



2024 Influenza A Virus HPAI H5N1 Outbreak Report May 23, 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 especially from isolates collected since 2024 in North America.

Statistics (As of May 20, 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. Unless otherwise indicated, the number of sequences reported includes sequences from all the influenza A genomic segments. For the 2024 outbreak, where we have isolate-specific information, we report the number of isolates along with the number of sequenced genomic segments. These numbers include the sequences generated by the USDA as well as sequences submitted from all other sources.

- Influenza A virus, total sequences to-date (all time): 1,061,803.
- Influenza A virus, HPAI H5N1 sequences to-date (all time): 53,046.
- Influenza A virus, HPAI H5N1 sequences collected in 2024: 2,395 genomic sequences from 298 virus isolates.

H5N1 virus isolates collected and sequenced in 2024 by host:

Host	Number of Virus Isolates
American crow	1
Australian wood duck	1
Aythya americana (Redhead duck)	1
Bald eagle	1
Blackbird	2
Bovine	5
Canada goose	8
Cattle	185
Chicken	21
Common raven	1
Crow	2
Domestic cat	12
Duck	1
Feline	2
Goat	15
Grackle	3
Great horned owl	1
Harris-hawk	1
Homo sapiens	1
Lophodytes cucullatus (Hooded Merganser)	1
Mallard	1
Mountain-lion	2
Mute swan	1
Pelecanus erythrorhynchos	1
Peregrine falcon	1
Pigeon	1
Raccoon	1
Red-tailed hawk	2
Skunk	9
Snow goose	3
Turkey	9
Turkey vulture	1
Western gull	1

H5N1 virus isolates collected and sequenced in 2024 by location:

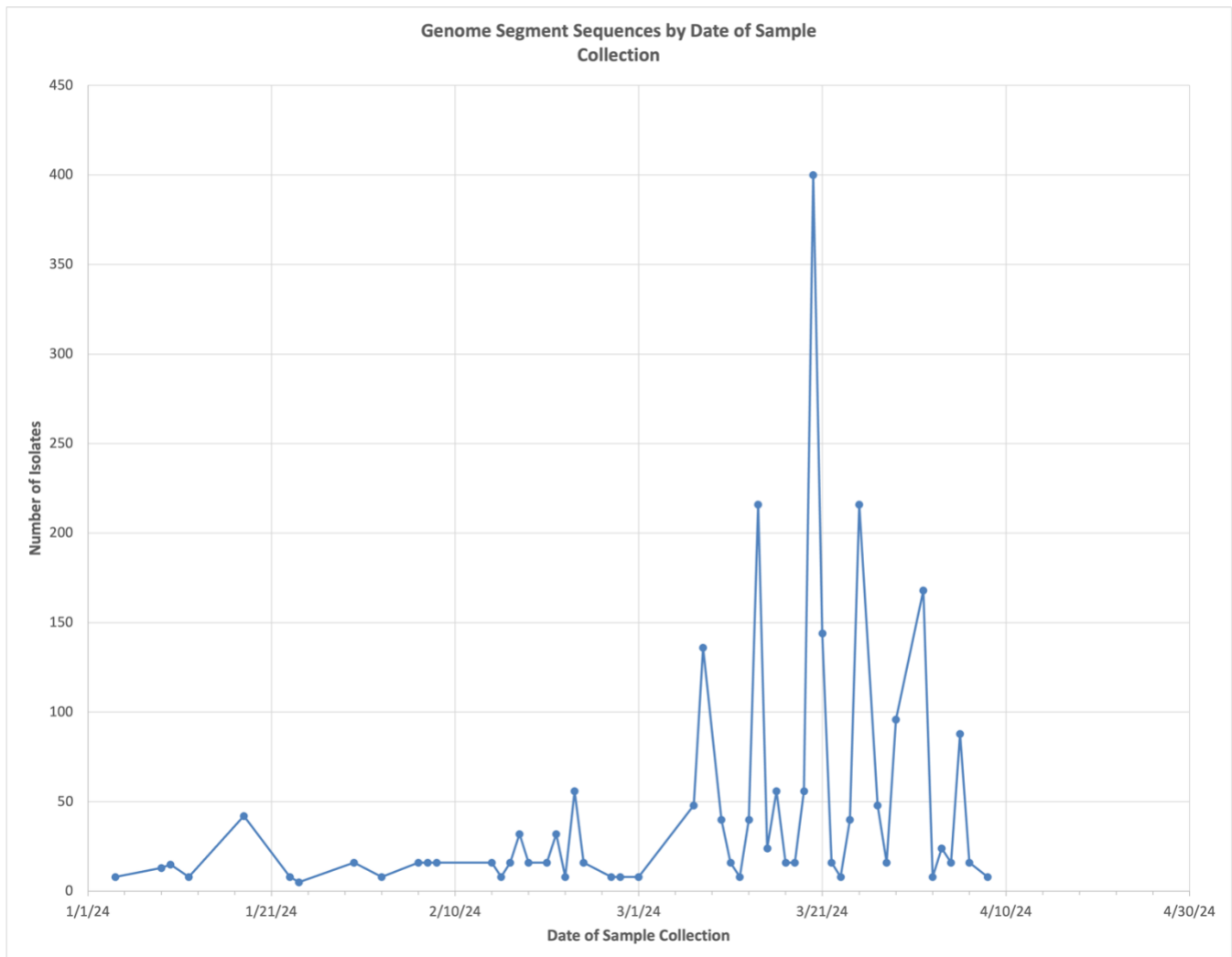
US State	Number of Virus Isolates
California	7
Colorado	1
Idaho	6
Illinois	2
Indiana	5
Iowa	1
Kansas	14
Maryland	2
Michigan	21
Minnesota	21
Missouri	7
Montana	4
New Mexico	24
North Carolina	8
Ohio	14
Oklahoma	1
Oregon	3
South Carolina	3
South Dakota	10
Texas	134
United States	1
Utah	2
Washington	7

H5N1 virus isolates collected and sequenced in 2024 by location/host:

