



## 2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report September 24, 2024

### Introduction

In March 2024, several cases of highly pathogenic avian influenza A (HPAI) H5N1 virus were confirmed in dairy cattle in Texas, with cases spreading to at least eight other states (<https://www.biorxiv.org/content/10.1101/2024.05.01.591751v1>). In addition, a human case of influenza from the same clade and genotype was also diagnosed in a dairy worker from Texas around the same time. As part of an effort to track this outbreak, the United States Department of Agriculture (USDA) Agricultural Research Service (ARS) and the USDA National Veterinary Services Laboratories (NVSL) have been working to collect and sequence samples from additional cattle as well as avian species and other animals that also appeared to be infected with HPAI that might be related to the virus from the Texas dairy cattle. The genomic sequences of each virus isolate (consisting of the eight genomic segments sequenced for each individual isolate) are assembled from the sequenced short read data, and after undergoing quality control, are submitted to the GenBank sequence repository where they become publicly available. To enhance the ability of the USDA to rapidly submit sequences to GenBank, personnel from the Bacterial and Viral Bioinformatics Resource Center (BV-BRC) have been collaborating with USDA scientists to assist them with the submission of assembled HPAI genomic sequences to GenBank. The Centers for Disease Control and Prevention (CDC) in a similar manner, track human cases of H5N1 influenza.

The BV-BRC provides a database of complete and partially sequenced microbial genomes from both viral and bacterial pathogens. This data is derived from the GenBank repository and includes metadata obtained from the GenBank record as well as associated NCBI BioProject, BioSample, and SRA repository records. All this metadata provides users with the ability to search for specific datasets from the BV-BRC web site using the filtering and sorting features built into BV-BRC web-retrieval tools. To provide rapid access to sequences and other data and information from the 2024 HPAI outbreak, the BV-BRC provides an outbreak-specific web page with links to this information: ([https://www.bv-brc.org/outbreaks/H5N1/#view\\_tab=overview](https://www.bv-brc.org/outbreaks/H5N1/#view_tab=overview)).

### Human Cases

Human cases of H5N1 Influenza A virus infection from North America. (One new case 8/22/24.)

Case Report Dates	Location (#cases)	Likely Infection Source	Total Number	Number Confirmed by Sequencing
04/01/2024 – 07/03/2024	Texas (1) Michigan (2) Colorado (1)	Dairy cows	4	1 (Texas 2024) 2 (Michigan 2024) 1 (Colorado 2024)
04/28/2022 – 07/25/2024	Colorado (10)	Poultry	10	1 (2022); 4 (2024)
8/22/2024	Missouri (1)	Unknown	1	1 (partial; 4 segments)

A current summary of human avian influenza virus infections can be found at <https://www.cdc.gov/bird-flu/situation-summary/index.html>.

### Sequence Statistics (As of September 24, 2024)

The numbers below provide statistics on the publicly available H5N1 genomic sequences collected from North American isolates in 2024. These sequences are available from the BV-BRC database using the links in the table below. We report the number of isolates along with the number of sequenced genomic segments (usually 8 per isolate). These numbers include sequences generated by the USDA and submitted to GenBank by both the USDA and BV-BRC; USDA sequences assembled by the BV-BRC from SRA data not yet submitted to GenBank; and sequences submitted to GenBank from all other sources. No new Human sequences have been reported or submitted to SRA or GenBank.

#### Influenza A sequence counts from the BV-BRC database

Outbreak Report Date	All Influenza A virus Sequences	All H5N1 Sequences	2024 H5N1 Sequences
May 22, 2024	1,061,787	53,030	2,379 (296 isolates)
May 29, 2024	1,065,763	54,632	2,563 (318 isolates)
June 12, 2024	1,082,498	57,301	5,132 (641 isolates)
June 19, 2024	1,087,487	58,045	5,728 (714 isolates)
June 26, 2024	1,091,952	59,465	7,112 (889 isolates)
July 3, 2024	1,092,769	60,280	7,927 (991 isolates)
July 10, 2024	1,096,341	61,469	8,863 (1,108 isolates)
July 17, 2024	1,098,276	63,324	10,534 (1,317 isolates)
July 26, 2024	1,099,887	63,650	10,812 (1,350 isolates)
July 31, 2024	1,106,264	67,556	14,619 (1,875 isolates)
August 8, 2024	1,106,782	68,079	15,140 (1,941 isolates)
August 16, 2024	1,111,297	66,272	12,883 (1,658 isolates)
August 22, 2024	1,116,181	66,560	13,274 (1,694 isolates)
August 28, 2024	1,114,197	67,438	14,058 (1,792 isolates)
September 3, 2024	<a href="#">1,114,657</a>	<a href="#">67,590</a>	<a href="#">14,210</a> (1,811 isolates)
September 24, 2024	<a href="#">1,138,843</a>	<a href="#">68,767</a>	<a href="#">14,877</a> (1,895 isolates)

<sup>1</sup>The BV-BRC genomic database links provided for these totals are dynamic and provide current numbers at the time the link is followed. Therefore, these numbers will increase over time.

