



2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report June 19, 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.

Updates

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 19, 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 newly submitted sequences may take a few days to be available from the BV-BRC database. 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)
May 29	1,065,779	54,648	2,579 (320 isolates)
June 12	1,082,514	57,317	5,148 (643 isolates)
June 19¹	1,087,503	58,061	5,744 (716 isolates)²

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.

²This includes 16 sequences from 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 560 H5N1 genomic segment sequences from 70 isolates were identified, assembled, and loaded into the BV-BRC database. These SRA records were deposited by the USDA and contain U.S. isolates from cattle, turkeys, cats, and chickens. The states where these isolates have been obtained have not yet been provided.

The tables below summarize North American H5N1 isolates collected in 2024 as of June 19, 2024 and includes both GenBank and SRA-derived isolates.

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

Host	# Isolates
American white pelican	1
American Wigeon	1
Australian wood duck	1
Bald Eagle	3
Blackbird	2
CAGO	1
Chicken	63
Common raven	2
Common grackle	1
Cow	440
Crow	8
Domestic Cat	36
Duck	2
Goat	30
Goose	13
Grackle	3
Great horned owl	2
Harris Hawk	2
Hawk	5
Hooded Merganser	1
Human	2
Mallard	2
Mountain Lion	4
Mute Swan	2
PEFA	1
Peregrine Falcon	1
Pigeon	2
Raccoon	4
Red Fox	5
Red Tailed Hawk	3
Redhead duck	3
Ruddy Turnstone	1
Sanderling	9
Skunk	18
Snow Goose	6
Turkey	31
Turkey vulture	2
Western gull	2
Western Sandpiper	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)	358

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 updated on June 17, 2024, and do not contain the last batch of assembled SRA sequences that were uploaded to the BV-BRC database on June 19, 2024.

News

Title	Date	Source
Studies find little to no immunity to H5N1 avian flu virus in Americans	June 17	CIDRAP
A Bird-Flu Pandemic in People? Here's What It Might Look Like.	June 17	NY Times
NIAID experiments show H5N1 levels plummet after heat treatment, but not to zero in some cases	June 14	CIDRAP
Infectious H5N1 influenza virus in raw milk rapidly declines with heat treatment	June 14	NIH
CDC A(H5N1) Bird Flu Response Update June 14, 2024	June 14	CDC
Study Shows Ferrets Became Sick with A(H5N1) Virus After Eye Exposure	June 14	CDC
Researcher Warns Pet Cats Risk Getting Bird Flu and Possibly Infecting People	June 14	UMD
USDA reports reveal biosecurity risks at H5N1-affected dairy farms	June 13	AP
Influenza Diagnostic Tests	May 21	FDA Guidance

Publications

Title	Date	Source
Does pasteurization inactivate bird flu virus in milk?	June 16	Emerging microbes and infections

<u>Inactivation of Avian Influenza A(H5N1) Virus in Raw Milk at 63°C and 72°C</u>	June 14	NEJM
<u>Efficacy of live and inactivated recombinant Newcastle disease virus vaccines expressing clade 2.3.4.4b H5 hemagglutinin against H5N1 highly pathogenic avian influenza in SPF chickens, Broilers, and domestic ducks</u>	Early Release	Vaccine
<u>Fatal Infection in Ferrets after Ocular Inoculation with Highly Pathogenic Avian Influenza A(H5N1)</u>	Early Release	CDC
<u>Waste Water Scan in Michigan High</u>	June 10	WastewaterSCAN Dashboard
<u>Epidemiological Investigations of HPAI H5N1 Genotype B3.13 in Michigan Dairy Herds and Poultry Flocks: Observations on viral spread between premises and mitigation recommendations</u>	June 9	USDA
<u>Pigs are highly susceptible to but do not transmit mink-derived highly pathogenic avian influenza virus H5N1 clade 2.3.4.4b</u>	May 3 (early release)	Emerging microbes and infections
<u>HA N193D substitution in the HPAI H5N1 virus alters receptor binding affinity and enhances virulence in mammalian hosts</u>	February 3 (early release)	Emerging microbes and infections