



# Genome Sequence of an H9N2 Avian Influenza Virus Strain with Hemagglutinin-Neuraminidase Combination, Isolated from a Quail in Guangxi, Southern China

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**ABSTRACT** We isolated a strain of H9N2 avian influenza virus from a quail in southern China in May 2015 and named it A/quail/Guangxi/198Q39/2015. All eight gene segments of the strain were sequenced. Sequence analysis indicated that the amino acid motif of the hemagglutinin cleavage site of this H9N2 virus was RSSR↓GLF, which is a typical characteristic of the low pathogenic avian influenza virus. This study will help in better understanding the epidemiology and molecular characteristics of avian influenza virus in wild birds.

The avian influenza virus is a negative-sense, segmented RNA virus that belongs to the genus Influenza type A virus of the family *Orthomyxoviridae* (1, 2). At present, there are 18 hemagglutinin (HA) and 11 neuraminidase (NA) subtypes of avian influenza virus based on the antigenic differences of the HA and NA proteins, which are surface glycoproteins on the viral envelope (3, 4).

The H9N2 subtype avian influenza virus is widespread in the world and is the most prevalent subtype of avian influenza viruses reported in China over the past decade (5, 6). Although H9N2 is characterized as a low-pathogenic avian influenza virus, occasional infections of humans (7–10) have caused great concerns. So far, H9N2 subtype avian influenza viruses are isolated mainly from domestic birds (11); however, wildfowl and shorebirds are the natural hosts of avian influenza, virus and they facilitate the transmission of avian influenza (6, 12).

An H9N2 subtype avian influenza virus was isolated from a quail in Guangxi, China, in May 2015 and named A/quail/Guangxi/198Q39/2015 (H9N2). All eight gene segments were amplified by reverse transcription-PCR using avian influenza virus universal primers (13, 14). The amplified products were gel purified and cloned into the pMD-18T vector (TaKaRa, Dalian, China) and sequenced (TaKaRa). The sequences were assembled using the SeqMan program and manually edited to generate the final full-length genome sequence.

The complete genome of the A/quail/Guangxi/198Q39/2015 strain consists of eight segments of the HA, NA, NS, M, NP, PA, PB1, and PB2 genes. The full lengths of these segments are 1,742, 1,457, 890, 1,027, 1,565, 2,233, 2,341, and 2,341 nucleotides, respectively. The amino acid (aa) lengths of the proteins encoded by the eight genes are 560 aa (HA), 466 aa (NA), 121 aa (NS2), 217 aa (NS1), 252 aa (M1), 97 aa (M2), 498 aa (NP), 716 aa (PA), 758 aa (PB1), and 259 aa (PB2).

The amino acid residues at the cleavage site (aa 335 to 341) of the HA molecule are RSSR↓GLF, which is characteristic of low-pathogenic avian influenza virus. Sequence analysis revealed that the nucleotide sequences of the HA and NA genes of the

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A/quail/Guangxi/198Q39/2015 strain both belong to the Eurasian lineage. The A/quail/Guangxi/198Q39/2015 strain has Leu234 and Gly236 at the receptor-binding site in the HA protein, which suggests that it might have the ability to bind a sialic acid–2,6-NeuAcGal linkage and might have the potential to infect humans (9).

The nucleotide homology comparisons revealed that the HA gene of this strain shared the highest sequence homology (98%) with the HA gene of a Beijing avian influenza virus strain, A/chicken/Beijing/0309/2013 (GenBank accession number KM609599). The NA gene shared the highest sequence homology (98%) with A/turtle-dove/Guangxi/49B6/2013 (GenBank accession number KJ725014). These results are useful for future analyses of the molecular epidemiology and evolutionary characteristics of avian influenza virus.

**Accession number(s).** The genome sequence of A/quail/Guangxi/198Q39/2015 (H9N2) was deposited in GenBank under the accession numbers [MF425642](#) to [MF425649](#).

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