Host by State	# Isolates
California	7
common raven	1
mute swan	1
Peregrine falcon	1
snow_goose	2
turkey vulture	1
western gull	1
Colorado	1
snow goose	1
Idaho	6
cattle	6
Illinois	2
crow	2
Indiana	5
canada goose	2
chicken	3
Iowa	1
american crow	1
Kansas	14
cattle	12
chicken	1
Dairy cattle	1
Maryland	2
chicken	2
Michigan	21
cattle	16
chicken	5
Minnesota	21
chicken	3
duck	1
goat	15
mallard	1
turkey	1
Missouri	7
canada goose	1
turkey	6
Montana	4
domestic cat	1
mountain_lion	2
skunk	1
New Mexico	24
canada goose	1

cattle	17
domestic cat	4
raccoon	1
skunk	1
North Carolina	8
American white pelican	1
canada goose	3
cattle	2
redhead duck	1
wood duck	1
Ohio	14
bovine	3
cattle	9
chicken	2
Oklahoma	1
domestic cat	1
Oregon	3
chicken	1
great horned owl	1
red-tailed hawk	1
South Carolina	3
hooded merganser	1
red-tailed hawk	2
South Dakota	10
cattle	8
turkey	2
Texas	134
blackbird	2
cattle	116
chicken	4
domestic cat	5
feline	2
grackle	3
human	1
pigeon	1
United States	1
domestic cat	1
Utah	2
harris-hawk	1
skunk	1
Washington	7
bald eagle	1
skunk	6

HPAI, H5N1 virus isolates collected and sequenced in 2024 by collection date:



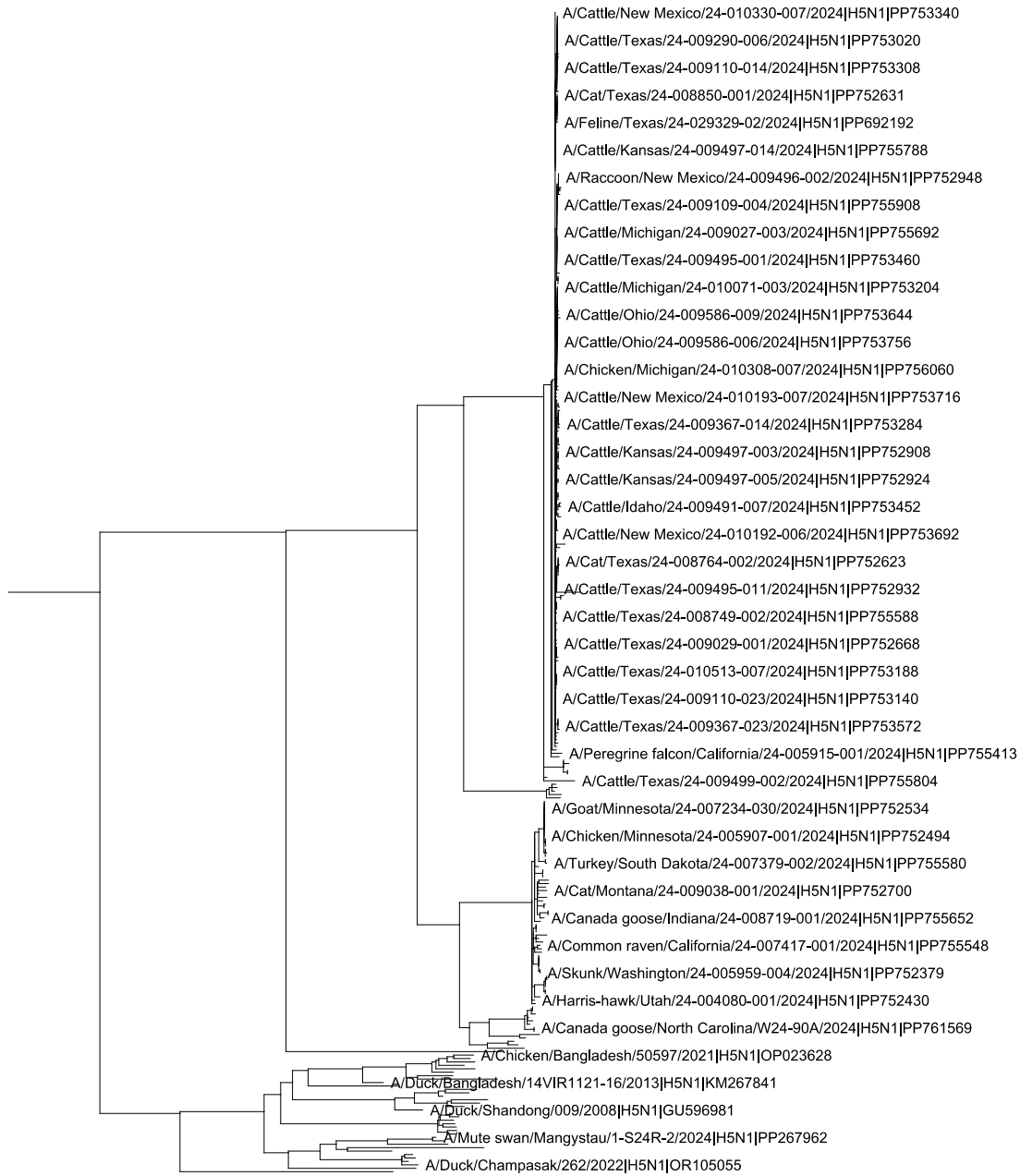
Phylogenetic Analysis

The next 16 figures provide two phylogenetic trees per genome segment. The trees include all 2024 genomic isolates from North America and a selected sample of other isolates from recent years. For isolates collected prior to 2024, representative sequences were selected by using isolates for which all 8 segments were sequenced. These were then clustered using cd-hit with a cutoff of 0.98% to remove closely related sequences. For this release there were ~450 sequences for each segment with ~150 collected prior to 2024 and ~300 from 2024.

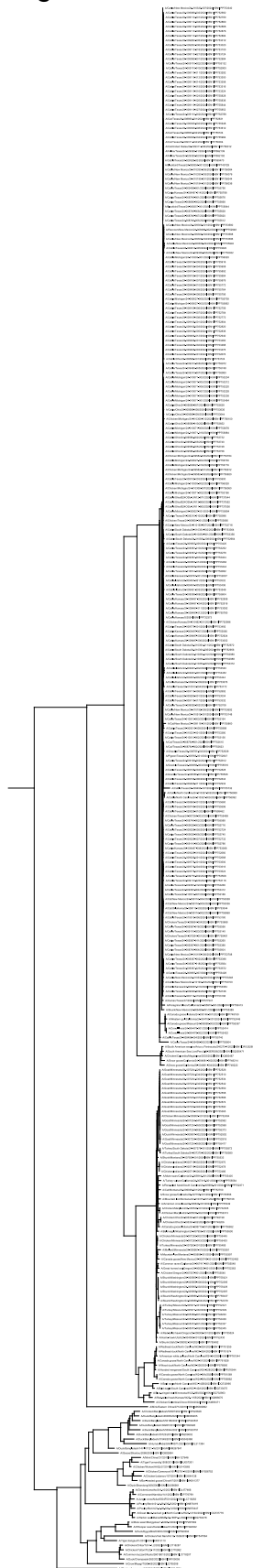
Multiple sequence alignments were performed using MAFFT v7.520 with the options --maxiterate 1000 and --localpair. Trees were then inferred using RAXML-NG v1.2.0 using the GTR model and four gamma distributed rates with 100 non-parametric bootstraps.

