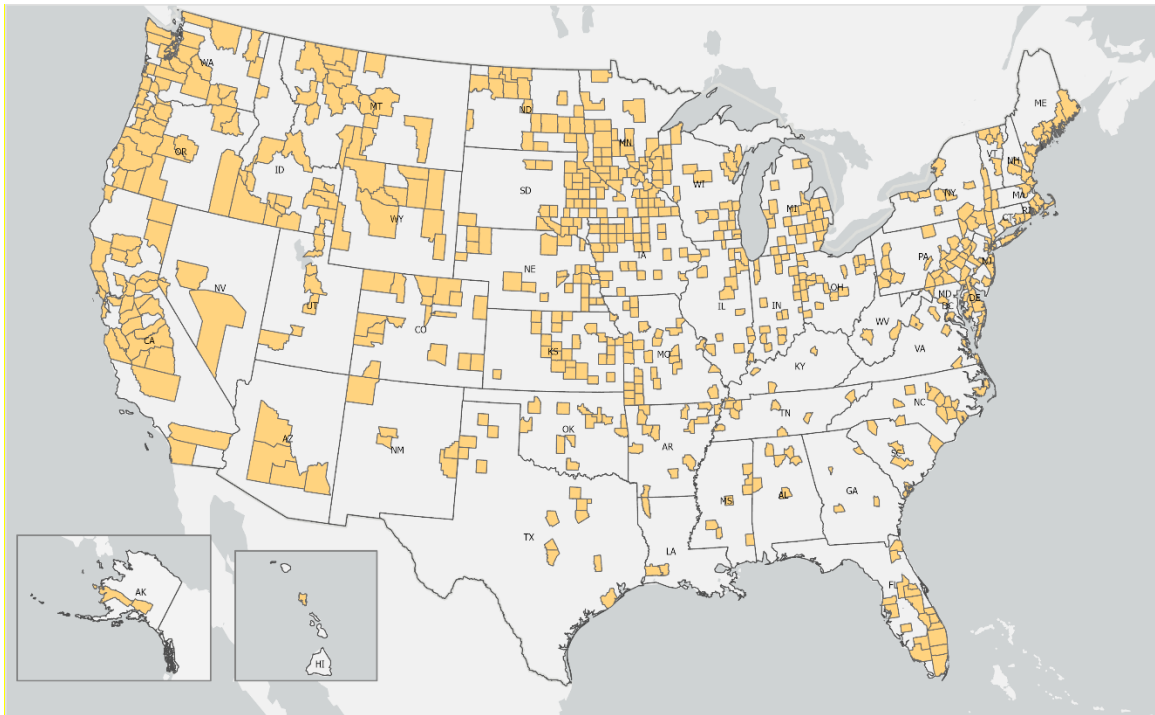




Status and Epidemiologic Analyses of HPAI-affected Poultry Flocks June 30, 2025 Interim Report



Suggested bibliographic citation for this report:

Center for Epidemiology and Animal Health. (2025). *Status and Epidemiologic Analyses of HPAI-affected Poultry Flocks June 30, 2025 Interim Report*. United States Department of Agriculture, Animal and Plant Health Inspection Service.

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ITEMS OF NOTE

A. Entire Event to Date: February 2022 to June 2025

- As of June 30, 2025, the 2022 HPAI event has impacted all 50 States and the territory of Puerto Rico with a total of 1,707 premises infected and over 175 million birds affected.
- There have been at least six distinct introductions of fully Eurasian viruses (“A” genotypes) in North America during the current event, and over 100 reassortant genotypes have been described, to date.
- Between December 30, 2021 and June 30, 2025, wild bird surveillance has resulted in 13,754 detections of H5Nx HPAI in wild birds, with 6,554 detections in apparently healthy birds and 7,200 detections in sick or dead birds.
- Over the entire HPAI event, 70.2 percent (1178 out of 1677) of detections are attributed to independent wild bird introductions and 29.8 percent (499 out of 1677) of detections are attributed to common source or lateral transmission (CSLT).
- The percentage of annual detections attributed to CSLT has increased since the event started in 2022, accounting for 15.5 percent in 2022 (110 out of 708), 20.4 percent (68 out of 333) in 2023, 43.4 percent (136 out of 314) in 2024, and for the first 6 months of 2025, 57.4 percent (185 out of 322).
- The increase in CSLT observed in 2024 is largely attributed to the B3.13 genotype, which was an initial spillover into dairy cattle with subsequent transmission between dairy premises, and multiple transmission events into poultry premises with subsequent poultry-to-poultry transmission.

B. Reporting Period: January 1, 2025 to June 30, 2025

- During the current reporting period, the event has impacted 43 States and affected 331 premises and approximately 45 million birds.
- Monthly cases were the greatest in January 2025, with subsequent monthly decline observed through June 2025.
- Genotype D1.1 has predominated in both wildlife and domestic poultry during the current reporting period.
- The increase in CSLT observed in 2025 is largely attributed to sustained transmission events in commercial premises in Ohio and Indiana; the live bird markets in New Jersey, New York, and Pennsylvania; and commercial premises in Missouri.
- Between January 20, 2025 and June 30, 2025, the USDA biosecurity audit and assessment programs completed 528 audits.
- Common remediations required by the biosecurity audits and assessments are related to mortality management, mitigating wildlife access to clean bedding and vacant production buildings, and visitor documentation.