#### Influenza A sequences from SRA and not yet submitted to GenBank

The BV-BRC checks the sequence read archive (SRA) database each week for submitted raw sequence read data that has not yet been assembled and submitted to GenBank. Since our last report (9/4/24) the USDA submitted 23 isolates (184 genome sequenced segments) to SRA. These SRA records have been assembled, annotated and loaded in BV-BRC. Since 9/4 the USDA also submitted 480 segment sequences from 60 isolates to GenBank. Most, if not all of these, duplicate sequences previously assembled by the BV-BRC from USDA-submitted SRA records. These duplicates are still in the BV-BRC database. The BV-BRC is in the process of identifying the duplicate records and removing them from the database.

The following tables summarize North American H5N1 2024 isolates collected in 2024 as of September 24, 2024, and include both GenBank and SRA-derived isolates.

**H5N1 US virus isolates collected and sequenced in 2024 by host**

<b>Host</b>	<b># Isolates</b>
Alpaca	5
American Wigeon	1
American Robin	2
Bald Eagle	13
Black Scoter	1
Blackbird	4
Brandt goose	1
Canada goose	50
Cat	52
Cat, domestic	23
Cattle	1238
Chicken	170
Common Eider	1
Common grackle	10
Common Loon	6
Crow	17
Duck	2
Eurasian collared dove	1
Goat	30
Great-Horned Owl	4
Gull	10
Harris hawk	2
Hawk	9
Herring Gull	9
Hooded Merganser	1
Human	9
Lesser Scaup	1

Mallard	2
Mountain lion	4
Mouse	2
Mute Swan	2
Pelican	1
Peregrine Falcon	2
Pigeon	1
Raccoon	8
Raven	3
Redhead duck	1
Red Fox	6
Red-tailed hawk	6
Ruddy Turnstone	1
Sanderling	29
Sandpiper	1
Scoter	3
Skunk	18
Snow Goose	6
Sparrow	3
Turkey	95
Vulture	8
Western gull	2
Western Kingbird	1
White-Winged Scoter	16
Wild bird	1
Wood duck	1
<b>Grand Total</b>	<b>1895</b>

## H5N1 US virus isolates collected and sequenced in 2024 by state

<b>State</b>	<b># Isolates</b>
California	8
Colorado	48
Idaho	160
Illinois	2
Indiana	5
Iowa	36
Kansas	20
Maine	1
Maryland	2
Massachusetts	128
Michigan	102
Minnesota	153
Missouri	8
Montana	4
New Hampshire	3
New Mexico	83
North Carolina	11
Ohio	43
Oklahoma	1
Oregon	3
Rhode Island	5
South Carolina	3
South Dakota	49
Texas	215
Utah	2
Virginia	14
Washington	7
Wyoming	46
USA (no state designated)	733
<b>Grand Total</b>	<b>1895</b>

## Phylogenetic Analysis

Phylogenetic trees for all eight segments can be accessed using the URL below, which includes all human isolates with available sequence data [https://www.bv-brc.org/outbreaks/H5N1/#view\\_tab=phylogenetics](https://www.bv-brc.org/outbreaks/H5N1/#view_tab=phylogenetics). The new, updated trees should be available in a few days and will contain all new sequences uploaded to the BV-BRC database by September 24, 2024. There are two tabs on the outbreak page that provide phylogenetic trees. The trees on the 'Phylogenetics' tab contain all 2024 H5N1 sequences from North America along with representative pre-2024 isolates. A new tab on the H5N1 Outbreak page, 'Clustered Phylogenetics' ([https://www.bv-brc.org/outbreaks/H5N1/#view\\_tab=clusteredPhylogenetics](https://www.bv-brc.org/outbreaks/H5N1/#view_tab=clusteredPhylogenetics)) starts with the same set of sequences, but first clusters sequences together that are at least 99% identical across all genomic segments and then uses one representative sequence for tree building.

## News

Title	Date	Source
<a href="#">Symptomatic contacts reported in probe into Missouri H5N1 flu case</a>	September 16	CIDRAP
<a href="#">No clear exposure source in Missouri H5 avian flu case   CIDRAP</a>	September 12	CIDRAP
<a href="#">Bird Flu Has Already Appeared in New York's Animal Markets. What's Next?</a>	September 9	The New York Times
<a href="#">Officials await testing clues from Missouri H5 avian flu case as Michigan reports more affected cows   CIDRAP</a>	September 9	CIDRAP
<a href="#">CDC Confirms Human H5 Bird Flu Case in Missouri</a>	September 6	CDC
<a href="#">Who is at risk for getting H5N1 bird flu?</a>	September 5	CDC

## Publications

Title	Date	Source
<a href="#">Sequencing-Based Detection of Avian Influenza A(H5N1) Virus in Wastewater in Ten Cities   New England Journal of Medicine</a>	September 11	NEJM
<a href="#">Full article: Phylodynamics of high pathogenicity avian influenza virus in Bangladesh identifying domestic ducks as the amplifying host reservoir</a>	September 10	Emerging Microbes and Infections
<a href="#">Estimating public health risks of infectious disease events: A Canadian approach to rapid risk assessment</a>	September 5	Canada Communicable Disease Reports
<a href="#">Acute and persistent responses after H5N1 vaccination in humans</a>	September	Cell Reports
<a href="#">Highly pathogenic avian influenza virus H5N1 clade 2.3.4.4b in wild rats in Egypt during 2023</a>	August	Emerging Microbes and Infections