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Complete Genome Sequence of Influenza Virus H9N2 Associated with a Fatal Outbreak among Chickens in Dubai

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We report the complete genome sequence of influenza virus H9N2 associated with a fatal outbreak among chickens in Dubai. All segments are clustered with avian H9N2 viruses circulating in the Middle East but distinct from those in southeast Asia. It is not a reassortant virus or transmitted from other regions.

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Influenza virus outbreaks due to H5N1, H5N6, H5N2, and H7 subtypes are common in poultry and have led to huge economic loss worldwide and are occasionally associated with human infections (1–3). However, outbreaks associated with influenza virus H9N2 have been extremely uncommon over the two decades since this subtype adapted and has been prevalent in chicken. Chickens infected with H9N2 virus are asymptomatic and egg production may be affected. In a previous report of an influenza virus H9N2 outbreak in chickens in the Republic of Korea, comparative genome analysis showed high sequence similarity to genes of reassortant H9N2 viruses in slaughterhouses and live bird markets (4).

In November 2015, ~30 chickens died in a chicken farm in Dubai, the United Arab Emirates, and all the chickens in the farm were culled. The farm has 20,000 layers of different breeds of leghorn chickens around 60 weeks old from Saudi Arabia. The farm consisted of four blocks with four houses per block, with the farm completely fenced. Altogether there were 19 staff members with one looking after the chickens in each house. There was no contact between chickens in the farm and other chickens or birds. The chickens received the influenza virus H9N2 vaccine and 85% of the chickens were H9 antibody-positive. Influenza virus A/Chicken/Dubai/D2506.A/2015 was isolated from the lung fluid of the chickens using 9 to 11-day-old embryonated chicken eggs and complete genome sequencing showed H9N2 subtype. In this article, we report the complete genome sequence of the influenza virus H9N2 strain associated with this outbreak.

Viral RNA was extracted using a QIAamp Viral RNA minikit (QIAGEN) and cDNAs were synthesized by reverse transcription (TaKaRa). The full length viral genome was sequenced as previously described (5). Sequence fragments were assembled with Lasergene (version 6.0; DNASTAR) then aligned and residue analyzed using BioEdit version 7. Sequences of avian H9N2 virus were used for comparison. A/Chicken/Dubai/D2506.A/2015 contains no known virulent elements in the hemagglutinin, such as the avian type 627E residue observed in multiple basic motif H5 or H7 subtypes and PB2. Using sequences of other H9N2 viruses extracted from GenBank, phylogenetic trees were constructed using the neighbor-joining method with the Tamura-Nei model of nucleotide substitutions in the MEGA program (version 5.05). It is shown that all segments are clustered with avian H9N2 viruses circulating in the Middle East but distinct from H9N2 viruses in southeast Asian countries (6, 7). Based on these findings, we conclude that A/Chicken/Dubai/D2506.A/2015 is not a reassortant virus and not transmitted from other regions. While no known virulent element was identified in the viral genome from A/Chicken/Dubai/D2506.A/2015, several mutations were observed in HA, NA, and other internal genes. It is possible that there are uncharacterized virulent mutations contributing to the outbreak in chickens. Pathogenicity in poultry and other animal models may be necessary to assess the pathogenic properties of this variant. Surveillance for any potential virulence change in H9N2 virus is warranted.

Accession number(s). This genome has been deposited at DDBJ/EMBL/GenBank under accession no. KX351195 to KX351202.

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