Two trees are provided for each segment. The first provides an overview tree that displays a subset of isolates so that the tree is visible on a single page. The second tree provides a visualization of all isolate sequences with detailed isolate descriptors for each node. This tree is very large since every isolate is visible. Both the overview and detailed trees are topologically the same.

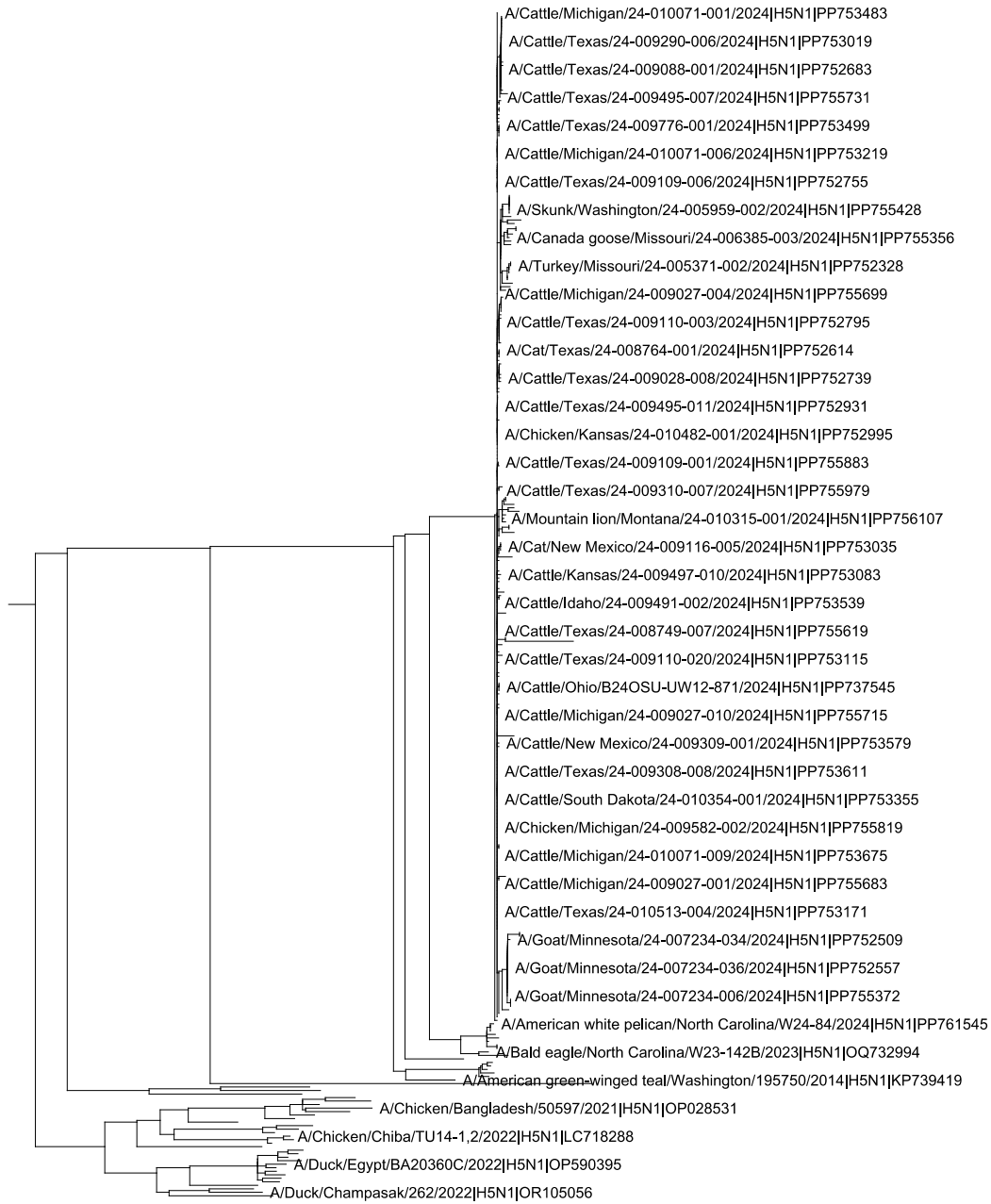
Segment 1, PB2 Overview



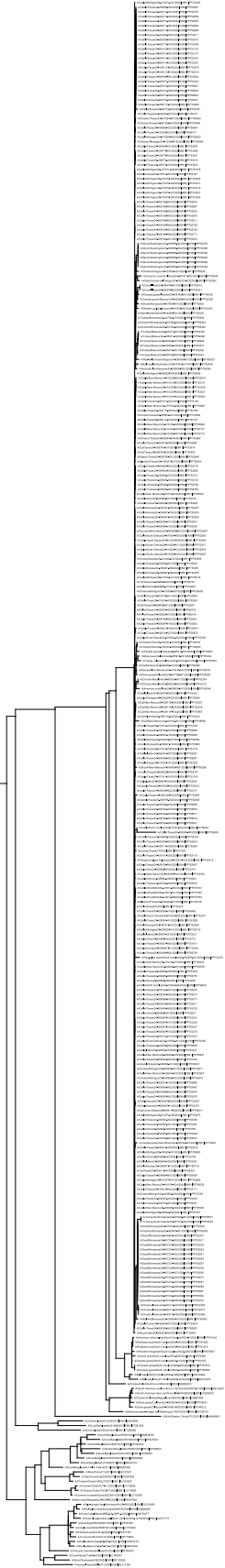
Segment 1, PB2 Detailed



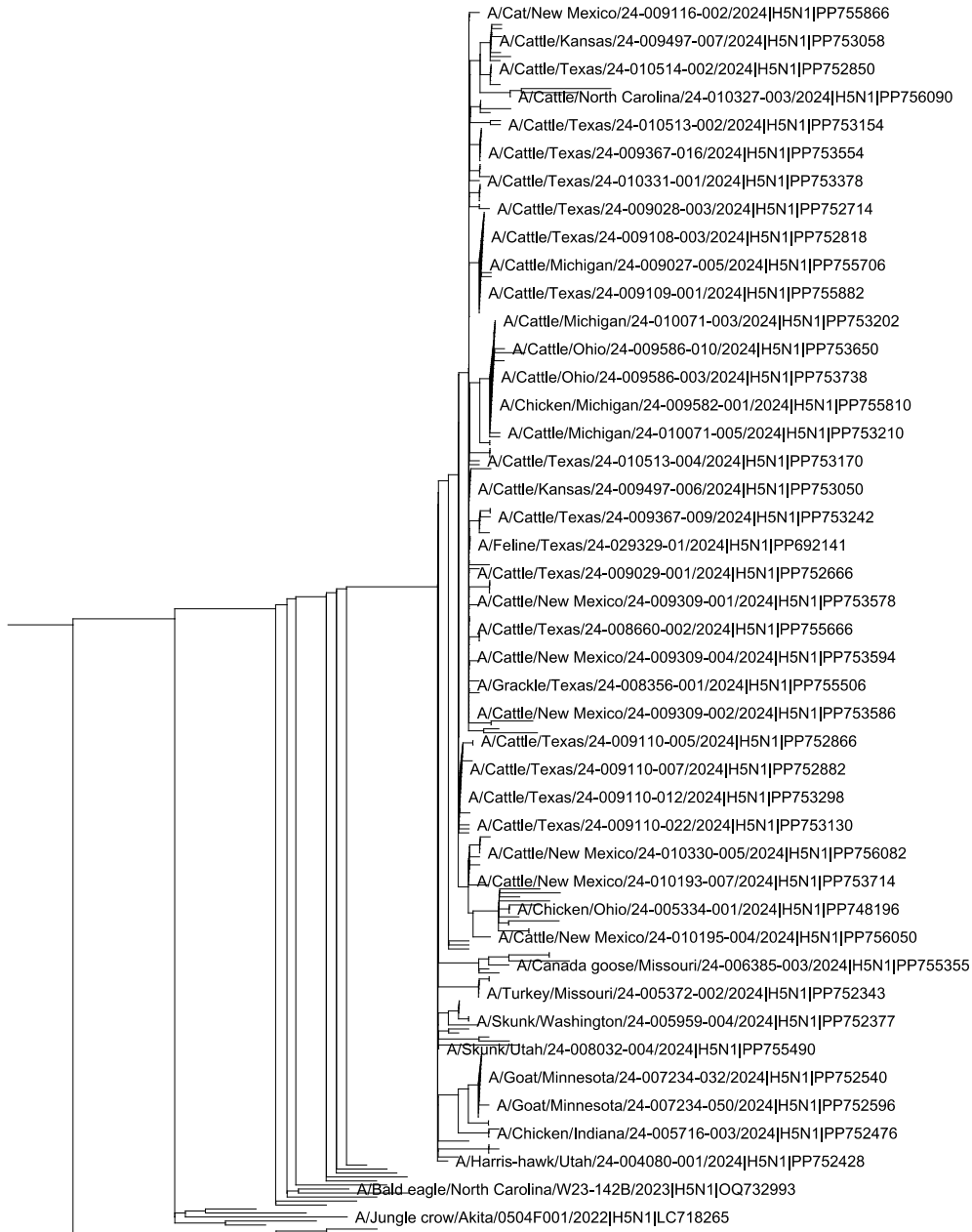
Segment 2, PB1 Overview



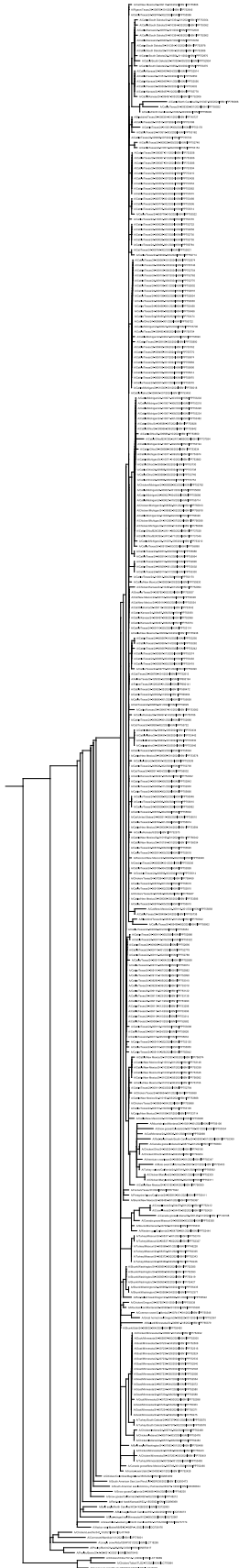
Segment 2, PB1 Detailed



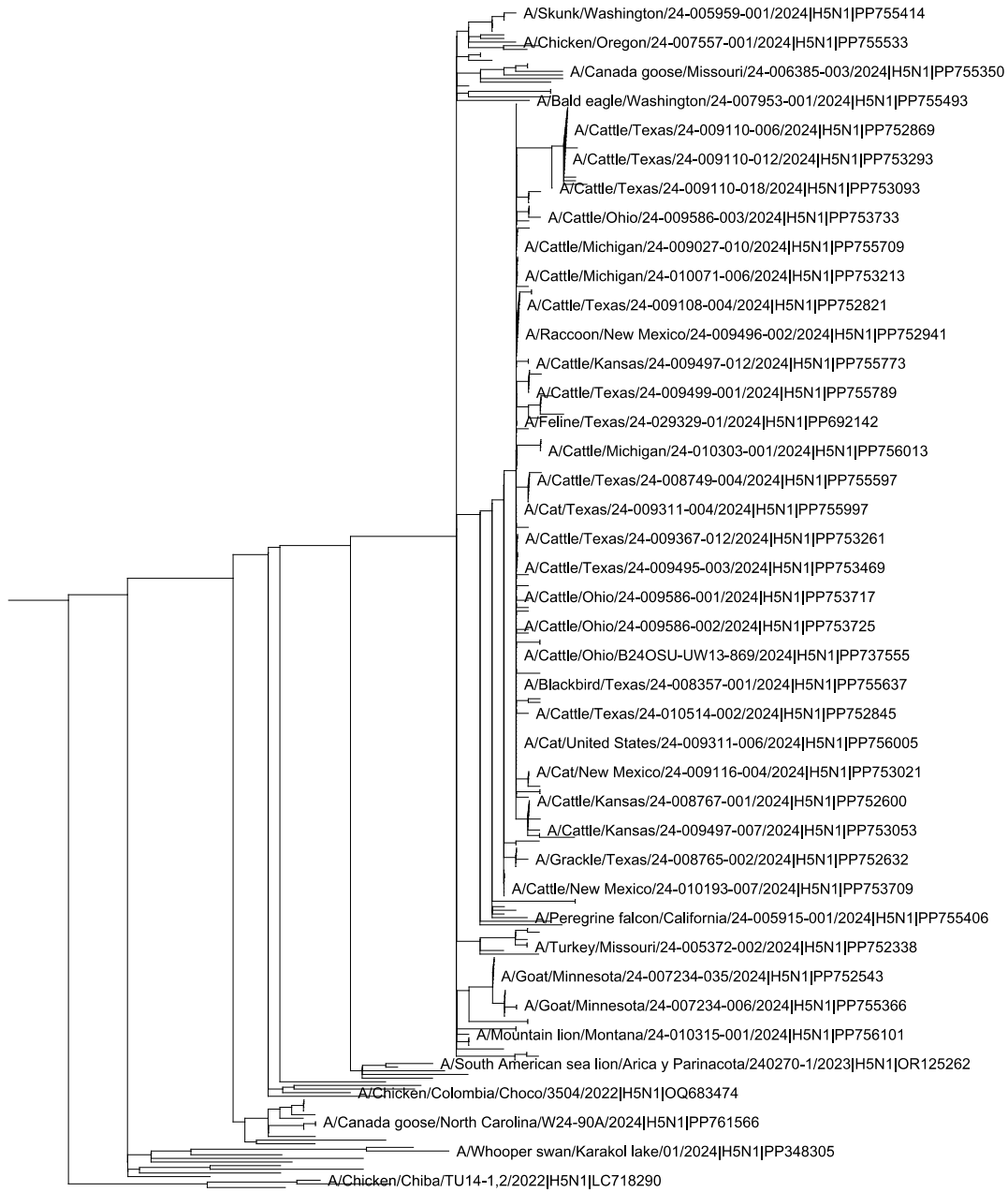
Segment 3, PA Overview



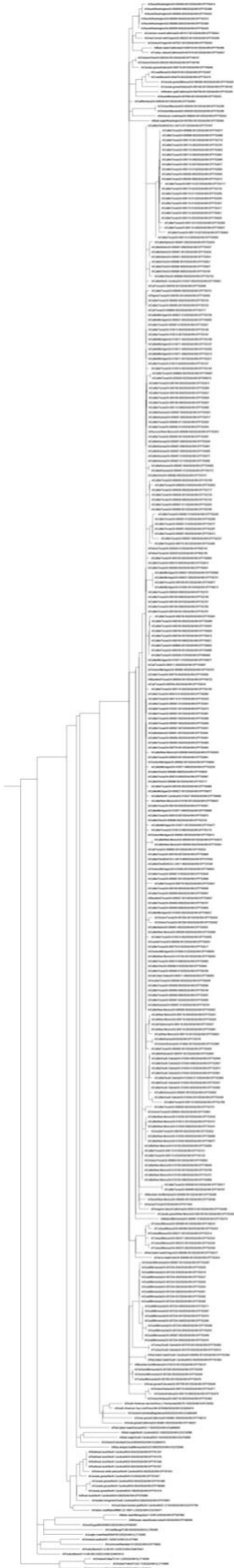
Segment 3, PA Detailed



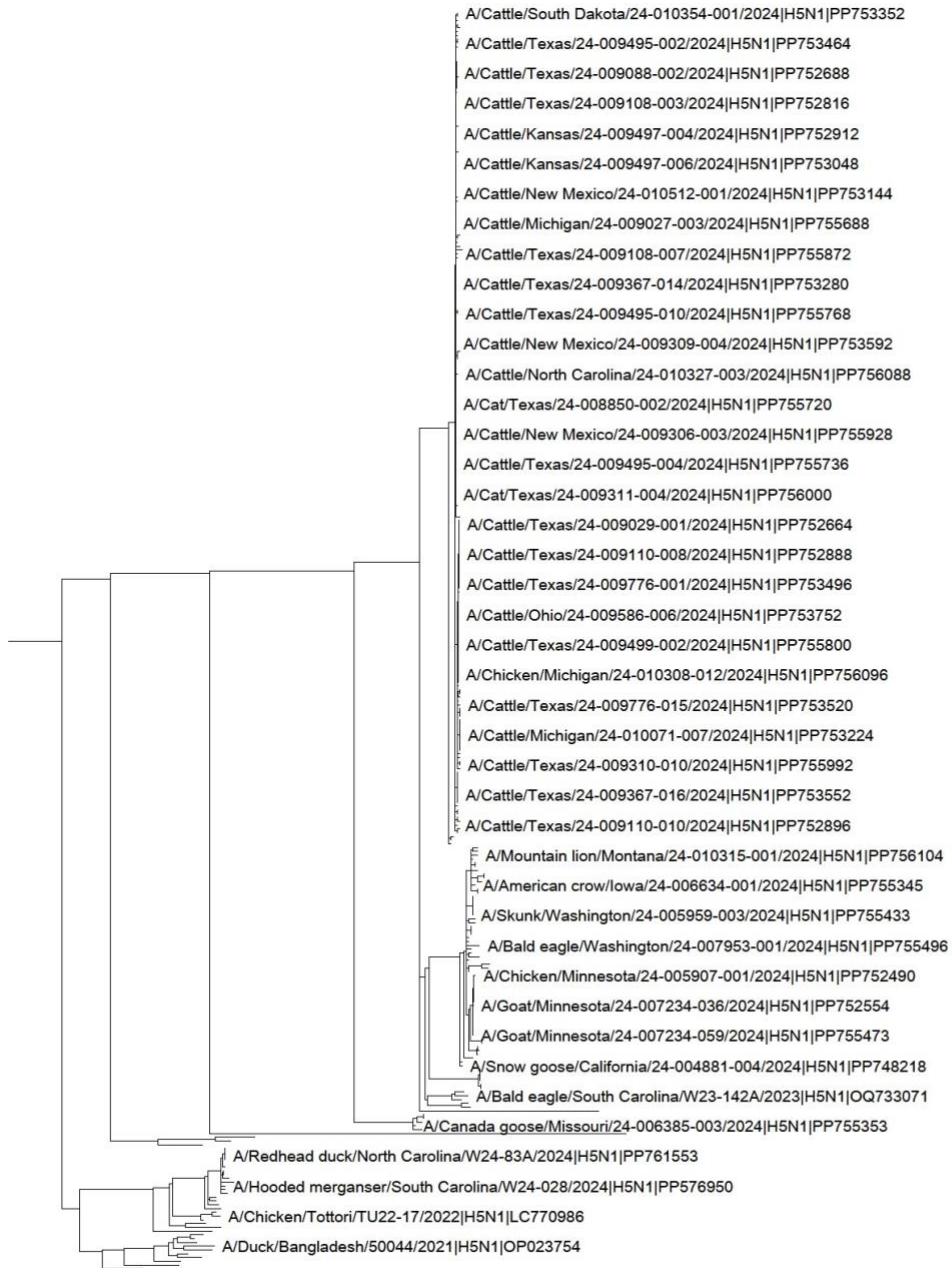
