



## **2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report June 26, 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 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)).

This report provides statistics on the public availability of HPAI H5N1 genomic sequences historically, and from isolates collected since 2024.

## Human Cases

Since the second case of human H5N1 influenza associated with the dairy cow outbreak in Michigan was reported on May 30, no additional human cases have been reported by the CDC. Therefore, the total number of human cases reported in 2024 of H5N1 influenza A virus remains at three, two from Michigan and one from Texas. In their reporting of all recent U.S. human cases of H5N1 influenza A virus infection, the CDC also includes a fourth case from Colorado in April, 2022 that was due to poultry exposure (<https://www.cdc.gov/media/releases/2022/s0428-avian-flu.html>).

## Statistics (As of June 26, 2024)

The numbers provided below are obtained from the BV-BRC database. These numbers should be equivalent to those available from GenBank with the exception that new sequences that have been deposited into GenBank may take a few days to be available from the BV-BRC. In addition, sequences present in H5N1 SRA records that have not yet been submitted to GenBank have been assembled and loaded into the BV-BRC database by BV-BRC personnel. (See below.)

For the 2024 outbreak, where we have isolate-specific information, we report the number of isolates along with the number of sequenced genomic segments (generally 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	All Influenza A Sequences	All H5N1 Sequences	2024 H5N1 Sequences
May 22	1,061,803	53,046	2,395 (298 isolates) <sup>2</sup>
May 29	1,065,779	54,648	2,579 (320 isolates) <sup>2</sup>
June 12	1,082,514	57,317	5,148 (643 isolates) <sup>2</sup>
June 19	1,087,503	58,061	5,744 (716 isolates) <sup>2</sup>
June 26 <sup>1</sup>	<a href="#">1,091,952</a>	<a href="#">59,465</a>	<a href="#">7,112</a> (891 isolates) <sup>3</sup>

<sup>1</sup>The BV-BRC genomic database links provided for these totals, provide summary numbers as of the time the link is followed. Therefore, these numbers will increase over time.

<sup>2</sup>These numbers include 16 sequences from 2 isolates from Kazakhstan.

<sup>3</sup>These numbers no longer include the 2 isolates from Kazakhstan.

### 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, an additional 1,384 H5N1 genomic segment sequences from 173 isolates were identified, assembled, and loaded into the BV-BRC database. The states where these isolates have been obtained have not yet been provided.

The tables below summarize North American H5N1 2024 isolates collected in 2024 as of June 26, 2024, and include both GenBank and SRA-derived isolates.

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

Host	# Isolates
Alpaca	3
American White Pelican	1
American Wigeon	1
Bald Eagle	3
Blackbird	2
CAGO	1
Cat	7
Chicken	71
Common Raven	1
Cow	591
Crow	8
Domestic Cat	32
Duck	2
Goat	30
Goose	13
Grackle	4
Great-Horned Owl	2
Gull	1
Harris-Hawk	1
Hawk	9
Hooded Merganser	1
Human	2
Mallard	2
Mountain Lion	4
Mute Swan	2
PEFA	1
Peregrine Falcon	1
Pigeon	2
Raccoon	4
Raven	1
Red Fox	5
Redhead Duck	3
Ruddy Turnstone	1
Sanderling	9
Sandpiper	1
Skunk	18
Snow Goose	6
Turkey	39
Turkey Vulture	1
Vulture	1
Western Gull	1
Wood Duck	1

State	# Isolates
California	8
Colorado	1
Idaho	6
Illinois	2
Indiana	5
Iowa	1
Kansas	15
Maryland	2
Michigan	25
Minnesota	21
Missouri	7
Montana	4
New Mexico	32
North Carolina	12
Ohio	30
Oklahoma	1
Oregon	3
South Carolina	3
South Dakota	21
Texas	139
Utah	2
Virginia	12
Washington	7
USA (no state designated)	531

## 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 June 21, 2024, and do not contain the last batch of assembled SRA sequences that were uploaded to the BV-BRC database on June 22, 2024.

## News

Title	Date	Source
<a href="#">Bird Flu Hits Texas, Kansas Milk in First Sign of Impact</a>	June 20	Bloomberg
<a href="#">Experiments show H5N1 risk to dairy cows not exclusive to subtype infecting US herds</a>	June 20	CIDRAP
<a href="#">Is New York Prepared for a Bird Flu Pandemic?</a>	June 25	NY Times

## Publications

Title	Date	Source
<a href="#">Highly Pathogenic Avian Influenza A(H5N1) Virus in Animals: Interim Recommendations for Prevention, Monitoring, and Public Health Investigations</a>	June 20	CDC
<a href="#">CDC Public Health Science Agenda for Highly Pathogenic Avian Influenza A(H5N1) – June 2024</a>	June 24	CDC
<a href="#">Persistence of Influenza H5N1 and H1N1 Viruses in Unpasteurized Milk on Milking Unit Surfaces</a>	June 24	CDC
<a href="#">Highly pathogenic avian influenza A(H5N1) virus infections on fur farms connected to mass mortalities of black-headed gulls, Finland, July to October 2023</a>	June 20	Eurosurveillance
<a href="#">FDA Research Agenda for 2024 Highly Pathogenic H5N1 Avian Influenza</a>	June 24	FDA
<a href="#">Genetic diversity of H5N1 and H5N2 high pathogenicity avian influenza viruses isolated from poultry in Japan during the winter of 2022-2023</a>	Early Release	Virus Research