



## 2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report August 16, 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.

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)

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 August 13, 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.

### 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 <sup>1</sup>	<a href="#">1,111,297</a>	<a href="#">66,272</a>	<a href="#">12,883</a> (1,658 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.

**\*Important note:** The total number of sequences and isolates have decreased in this week's report compared to the number reported last week. Last week's report contained numbers that included duplicate sequences due to the addition of newly submitted GenBank sequences from the USDA that they assembled from their SRA data. The BV-BRC assembled sequences from USDA SRA records that correspond to the newly submitted GenBank records had not been removed from the numbers reported last week. For this week's report, we have removed these duplicated records (3543 genomes, 442 strains were duplicated).

### 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. This past week, the USDA submitted GenBank records for 3,543 of these sequences that were previously only available from SRA but had been assembled and added to the BV-BRC web site by BV-BRC personnel. These records have been reconciled to remove the duplicate data from BV-BRC records.

Sequences from 3 new human isolates (24 sequences) from Colorado mentioned in last week's report have now been loaded into the BV-BRC database.

The following tables summarize North American H5N1 2024 isolates collected in 2024 as of August 13, 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
Bald Eagle	13
Black Scoter	1
Blackbird	4
Brandt goose	1
Canada goose	50
Cat	45
Cat, domestic	23
Cattle	1059
Chicken	135
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	8
Lesser Scaup	1

Mallard	2
Mountain lion	4
Mouse	2
Mute Swan	2
Pelican	1
Peregrine Falcon	2
Pigeon	1
Raccoon	8
Raven	3
Readhead duck	1
Red Fox	6
Red-tailed hawk	6
Ruddy Turnstone	1
Sanderling	29
Sandpiper	1
Scoter	3
Skunk	18
Snow Goose	6
Sparrow	2
Turkey	83
Vulture	8
Western gull	2
Western Kingbird	1
White-Winged Scoter	16
Wild bird	1
Wood duck	1
<b>Grand Total</b>	<b>1658</b>

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

<b>State</b>	<b># Isolates</b>
California	8
Colorado	31
Idaho	156
Illinois	2
Indiana	5
Iowa	32
Kansas	20
Maine	1
Maryland	2
Massachusetts	128
Michigan	73
Minnesota	138
Missouri	7
Montana	4
New Hampshire	3
New Mexico	72
North Carolina	11
Ohio	42
Oklahoma	1
Oregon	3
Rhode Island	5
South Carolina	3
South Dakota	47
Texas	207
Utah	2
Virginia	14
Washington	7
Wyoming	46
USA (no state designated)	588
<b>Grand Total</b>	<b>1658</b>

## Phylogenetic Analysis

The latest 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). These trees were generated on August 14, 2024, and contain the last batch of assembled SRA sequences that were uploaded to the BV-BRC database on August 13, 2024.

## News

Title	Date	Source
<a href="#">Updated joint FAO/WHO/WOAH assessment of recent influenza A(H5N1) virus events in animals and people</a>	August 14	WHO
<a href="#">Federal testing on more retail dairy products finds no live H5N1 virus</a>	August 13	CIDRAP
<a href="#">CDC pandemic review of US H5N1 virus on par with earlier assessments from same clade   CIDRAP</a>	August 12	CIDRAP
<a href="#">CDC's Influenza Risk Assessment Tool (IRAT)   NCIRD   CDC</a>	August 9	CDC
<a href="#">Clinicians detail H5N1 infections in 2 Michigan farm workers</a>	August 8	CIDRAP

## Publications

Title	Date	Source
<a href="#">Descriptive epidemiology and phylogenetic analysis of highly pathogenic avian influenza H5N1 clade 2.3.4.4b in British Columbia (B.C.) and the Yukon, Canada, September 2022 to June 2023</a>	August 15	Emerging Microbes & Infections
<a href="#">The highly pathogenic H5N1 virus found in U.S. dairy cattle has some characteristics that could enhance infection and transmission among mammals</a>	August 14	Labanimal
<a href="#">The panzootic spread of highly pathogenic avian influenza H5N1 sublineage 2.3.4.4b: a critical appraisal of One Health preparedness and prevention - The Lancet Infectious Diseases</a>	August 9	The Lancet Infectious Disease
<a href="#">Influenza A(H5N1) Virus Infection in Two Dairy Farm Workers in Michigan   New England Journal of Medicine</a>	August 7	NEJM