Segment 4, HA Overview



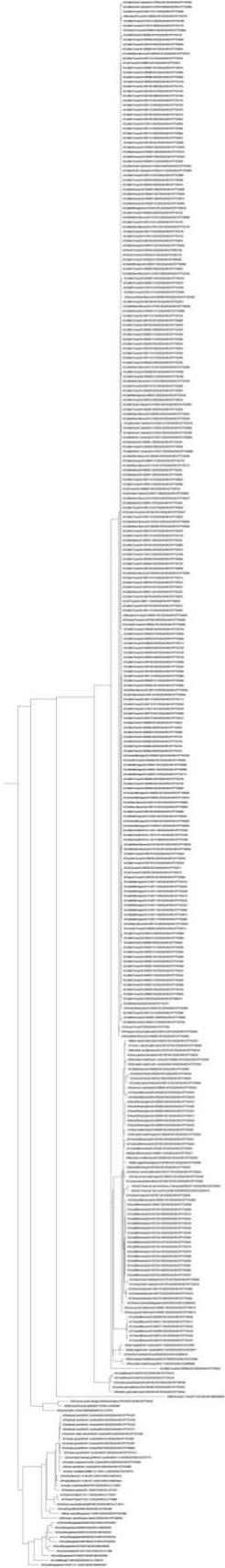
Segment 4, HA Detailed



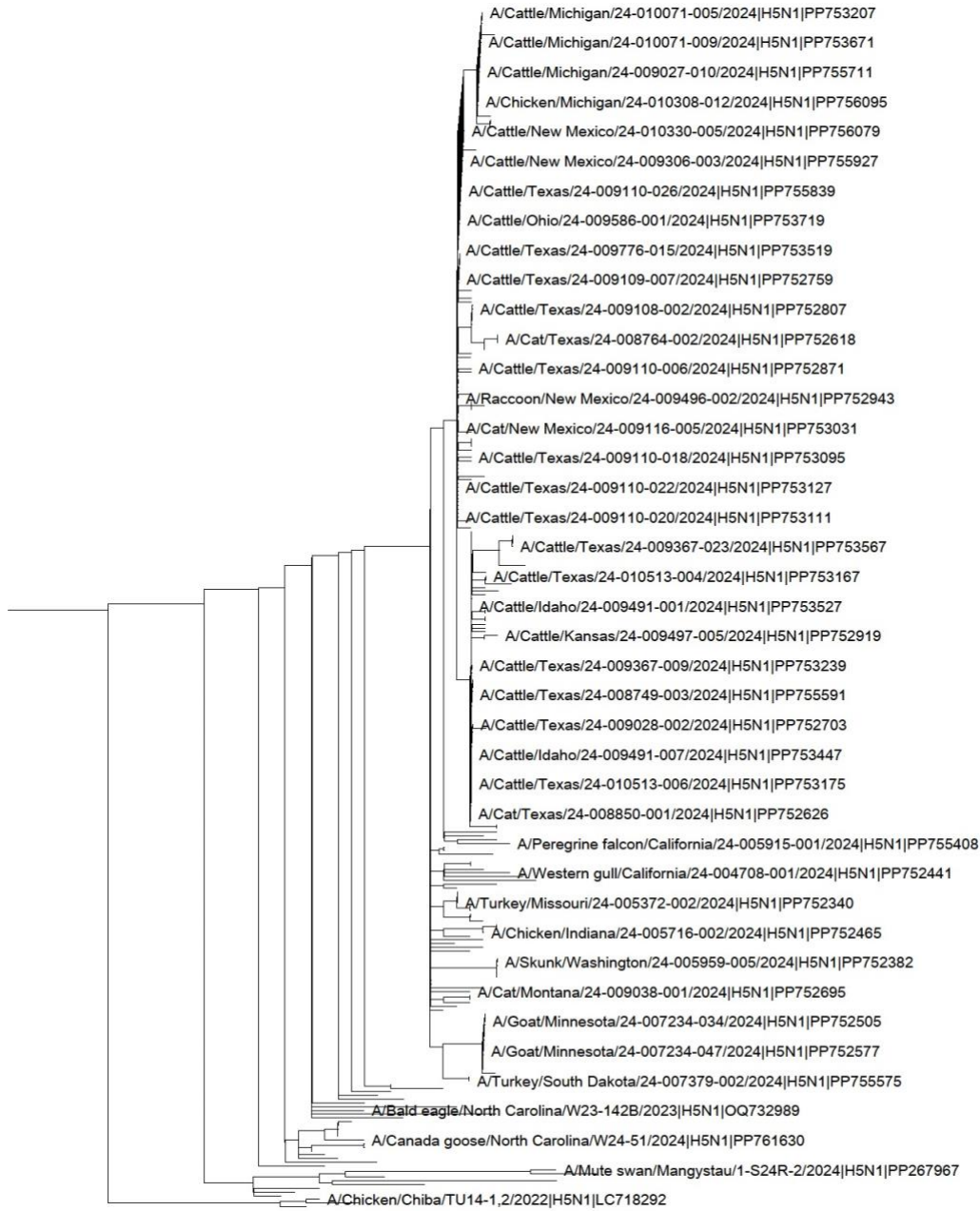
Segment 5, NP Overview



Segment 5, NP Detailed



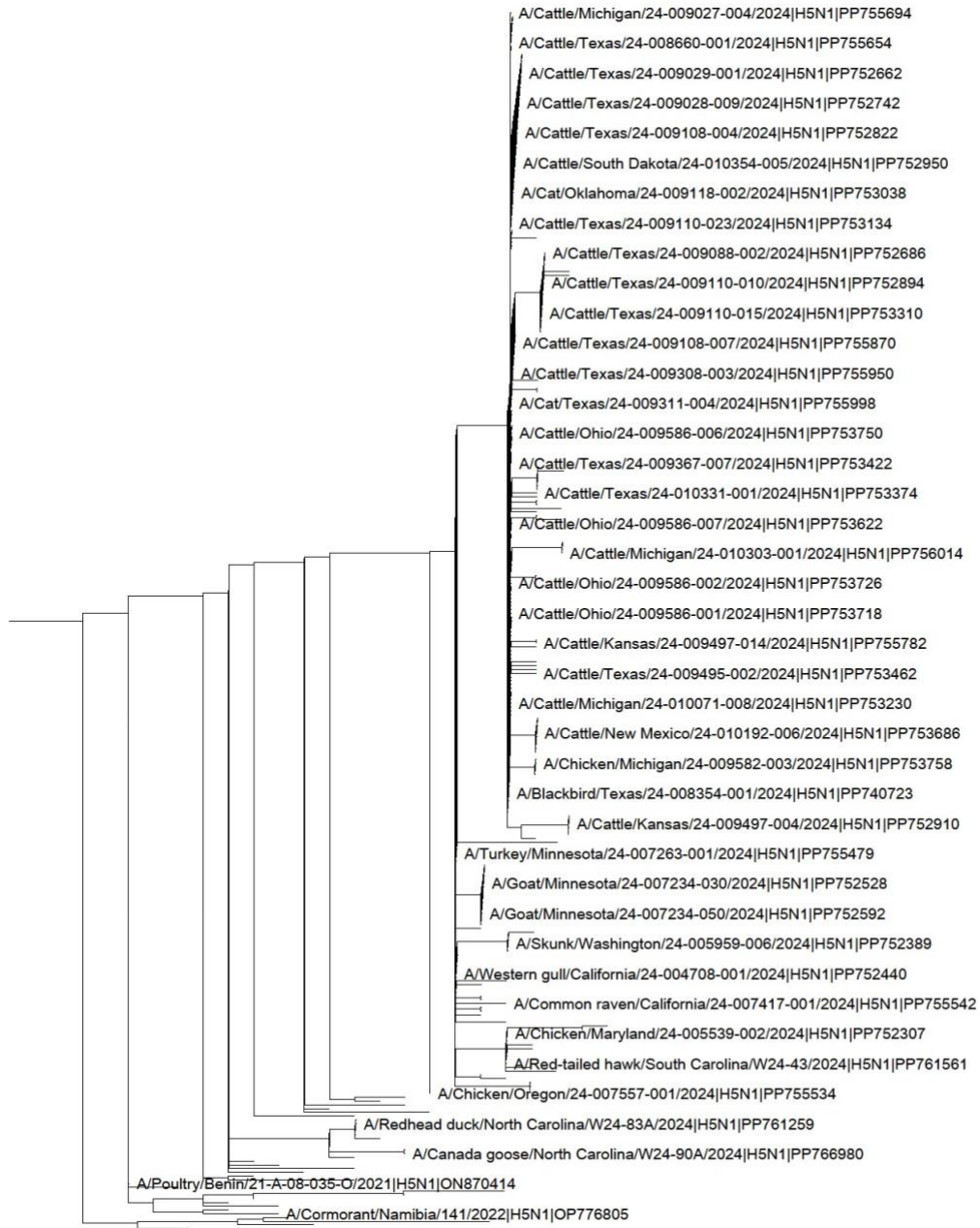
Segment 6, NA Overview



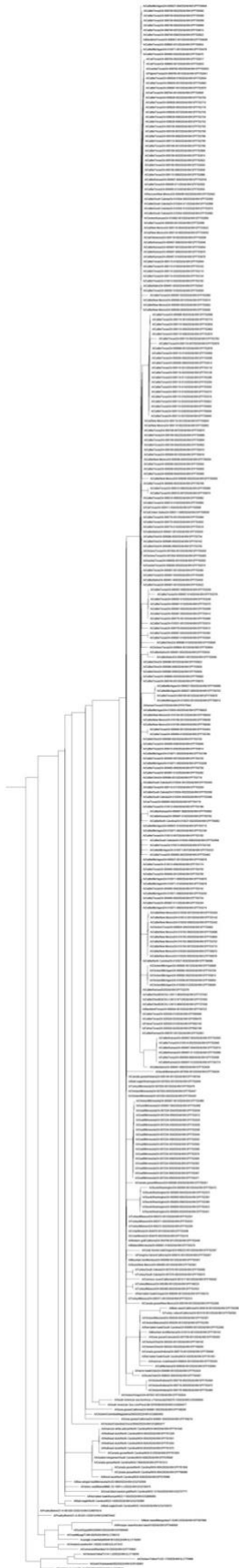
Segment 6, NA Detailed



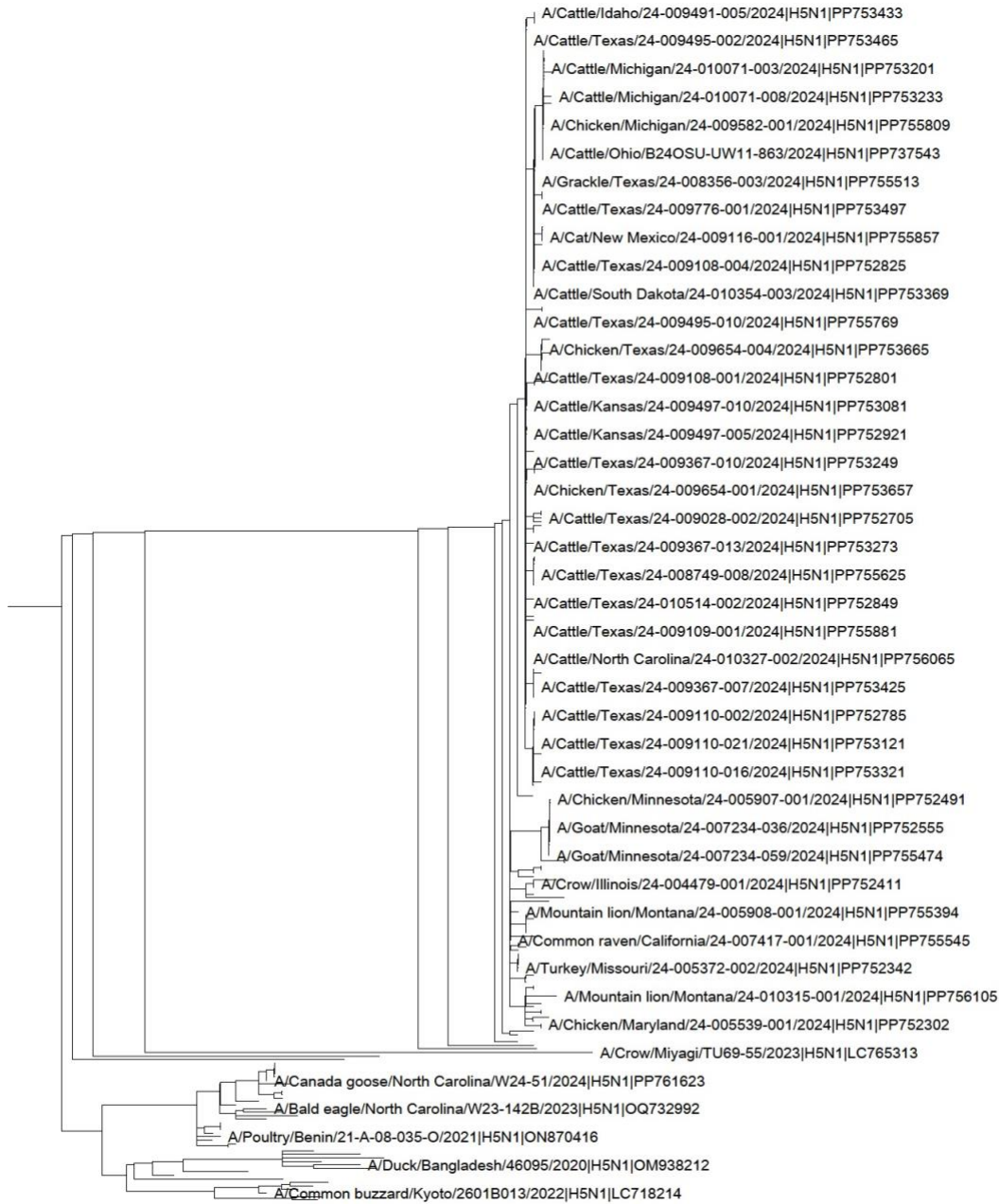
Segment 7, M1, M2 Overview



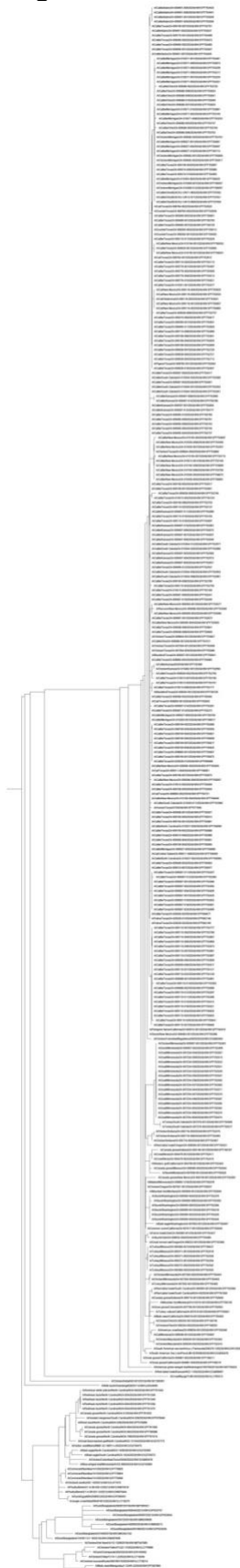
Segment 7, M1, M2 Detailed



Segment 8, NS1, NEP Overview



Segment 8, NS1, NEP Detailed



News

Title	Date	Source
Sick cows in 2 states test positive for avian flu	March 25	CIDRAP
Joint FAO/WHO/WOAH preliminary assessment of recent influenza A(H5N1) viruses	April 23	WHO
Bird flu in US cows: is the milk supply safe?	April 25	Nature
Bird flu virus has been spreading among US cows for months, RNA reveals	April 27	Nature
