A Discussion on H5N1 Avian Flu

Nahid Bhadelia, MD, MALD Davidson Hamer, MD, FACP Catherine Brown, DVM, MSc, MPH Tim Uyeki, MD, MPH, MPP







June 14, 2024

Acknowledgement

This webinar is presented by the Region 1 Disaster Health Response System (RDHRS) in collaboration with the Regional Emerging Special Pathogens Treatment Center (RESPTC). Both programs are funded by the Administration for Strategic Preparedness and Response (ASPR) within the US Department of Health and Human Services.



Disclosure

- The content provided in this webinar is presented by the individual speakers only and does not represent of reflect the official policy or position of any portion of the United States Government or the Henry M. Jackson Foundation, Inc.
- The content is not meant to be a substitute for medical professional advice, diagnosis, or treatment. The information herein should be adapted to each specific patient based on the treating medical professional's independent professional judgment and consideration of the patient's needs, the resources available at the location from where the medical professional services are being provided (e.g., healthcare institution, ambulatory clinic, physician's office, etc.), and any other unique circumstances. This information should not be used to replace, substitute for, or overrule a qualified medical professional's judgment.
- The speakers have no affiliation or financial interests/relationships to disclose.

Moderators & Speakers

Moderator:

Erica S. Shenoy, MD, PhD

Chief of Infection Control, Mass General Brigham Physician, Division of Infectious Diseases, Massachusetts General Hospital Medical Director, Region 1 Emerging Special Pathogens Treatment Center

Speakers:

David Hamer, MD

Professor of Global Health and Medicine, Boston University Co-lead, climate change and emerging infectious diseases, BU Center on Emerging Infectious Diseases

Nahid Bhadelia, MD, MALD

Associate Professor, BU School of Medicine, Founding Director, BU Center on Emerging Infectious Diseases

Tim Uyeki, MD, MPH, MPP

Chief Medical Officer, Influenza Division, Centers for Disease Control and Prevention

Catherine Brown, DVM, MSc, MPH

State Public Health Veterinarian and State Epidemiologist, Massachusetts Department of Health

Learning Objectives

1. Understand updated information on H5N1 viruses, the epidemiology of human cases of

H5N1, and the associated risk to humans.

- 2. Identify and access quality and up-to-date resources and guidance on H5N1, an evolving landscape.
- 3. Assess risk to individual patients and mitigate risk to healthcare providers and facilities through the implementation of the Identify, Isolate, Inform approach.

Overview of Human HPAI A(H5N1) Cases

- Highly Pathogenic Avian Influenza (HPAI) A(H5N1) virus first detected in a poultry outbreak in Scotland (1959)
 - Continue to evolve (classified into clades)
- First human infection identified in 1997 (Hong Kong)
 - 18 cases, 6 deaths
- 1997 to date: 912 human cases reported (24 countries)
 - >50% case fatality proportion
- Clade 2.3.4.4b viruses emerged in 2020 in wild birds
 - Detected in wild birds in N. America (end of 2021)
 - Poultry outbreaks, wild bird detections 2022 ongoing
 - Wide range of infected mammals
- Other virus clades are circulating among wild birds, poultry

Emergence and Evolution of H5N1 BIRD FLU





1996-1997 H5N1 bird flu virus first detected

In 1996, highly pathogenic avian influenza H5N1 virus is first identified in domestic waterfowl in Southern China. The virus is named A/goose/Guangdong/1/1996. In 1997, H5N1 poultry outbreaks happen in China and Hong Kong with 18 associated human cases (6 deaths) in Hong Kong. This virus would go on to cause more than 860 human infections with a greater than 50% death rate.

H5N1 spreads 2003-2005

For several years, H5N1 viruses were not widely detected; however, in 2003, H5N1 re-emerges in China and several other countries to cause widespread poultry outbreaks across Asia. In 2005, wild birds spread H5N1 to poultry in Africa, the Middle East and Europe. The hemagglutinin (HA) gene of the virus diversifies into many genetic groups (clades). Multiple genetic lineages (genotypes) are detected.



H5N8

2014-2016 H5N6 and H5N8 viruses emerge

Gene-swapping of H5 viruses from poultry and wild birds leads to emergence/detection of H5N6 and H5N8 virus subtypes. H4 diversifies further into clade 2.3.4.4 in Asia, Africa, Europe, the Middle East and North America. H5 viruses with various neuraminidase (NA) genes continue to be detected, including in U.S. wild birds and poultry.

2.3.4.4b viruses spread widely 2018-2020

H5N6 and H5N8 viruses become predominant globally, replacing the original H5N1 viruses. As of 2022, there have been more than 70 H5N6 human infections and 7 H5N8 human infections reported. The H5 HA diversifies further into clade 2.3.4.4b which becomes predominant in Asia, Africa, Europe, and the Middle East.



