Highly Pathogenic Avian Influenza A(H7N3) Virus in Poultry Workers, Mexico, 2012


Human infection with influenza A(H7) virus is rare but has been documented after direct contact with infected birds (1). Conjunctivitis or upper respiratory tract symptoms developed in patients infected with this virus, and outcomes ranged from mild disease to death (1,2). In North America, 6 persons infected with influenza A(H7) virus have been reported; all patients recovered (2–6). We report the cases of 2 poultry workers with conjunctivitis caused by highly pathogenic avian influenza (HPAI) A(H7N3) viruses during poultry-related outbreaks in Jalisco, Mexico (3).

The Study

In June 2012, outbreaks of (HPAI) A(H7N3) virus in poultry on farms throughout Jalisco State were reported by the National Service for Health, Safety, and Food Quality in Mexico (7,8). A 32-year-old poultry worker who reported irritation in her left eye was examined at a clinic in Jalisco on July 7. Bilateral conjunctival swab specimens were collected and sent to the Instituto de Diagnóstico y Referencia Epidemiológica (IndRE) in Mexico City, where H7 subtype virus infection was confirmed by real-time reverse transcription PCR (RT-PCR). HPAI A(H7N3) virus had been suspected because the patient collected eggs on a farm that had had HPAI A(H7N3) virus infection among poultry. The Mexican International Health Regulation authority reported the case to the World Health Organization on July 19.

Several days later, a 52-year-old man, who was related to the first patient and worked on the same farm, visited a local clinic and reported conjunctivitis. Conjunctival swab specimens from this patient were also positive for H7 subtype virus infection by real-time RT-PCR. Both patients were treated symptomatically and recovered without sequelae (5). We describe characteristics of the virus isolated from the 32-year-old woman.

Although wild birds might be infected with influenza A(H7) viruses, outbreaks among poultry are rare.

DOI: http://dx.doi.org/10.3201/eid1909.130087

1These authors contributed equally to this article.
2Deceased.
Nucleotide sequences of 8 influenza A gene segments from a virus isolate were generated by semiconductor next-generation sequencing with Ion PGM (Life Technologies, Carlsbad, CA, USA) and MBTuni12 and MBTuni13 primers as described (9) at InDRE/Instituto Nacional de Enfermedades Respiratorias and by RT-PCR of overlapping fragments of each gene by using H7N3 subtype and avian influenza virus–specific primers at the Centers for Disease Control and Prevention. Sequences were aligned and phylogenetic trees were constructed from each gene alignment by using a neighbor-joining approach implemented in MEGA5 (www.megasoftware.net/) with 1,000 bootstrap replicates. Genomic sequences confirmed that the conjunctivitis was caused by infection with an HPAI A(H7N3) virus closely related to HPAI A(H7N3) viruses collected during poultry outbreaks in Jalisco State (Figure 1, Appendix, wwwnc.cdc.gov/EID/article/19/9/13-0087-Techapp1.pdf). Like reported avian A(H7N3) virus sequences from Jalisco, the human isolate had a multibasic cleavage site indicative of an HPAI A virus (7) (Figure 2). Genetic similarity of nucleotides at the cleavage site suggested that this region was inserted into the H7 HA gene at the site of HA0 protein cleavage by nonhomologous recombination of host rRNA from an unknown source (7). Comparison of this protein sequence motif with other HPAI and low pathogenicity avian influenza (LPAI) H7 viruses showed that this sequence indicated a novel cleavage site not observed in influenza A virus HA gene sequences (Figure 2). However, multiple arginine amino acids in this motif would be predicted to result in a highly pathogenic phenotype in chickens. Phylogenetic trees of HA and neuraminidase (NA) genes indicated high similarity of HPAI A(H7N3) viruses detected in Mexico and LPAI viruses collected from wild birds and poultry in North America (Figure 1). HA genes clustered with LPAI A(H7N9) viruses from turkeys, geese, and guinea fowl in the United States during 2011 (10). The N3 NA genes grouped with LPAI viruses of various subtypes, clustering most closely with viruses collected from wild birds in the midwestern United States in 2009. Internal genes also clustered with LPAI viruses from various subtypes collected primarily in California in 2010, except for the polymerase acidic gene, which was most closely related to an H11N9 subtype virus from Mississippi.

HA and other protein gene alignments were assessed for putative markers of virulence, mammalian adaptation, receptor-binding specificity, and antiviral drug resistance. Besides the multibasic cleavage site, the virus had typical avian consensus amino acid residues in the HA protein at positions involved in preferential receptor binding to avian sialic acid receptors (amino acids Q226 and G228 by H3 numbering). Avian consensus sequences at other
motifs/amino acid positions in proteins of interest were identified, suggesting that the virus had not accumulated described mammalian host adaptive mutations or known virulence markers.

Antigenic characterization was performed by using a panel of ferret antisera in hemagglutination inhibition (HI) tests with turkey erythrocytes as described (11). The HI assay demonstrated relatedness of HPAI A(H7N3) virus with several amino acid differences compared with older North American and Eurasian lineage H7 viruses (Table). Antiserum against HPAI A(H7N3) virus was cross-reactive with North American and Eurasian lineage H7 subtype viruses but showed higher levels of heterologous titers was cross-reactive with North American and Eurasian lineage H7 viruses (Table). Antiserum against HPAI A(H7N3) virus with and contact with poultry in areas with known avian influenza outbreaks.

Acknowledgment

We thank the originating and submitting laboratories for providing sequences from the Global Initiative On Sharing All Influenza Data EpiFluTM database, which were used in this analysis.

Ms. Lopez-Martinez is chief of the virology department at the Institute for Epidemiological Diagnosis and Reference in Mexico City, Mexico. Her research interests include the epidemiology of influenza and other viral infectious diseases.

References


Address for correspondence: C. Todd Davis, Centers for Disease Control and Prevention, 1600 Clifton Rd NE, Mailstop D30, Atlanta, GA 30333, USA; email: ctdavis@cdc.gov