Attempted Influenza Virus Isolation From A(H5) RT-PCR Positive Supermarket Milk Samples	April 30	CEIRR
FDA finds no live H5N1 avian flu virus in sour cream or cottage cheese, will assess raw milk	May 1	CIDRAP
NPR: The US May be missing human cases of bird flu, scientists say	May 2	NPR
NIAID Monovalent Inactivated Influenza A/H5N8 Clinical Trials	May 3	CEIRR
With H5N1 avian flu silently spreading in US cattle, wastewater testing could be key	May 7	CIDRAP
No sign yet of H5N1 bird flu spreading between humans, says WHO chief	May 8	UN
CDC's Flu Surveillance Systems Can Detect Avian Influenza A(H5N1) Virus Infections	May 8	CDC
Colorado officials probe source of H5N1 in cows as USDA confirms more infected mammals	May 8	CIDRAP
To probe outbreak, BSL-3 labs plan to infect cows with flu virus	May 10	Science
Feds announces assistance for US farmers affected by H5N1 avian flu	May 10	CIDRAP
Updates on Highly Pathogenic Avian Influenza (HPAI)	May 10	FDA
USDA confirms 3 more H5N1 outbreaks in dairy herds	May 15	CIDRAP
H5N1 virus from 2022 mink outbreak capable of inefficient airborne transmission	May 16	Penn State
Labs in U.S., Germany and Canada to infect cows with H5N1 influenza A virus	May 17	Infectious Disease Society of America
The Disease Detectives Trying to Keep the World Safe From Bird Flu	May 20	NY Times
Farm Animals Are Hauled All Over the Country. So Are Their Pathogens	May 20	NY Times

Publications

Title	Date	Source
Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b Virus Infection in Domestic Dairy Cattle and Cats, United States, 2024	May 1	Emerging Infectious Diseases
Emergence and interstate spread of highly pathogenic avian influenza A(H5N1) in dairy cattle	May 1	bioRxiv Pre-print
