condor/Guangdong/139/2003 [GD139]) was isolated from a sick condor in southern China in 2003. To investigate more information about this recombinant virus, we determined the complete genomic sequence with an ABI 3730 genetic analyzer using the Sanger method, which is based on DNA fragments amplified by PCR with a previous primer (5). Sequence fragments were assembled using Sequencher 5.0. The 8 genome segments of the virus encode 10 proteins (PB2, PB1, PA, HA, NP, NA, M1, M2, NS1, and NS2) with lengths of 759, 757, 716, 568, 498, 449, 252, 97, 225, and 121 amino acids, respectively. There are 20- and 5-amino-acid deletions in NA and NS1, respectively. The GD139 virus has a series of basic amino acids at the cleavage site of the HA (RRKKR) that is characteristic of HPAI viruses. The receptor-binding pocket of HA1 retains the amino acid residues Q226 and G228 (H3 numbering), which preferentially bind to the avian influenza virus receptor (4). The PB2 protein has E and D at positions 627 and 701, which are characteristic of the avian influenza virus (6, 7).

Phylogenetic analysis of GD139 revealed that the HA and NA genes belong to the Eurasia gene pool (A/Hong Kong/213/2003 [H5N1]-like virus) and share 99% and 94.7% nucleotide identity with HK213-like virus, respectively. The internal genes showed that PB1, PA, NP, M, and NS genes also belong to the Eurasia gene pool and exhibit more than 99%, 96%, 99% and 99% sequence identity to HK213-like virus, respectively. However, the PB2 gene

belongs to the North America gene pool and has 94% sequence identity with the A/Pheasant/NJ/9804570/1998(H5N2) virus. Thus, GD139 virus is a recombinant virus between the Eurasia gene pool and the North America gene pool which has rarely been reported in southern China.

The genomic information on this H5N1 natural recombinant virus from a condor will be helpful for analyses of the evolution of H5N1 AIV in southern China.

Nucleotide sequence accession numbers. The genome sequences of A/Condor/Guangdong/139/2003 (H5N1) have been deposited in GenBank under accession numbers [JQ966928](#) to [JQ966935](#).

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