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GENOME ANNOUNCEMENT

Complete Genomic Sequence of an H5N1 Influenza Virus from a Parrot in Southern China

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An H5N1 avian influenza virus (AIV) designated A/Parrot/Guangdong/C99/2005 (H5N1) was first isolated from a sick parrot in Guangdong in southern China in 2005. The complete genome of this strain was analyzed. Genome sequence analysis showed that all 8 gene segments of the virus nucleotide had 99.0% homology to A/chicken/Henan/12/2004 (H5N1). Phylogenetic analysis demonstrated that all 8 gene segments of the virus were derived from the Eurasian lineage. The availability of genome sequences is useful to investigate the host range and genetic evolution of the H5N1 avian influenza virus in Southern China.

Avian influenza (AI) virus belongs to the type A influenza viruses, which can infect a great variety of birds, including free-living birds, captive caged birds, domestic ducks, chickens, turkeys, and other domestic poultry (1). The isolation of AI viruses from psittacine birds is rarely reported (4, 9). The potential role of psittacine birds in the ecology, pathogenicity, and transmission of AI viruses among domestic birds is unclear (4, 9). In 1997 and 1998, H9N2 AI viruses were isolated from Indian ring-necked parakeets; these were closely related to the viruses isolated from affected people in Hong Kong (6, 8). Furthermore, H5N1 AI viruses can infect a broad range of birds and have crossed the species barrier to infect mammalian species (11). Clusters of AI H5N1 infection may increase the virus's capacity for human transmissibility, which could then lead to the emergence of a new influenza pandemic. In 2005, we first isolated one H5N1 avian influenza virus, designated A/Parrot/Guangdong/C99/2005 (C99), from a sick parrot with lethargy and severe respiratory symptoms in southern China. Accordingly, the parrot origin H5N1 virus raises significant questions concerning the impact of parrots on poultry and human health.

The complete genome of A/Parrot/Guangdong/C99/2005 (C99) virus was sequenced with an ABI 3730 genetic analyzer using the Sanger method, based on cDNA fragments amplified by PCR with special primers (5). Sequence fragments were assembled using Sequencher 5.0. The 8 gene segments of the virus encoded 10 proteins (PB2, PB1, PA, HA, NP, NA, M1, M2, NS1, and NS2) with the following amino acid lengths: 759, 757, 716, 568, 498, 450, 252, 80, 225, and 121, respectively. The virus contains the amino acid motif PQRERRRKKR ↓ G at the HA cleavage site, which is a characteristic of highly pathogenic influenza viruses (2, 3). The receptor-binding pocket of HA1 retains the amino acid residues Q222 and G224 (H5 numbering) (2), which preferentially bind to the avian influenza virus receptor. The consensus amino acid sequences revealed eight potential N-linked glycosylation sites in HA (26 or 27, 39, 181,209, 302, 500, and 559). The NA gene possesses a 20-amino-acid deletion in the stalk region. There were 5 amino acid deletions in the NS1 protein. Amino acid residue 627 of PB2 is E rather than K, and amino acid residue 701 of PB2 is D, characteristic of the avian influenza virus (7).

Genome sequence analysis showed that the nucleotide homology of all 8 gene segments of the virus was 99.0% when compared with A/chicken/Henan/12/2004 (H5N1). Phylogenetic analysis demonstrated that all 8 gene segments of C99 were derived from the Eurasian lineage. The HA of C99 clustered into clade 9, which is a clade of H5N1 AI virus that can infect mammalian species (10).

In conclusion, the genome sequence of A/Parrot/Guangdong/C99/2005(H5N1) virus, which was isolated from a caged parrot in southern China, is first reported here. These data are useful to investigate the host rang and genetic evolution of the H5N1 avian influenza virus in southern China.

Nucleotide sequence accession numbers. The genome sequences of A/Parrot/Guangdong/C99/2005 (H5N1) have been deposited in GenBank under accession numbers JX013485 to JX013492.

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REFERENCES

1. **Alexander DJ.** 2007. An overview of the epidemiology of avian influenza. Vaccine **25**:5637–5644.
2. **Chen H, et al.** 2006. Establishment of multiple sublineages of H5N1 influenza virus in Asia: implications for pandemic control. Proc. Natl. Acad. Sci. U. S. A. **103**:2845–2850.
3. **Chen H, Yu K, Bu Z.** 1999. Molecular analysis of hemagglutinin gene of a goose origin highly pathogenic avian influenza virus. Chin. Agric. Sci. **32**:87–92.
4. **Hawkins MG, et al.** 2006. Avian influenza A virus subtype H5N2 in a red-lored Amazon parrot. J. Am. Vet. Med. Assoc. **228**:236–241.
5. **Jiao P, et al.** 2008. A single-amino-acid substitution in the NS1 protein changes the pathogenicity of H5N1 avian influenza viruses in mice. J. Virol. **82**:1146–1154.
6. **Mase M, et al.** 2001. Imported parakeets harbor H9N2 influenza A viruses

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that are genetically closely related to those transmitted to humans in Hong Kong. J. Virol. **75**:3490–3494.
7. **Massin P, van der Werf S, Naffakh N.** 2001. Residue 627 of PB2 is a determinant of cold sensitivity in RNA replication of avian influenza viruses. J. Virol. **75**:5398–5404.
8. **Pillai SP, Suarez DL, Pantin-Jackwood M, Lee CW.** 2008. Pathogenicity and transmission studies of H5N2 parrot avian influenza virus of Mexican lineage in different poultry species. Vet. Microbiol. **129**:48–57.
9. **Steuler H, Rohde W, Scholtissek C.** 1984. Sequence of the neuraminidase gene of an avian influenza A virus (A/parrot/ulster/73, H7N1). Virology **135**:118–124.
10. **Sun H, et al.** 2011. Pathogenicity in quails and mice of H5N1 highly pathogenic avian influenza viruses isolated from ducks. Vet. Microbiol. **152**:258–265.
11. **Watanabe Y, Ibrahim MS, Suzuki Y, Ikuta K.** 2012. The changing nature of avian influenza A virus (H5N1). Cell **20**:11–20.