

CORRESPONDENCE

Highly Pathogenic Avian Influenza A(H5N1) Virus Infection in a Dairy Farm Worker

TO THE EDITOR: Sporadic human infections with highly pathogenic avian influenza (HPAI) A(H5N1) virus, with a wide spectrum of clinical severity and a cumulative case fatality of more than 50%, have been reported in 23 countries over more than 20 years.¹ HPAI A(H5N1) clade 2.3.4.4b viruses have spread widely among wild birds worldwide since 2020–2021,^{2,3} resulting in outbreaks in poultry and other animals.² Recently, HPAI A(H5N1) clade 2.3.4.4b viruses were identified in dairy cows, and in unpasteurized milk samples, in multiple U.S. states.^{4,5} We report a case of HPAI A(H5N1) virus infection in a dairy farm worker in Texas.

In late March 2024, an adult dairy farm worker had onset of redness and discomfort in the right eye. On presentation that day, subconjunctival hemorrhage and thin, serous drainage were noted in the right eye. Vital signs were unremarkable, with normal respiratory effort and an oxygen saturation of 97% while the patient was breathing ambient air. Auscultation revealed clear lungs. There was no history of fever or feverishness, respiratory symptoms, changes in vision, or other symptoms. The worker reported no contact with sick or dead wild birds, poultry, or other animals but reported direct and close exposure to dairy cows that appeared to be well and with sick cows that showed the same signs of illness as cows at other dairy farms in the same area of northern Texas with confirmed HPAI A(H5N1) virus infection (e.g., decreased milk production, reduced appetite, lethargy, fever, and dehydration⁵). The worker reported wearing gloves when working with cows but did not use any respiratory or eye protection.

Conjunctival and nasopharyngeal swab specimens were obtained from the right eye for influenza testing. The results of real-time reverse-transcription–polymerase-chain-reaction (RT-PCR) testing were presumptive for influenza A and A(H5) virus in both specimens. On the basis of a presumptive A(H5) result, home isolation was

recommended, and oral oseltamivir (75 mg twice daily for 5 days) was provided for treatment of the worker and for postexposure prophylaxis for the worker's household contacts (at the same dose). The next day, the worker reported no symptoms except discomfort in both eyes; reevaluation revealed subconjunctival hemorrhage in both eyes, with no visual impairment (Fig. 1). Over the subsequent days, the worker reported resolution of conjunctivitis without respiratory symptoms, and household contacts remained well.

On the basis of real-time RT-PCR and sequencing, the Centers for Disease Control and Prevention confirmed HPAI A(H5N1) virus infection in the conjunctival and nasopharyngeal swab specimens obtained on the day of symptom onset. Additional clinical specimens were not available for influenza testing. Although viral RNA purified from the nasopharyngeal swab specimen (cycle threshold [Ct] value, 33) yielded insufficient PCR amplicons for sequencing, complete genome sequences from the conjunctival swab specimen (Ct value, 18) confirmed that the virus belonged to clade 2.3.4.4b (genotype B3.13), and successful virus isolation from both the conjunctival and nasopharyngeal swab specimens yielded identical virus. All gene segments were closely related to viruses detected in Texas dairy cattle and other genotype B3.13 viruses detected in peridomestic wild birds in Texas during March 2024 (Fig. S1



Figure 1. Conjunctivitis with Subconjunctival Hemorrhage in Both Eyes.

in the Supplementary Appendix, available with the full text of this letter at NEJM.org). Sequence data from presumably infected cattle on the farm where the worker was exposed were not available for analysis.

Viral sequences from cattle and from the worker maintained primarily avian genetic characteristics and lacked changes in the hemagglutinin gene that would affect receptor-binding specificity (e.g., binding to α 2-6-linked sialic acid receptors, primarily located in the human upper respiratory tract) and transmission risk to humans. The virus identified in the worker's specimen had a change (PB2 E627K) that has been associated with viral adaptation to mammalian hosts and detected previously in humans and other mammals infected with HPAI A(H5N1) viruses and other avian influenza A virus subtypes, including A(H7N9) and A(H9N2). No genetic markers associated with reduced susceptibility to influenza antiviral drugs approved by the Food and Drug Administration were identified. Additional results and interpretation and discussion of findings, unanswered questions, recommendations, and references are provided in the Supplementary Appendix. The hemagglutinin of the virus was found to be closely related to two existing clade 2.3.4.4b A(H5N1) candidate vaccine viruses. Because influenza A(H5N1) viruses have pandemic potential, these candidate vaccine viruses are available to manufacturers and could be used to produce vaccine if needed.

Timothy M. Uyeki, M.D., M.P.H.

Centers for Disease Control and Prevention
Atlanta, GA
tmu0@cdc.gov

Scott Milton, M.D.

Cherissa Abdul Hamid, D.V.M., M.P.H.

Texas Department of State Health Services
Lubbock, TX

Cynthia Reinoso Webb, Ph.D.

Steven M. Presley, Ph.D.

Texas Tech University Bioterrorism Response Laboratory
Lubbock, TX

Varun Shetty, M.D.

Susan N. Rollo, D.V.M., Ph.D.

Diana L. Martinez, Ph.D., M.P.H.

Saroj Rai, Ph.D., M.P.H.

Emilio R. Gonzales, M.P.H.

Texas Department of State Health Services
Austin, TX

Krista L. Kniss, M.P.H.

Yunho Jang, Ph.D.

Julia C. Frederick, Ph.D.

Juan A. De La Cruz, M.S.

Jimma Liddell, M.S.

Han Di, Ph.D.

Marie K. Kirby, Ph.D.

John R. Barnes, Ph.D.

C. Todd Davis, Ph.D.

Centers for Disease Control and Prevention
Atlanta, GA

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Disclosure forms provided by the authors are available with the full text of this letter at NEJM.org.

This letter was published on May 3, 2024, at NEJM.org.

1. World Health Organization. Cumulative number of confirmed human cases for avian influenza A(H5N1) reported to WHO, 2003-2024. March 28, 2024 ([https://www.who.int/publications/m/item/cumulative-number-of-confirmed-human-cases-for-avian-influenza-a\(h5n1\)-reported-to-who--2003-2024-28-march-2024](https://www.who.int/publications/m/item/cumulative-number-of-confirmed-human-cases-for-avian-influenza-a(h5n1)-reported-to-who--2003-2024-28-march-2024)).
2. European Food Safety Authority (EFSA), European Centre for Disease Prevention and Control (ECDC), Adlhoch C, et al. Drivers for a pandemic due to avian influenza and options for One Health mitigation measures. *EFSA J* 2024;22(4):e8735.
3. Kandeil A, Patton C, Jones JC, et al. Rapid evolution of A(H5N1) influenza viruses after intercontinental spread to North America. *Nat Commun* 2023;14:3082.
4. United States Department of Agriculture Animal and Plant Health Inspection Service. Highly pathogenic avian influenza (HPAI) detections in livestock. April 30, 2024 (<https://www.aphis.usda.gov/livestock-poultry-disease/avian/avian-influenza/hpai-detections/livestock>).
5. Burrough ER, Magstadt DR, Petersen B, et al. Highly pathogenic avian influenza A(H5N1) clade 2.3.4.4b virus infection in domestic dairy cattle and cats, United States, 2024. *Emerg Infect Dis* 2024 April 29 (Epub ahead of print).

DOI: 10.1056/NEJMc2405371

Correspondence Copyright © 2024 Massachusetts Medical Society.