



2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report July 31, 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).

Human Cases

Human cases of H5N1 Influenza A virus infection reported in 2024 in North America. **Two new human cases have been reported from 07/22/24-07/30/24.**

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 – 07/14/2024	Colorado (9 or 10)	Poultry	9 or 10	1 (2022); 1* (2024)

*The sequence metadata does not indicate if these Colorado cases were from an individual exposed to dairy cattle or poultry.

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

Statistics (As of July 31, 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. 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	1,099,887	63,650	10,812 (1,350 isolates)
July 31, 2024	1,106,264	67,556	14,619 (1,875 isolates)

¹The 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. This past week, an additional 3807 H5N1 genomic sequences from 524 isolates were identified, assembled, and loaded into the BV-BRC database. These isolates were from alpaca (5), blackbird (2), cat (35), cow (361), chickens (56), goose (2), Grackle (7), hawk (2), mouse (2), racoon (3), red fox (6), sparrow (1), turkeys (41) and Wild-Bird (1). No new human sequences were loaded. The 524 isolates were identified from Colorado (24), Idaho (118), Iowa (12), Kansas (4), Michigan (45), Minnesota (42), New Mexico (53), North Carolina (2), Ohio (12), South Dakota (13), Taxes (66), Wyoming (46), New Hampshire (3) and all the others were from the USA with no further information on location. Note that there were additional changes to the BV-BRC sequence records this past week arising from updates to the associated metadata. These increases are reflected in the data provided in this report.

Note, 2592 sequences that were assembled and loaded from SRA were deprecated since the latest genomes were identified and loaded from GenBank.

The tables on the next page summarize North American H5N1 2024 isolates collected in 2024 as of July 31, 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	8
American Crow	13
American Wigeon	1
Arenaria interpres	1
Aythya americana	1
Bald Eagle	13
black scoter	1
Blackbird	4
Bovine	24
brandt goose	1
Branta canadensis	3
Buteo jamaicensis	1
CAGO	1
Calidris alba	10
Canada Goose	44
Cat	35
Cattle	1216
Chenonetta jubata	1
Chicken	135
Common Eider	1
Common grackle	5
common loon	6
Common Raven	3
COMON-GRACKLE	1
Corvus brachyrhynchos	2
Crow	2
Dairy cattle	2
Domestic Cat	32
Duck	2
Feline	10
Ganada Goose	1
Goat	30
Goose	3

Grackle	5
Great Black-Backed Gull	10
Great Horned Owl	4
Harris Hawk	2
Hawk	3
Herring Gull	9
Homo sapiens	5
House mouse	2
House sparrow	1
lesser scaup	1
Lophodytes cucullatus	1
Mallard	2
Mountain Lion	4
Mute Swan	2
PEFA	1
Pelecanus erythrorhynchos	1
Peregrine falcon	1
Pigeon	2
Raccoon	7
Red fox	11
Red Tailed Hawk	3
Red-Tailed Hawk	9
Sanderling	19
Scoter	2
Skunk	18
Snow Goose	6
surf scoter	1
Turkey	102
Turkey Vulture	8
Western Gull	2
Western Sandpiper	1
White-winged Scoter	16
Wild-bird	1
Grand Total	1875

State	# Isolates
California	8
Colorado	27
Idaho	124
Illinois	2
Indiana	5
Iowa	13
Kansas	19
Maryland	2
Massachusetts	137
Michigan	71
Minnesota	87
Missouri	7
Montana	4
New Hampshire	1
New Mexico	64
North Carolina	11
Ohio	42
Oklahoma	1
Oregon	3
South Carolina	3
South Dakota	34
Texas	205
Utah	2
Virginia	6
Washington	7
Wyoming	46
USA (no state designated)	944
Grand Total	1875

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 31, 2024, and contain the last batch of assembled SRA sequences that were uploaded to the BV-BRC database on July 30, 2024.

News

Title	Date	Source
To prevent a new supercharged flu virus, CDC pushes seasonal flu vaccines to farmworkers at risk for co-infection with bird flu CNN	July 30	CNN
New initiative launched to advance mRNA vaccine development against human avian influenza (H5N1)	July 29	WHO
Experts consider H5N1 avian flu unknowns as state fairs loom CIDRAP	July 29	CIDRAP
UK ups risk assessment for H5N1 in US dairy cattle CIDRAP	July 26	CIDRAP
Colorado reports 2 more avian flu infections in poultry cullers CIDRAP	July 25	CIDRAP

Publications

Title	Date	Source
Pinnipeds and avian influenza: a global timeline and review of research on the impact of highly pathogenic avian influenza on pinniped populations with particular reference to the endangered Caspian seal (<i>Pusa caspica</i>)	July 25	Frontiers
Alert and surveillance on H5N1 influenza virus: risks to agriculture and public health	July 24	Sage Journals
Mortality of H5N1 human infections might be due to H5N1 virus pneumonia and could decrease by switching receptor - The Lancet Infectious Diseases	July 24	The Lancet Infectious Disease
Influenza A genomic diversity during human infections underscores the strength of genetic drift and the existence of tight transmission bottlenecks	June 1	Virus Evolution