H5N1 clade 2.3.4.4b 2021-2023 H5N1 found in Canada, US A new H5N1 virus belonging to clade 2.3.4.4b with a wild bird



adapted N1 NA gene emerges. Clade 2.3.4.4b H5N1 viruses become predominant in Asia, Africa, Europe, and the Middle East by the end of 2021. The virus is detected in wild birds in Canada and the United States in late 2021. In February 2022, the virus begins causing outbreaks in U.S. commercial and backyard poultry. Rare, sporadic human infections with this H5N1 virus are detected, as well as sporadic infections in mammals. More information is available:

https://www.cdc.gov/flu/avianflu/inhumans.htm.



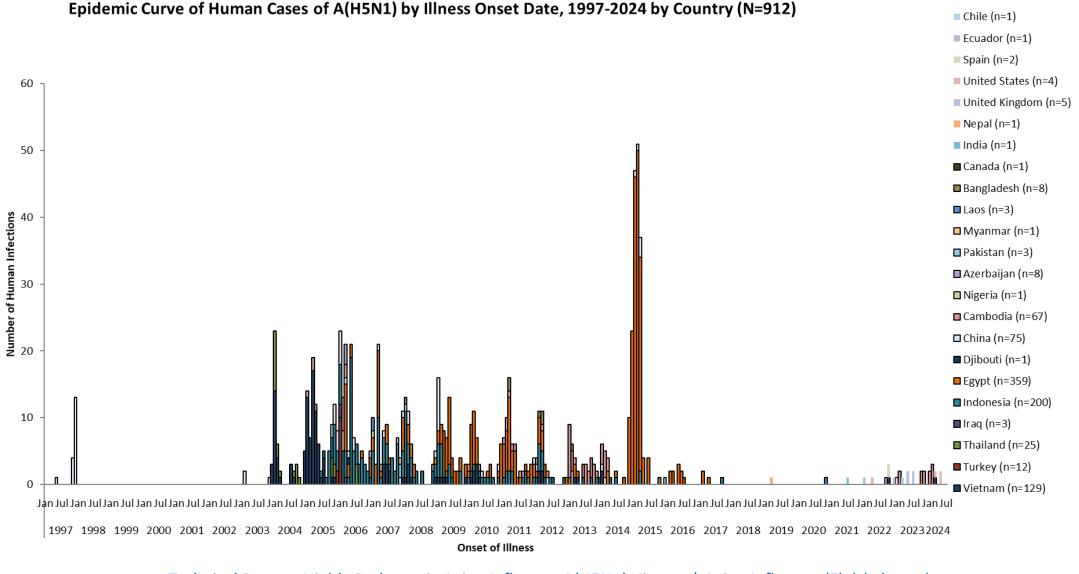


H5N1 Cases Since 1997

Influenza

2022-2024: 29 cases

(Australia 1, Cambodia 11, Chile 1, China 2, Ecuador 1, Spain 2, UK 5, US 4, Vietnam 2)



Technical Report: Highly Pathogenic Avian Influenza A(H5N1) Viruses | Avian Influenza (Flu) (cdc.gov)

Human Infections with HPAI A(H5N1) Viruses

- HPAI A(H5N1) viruses bind preferentially to receptors most prevalent in the human lower respiratory tract
 - Also found on conjunctivae
- Wide symptomatic clinical spectrum
 - Mild (conjunctivitis, upper respiratory illness)
 - Severe/critical (pneumonia, respiratory failure, sepsis)
- Unprotected exposures resulting in human infection
 - Direct contact with sick/dead poultry
 - Visiting a live poultry market

Influenza

- Preparing poultry for consumption that were sick/died
- Exposure to other infected animals (swans, dairy cows)
- Limited, non-sustained transmission from prolonged exposure to a symptomatic H5N1 patient



T Uyeki NEJM 2024



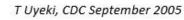


37-yo woman, illness day #7 Admission CXR Illness day #10; died day #11



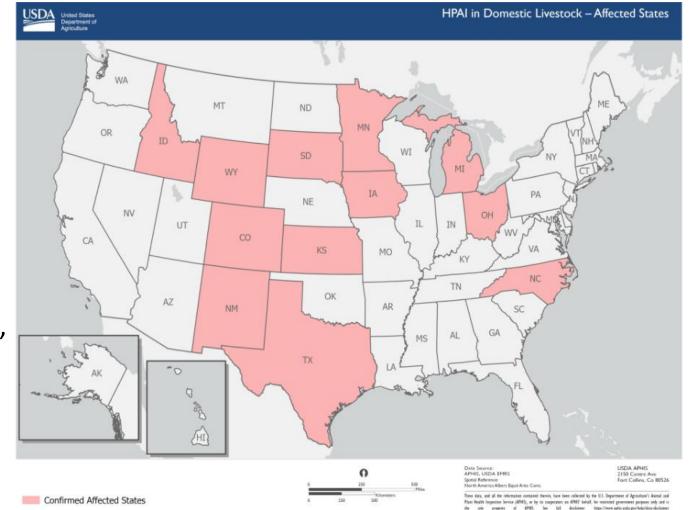
21-yo male, illness day #5 Admission CXR