Highly Pathogenic Avian Influenza A(H5N1) Virus Infection in a Dairy Farm Worker	May 3	New England Journal of Medicine
Structures of H5N1 influenza polymerase with ANP32B reveal mechanisms of genome replication and host adaptation	May 15	Nature Comm
Risk assessment of a highly pathogenic H5N1 influenza virus from mink	May 15	Nature Comm
Outbreak of Highly Pathogenic Avian Influenza A(H5N1) Virus in Seals, St. Lawrence Estuary, Quebec, Canada	May 17	Emerging Infectious Diseases
US Public Health Preparedness and Response to Highly Pathogenic Avian Influenza A(H5N1) Viruses	May 21	JAMA

Links

The following links provide access to the primary data used to assemble this report:

- BV-BRC web site: <https://www.bv-brc.org>
- BV-BRC HPAI H5N1 outbreak web page: https://www.bv-brc.org/outbreaks/H5N1/#view_tab=overview
- All 2024 North American H5N1 sequences: [https://www.bv-brc.org/view/Taxonomy/11320#view_tab=genomes&filter=and\(eq\(subtype,%22H5N1%22\),eq\(collection_year,%222024%22\),eq\(geographic_group,%22North%20America%22\)\)](https://www.bv-brc.org/view/Taxonomy/11320#view_tab=genomes&filter=and(eq(subtype,%22H5N1%22),eq(collection_year,%222024%22),eq(geographic_group,%22North%20America%22)))
- Phylogenetic trees; https://www.bv-brc.org/outbreaks/H5N1/#view_tab=phylogenetics
- NCBI GenBank sequence records: <https://www.ncbi.nlm.nih.gov/nuccore/?term=txid197911%5BOrganism%3Aexp%5D++AND+H5N1>
- NCBI Virus sequence records for all H5N1 isolates: https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/virus?SeqType_s=Nucleotide&VirusLineage_ss=Influenza%20A%20virus,%20taxid:11320&CollectionDate_dr=2024-01-01T00:00:00.00Z%20TO%202024-05-08T23:59:59.00Z&Serotype_s=H5N1