



2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report July 10, 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).

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

Human Cases

An additional human case of H5N1 influenza from Colorado was reported by the CDC on July 3, 2024 (<https://www.cdc.gov/media/releases/2024/p-0703-4th-human-case-h5.html>). The individual infected worked on a dairy farm and had an ocular infection from which they recovered after treatment with oseltamivir. Therefore, the total number of human cases reported in 2024 of H5N1 influenza A virus is now four, one from Colorado, 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/bird-flu/situation-summary/index.html?CDC_AA_refVal=https%3A%2F%2Fwww.cdc.gov%2Fbird-flu%2Fphp%2Favian-flu-summary%2Findex.html).

Statistics (As of July 10, 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) ²
May 29	1,065,779	54,648	2,579 (320 isolates) ²
June 12	1,082,514	57,317	5,148 (643 isolates) ²
June 19	1,087,503	58,061	5,744 (716 isolates) ²
June 26	1,091,952	59,465	7,112 (889 isolates) ³
July 3	1,092,769	60,280	7,927 (991 isolates) ³
July 10¹	1,096,341	61,469	8,863 (1,108 isolates) ³

¹The 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.

²These numbers include 16 sequences from 2 isolates from Kazakhstan.

³These 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 936 H5N1 genomic segment sequences from 117 isolates were identified, assembled, and loaded into the BV-BRC database. These isolates were from cows (107), turkeys (8), and cats (2). 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 July 8, 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	9
Chicken	72
Common Raven	1
Cow	792
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	54
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)	750

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. These trees were generated on July 10, 2024, and contain the last batch of assembled SRA sequences that were uploaded to the BV-BRC database on July 8, 2024.

News

Title	Date	Source
Twist Bioscience Launches Synthetic RNA Control for H5N1 Influenza A Business Wire	July 9	Businesswire
Features of H5N1 influenza viruses in dairy cows may facilitate infection, transmission in mammals National Institutes of Health (NIH)	July 8	NIH
H5N1 avian flu infects 2 children in Cambodia CIDRAP	July 8	CIDRAP
Animal experiments shed more light on behavior of H5N1 from dairy cows CIDRAP	July 8	CIDRAP
USDA Offers Expanded Emergency Livestock Assistance to Help Dairy Producers Offset Milk Loss Due to H5N1 - Quality Assurance & Food Safety	July 8	Quality Assurance & Food Safety
CDC A(H5N1) Bird Flu Response Update, July 5, 2024	July 5	CDC
Why Finland and others are vaccinating people against bird flu	July 5	Economist
CDC confirms 4th human case of H5N1 avian flu as more dairy herds in Colorado hit CIDRAP	July 3	CIDRAP

Publications

Title	Date	Source
Strong and consistent effects of waterbird composition on HPAI H5 occurrences across Europe	July 8	ESA
Pathogenicity and transmissibility of bovine H5N1 influenza virus	July 8	Nature
Does pasteurization inactivate bird flu virus in milk?	Preprint	Emerging Microbes & Infections