Illness day #12; survived (not ventilated)



H5N1 in Dairy Herds

- USDA confirmed H5N1 virus infections of dairy herds in 95 farms across 12 states
 - Clade 2.3.4.4b virus
 - High levels of virus in raw milk
- Other animal species reported:
 - Wild birds, cats, racoon, opossums, alpacas, baby goats in the U.S.
- Wide range of infected wild birds, terrestrial and marine mammal species worldwide





H5N1 Human Cases in 2024, U.S.

- Three human cases with cattle exposure detected:
 - April 1 Texas, farmworker, conjunctivitis
 - May 22 Michigan, farmworker, conjunctivitis
 - May 30 Michigan, farmworker, upper respiratory symptoms, watery eyes
- Not hospitalized, isolation recommended
- Antivirals recommended
- No human-to-human transmission
- Virus isolated from 2 cases





H5N1 Human Cases – Virus Sequences to Date

Diagnostics

- No impact to current CDC influenza diagnostic assay's ability to detect A(H5N1) viruses
- Public health laboratories have the CDC real-time RT-PCR A(H5) assay

Antivirals

- No known markers of resistance to FDA approved antiviral drugs (PA inhibitor: baloxavir; NA inhibitors: oseltamivir, peramivir, and zanamivir)
- Oseltamivir recommended for treatment and post-exposure prophylaxis

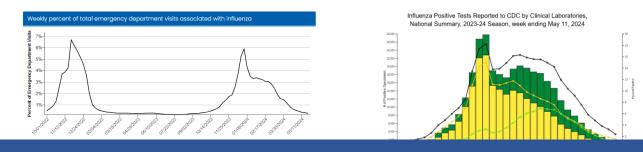
Candidate Vaccine Viruses (CVVs)

- H5N1 viruses (hemagglutinin gene) identified from the 3 human cases are very closely related to two available CVVs
- CVVs expected to provide good protection against clade 2.3.4.4b viruses



Surveillance, Human Monitoring, and Testing

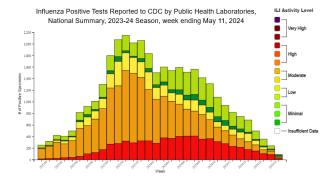
- Since March 24, >500 people monitored from affected farms, >45 tested
- CDC monitoring multiple surveillance systems for unusual activity



No indicators of unusual influenza activity in people, including avian influenza A(H5N1)



Influenza





3) 📕 A (H1H1)pdm09 📕 A (Subtyping not Performed) 📕 B (Lineage Unspecified) ctoria Lineage) https://www.cdc.gov/flu/avianflu/h5-monitoring.html

Summer Influenza Surveillance Priorities

- Continued monitoring of workers with recent exposure on confirmed farms
- Facilitate detection of A(H5N1) in the community through enhanced, national surveillance at seasonal influenza levels
 - Subtyping of influenza A positive specimens, expanded specimen sources
 - Continued surveillance of lab-confirmed influenza associated hospitalizations through FluSurv-NET
- Continued follow-up for areas that flag in syndromic and wastewater data
- Provider outreach to continue influenza testing through summer, particularly for patients with recent history of relevant exposures



Opening Poll Question

In terms of level of concern with respect to the current outbreak of H5N1, I have:

- Low concern continue to follow, no major changes recommended to preparedness activities.
- Moderate concern following closely; planning some changes to preparedness activities.
- **High concern** following very closely; planning and implementing major changes to preparedness activities.

Questions







Closing Poll Question

In terms of level of concern with respect to the current outbreak of H5N1, I have:

- Low concern continue to follow, no major changes recommended to preparedness activities.
- Moderate concern following closely; planning some changes to preparedness activities.
- **High concern** following very closely; planning and implementing major changes to preparedness activities.

Thank you!







MGHBRT@partners.org <u>www.massgeneral.org/disaster-medicine</u> @MGHDisasterMed

Center for Disaster Medicine – Region 1 Disaster Health Response System and Regional Emerging Special Pathogens Treatment Center