DESCRIPTION OF HPAI EVENT IN POULTRY

A. Entire Event to Date: February 2022 to June 2025

An event of highly pathogenic avian influenza in poultry in the United States has been ongoing since February 2022. As of June 30, 2025, the National Veterinary Services Laboratories (NVSL; National Centers for Animal Health, Ames, Iowa) have confirmed Eurasian clade 2.3.4.4b H5N1 highly pathogenic avian influenza (HPAI) in 1,707 premises across all 50 States and Puerto Rico. The production types affected include 786 WOAH poultry [commercial], 185 WOAH poultry [backyard], 680 WOAH non-poultry [backyard], and 55 WOAH poultry [live bird market; LBM] premises. The WOAH poultry [commercial] detections include 473 turkey, 142 table egg, 90 broiler, 44 duck, 33 upland gamebird, and 4 commercial breeders–multiple bird species premises. Over 175 million birds have been affected since the start of the event, varying annually from over 58 million birds in 2022 to approximately 22 million birds in 2023. The epidemiological curve in **Figure 1** shows the most prominent peaks occurred during the spring and fall months, which align with wild bird migratory seasons. A figure of overall detections by flyway, State, and production type is available in Appendix A (**Figure A1**).

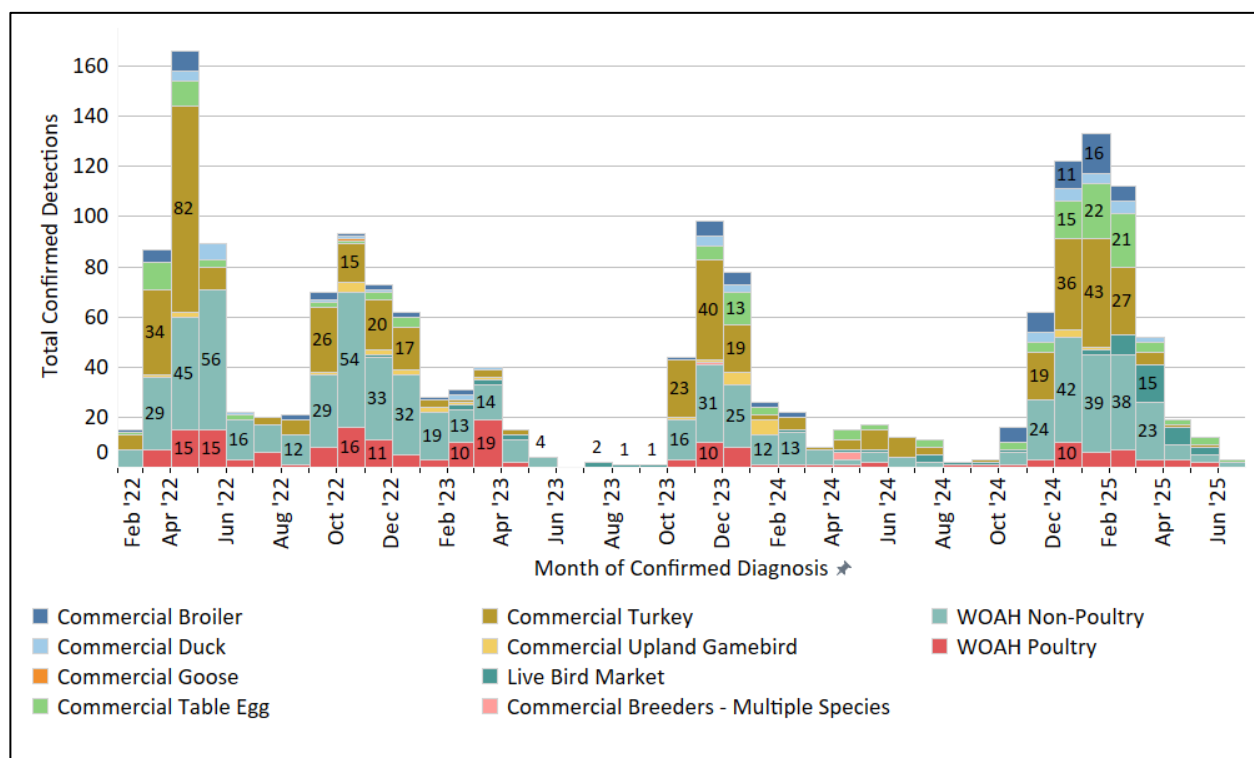


Figure 1. Monthly HPAI confirmed detections by premises and type, as of June 30, 2025.

B. Reporting Period: January 1, 2025 to June 30, 2025

During the current reporting period, a total of 331 detections occurred among 43 out of 50 States and Puerto Rico. NVSL-confirmed premises include 164 WOAH poultry [commercial], 21 WOAH poultry [backyard], 111 WOAH non-poultry [backyard], and 35 WOAH poultry [LBM] premises. The WOAH poultry [commercial] detections include 77 turkey, 53 table egg, 22 broiler, 11 duck, and 1 upland gamebird premises (**Figure 2**). Approximately 45 million birds have been affected in 2025, a greater number when compared to the same month span in past years of the current HPAI event. Reporting period detections by flyway, State, and production type are depicted in **Figure A2**.

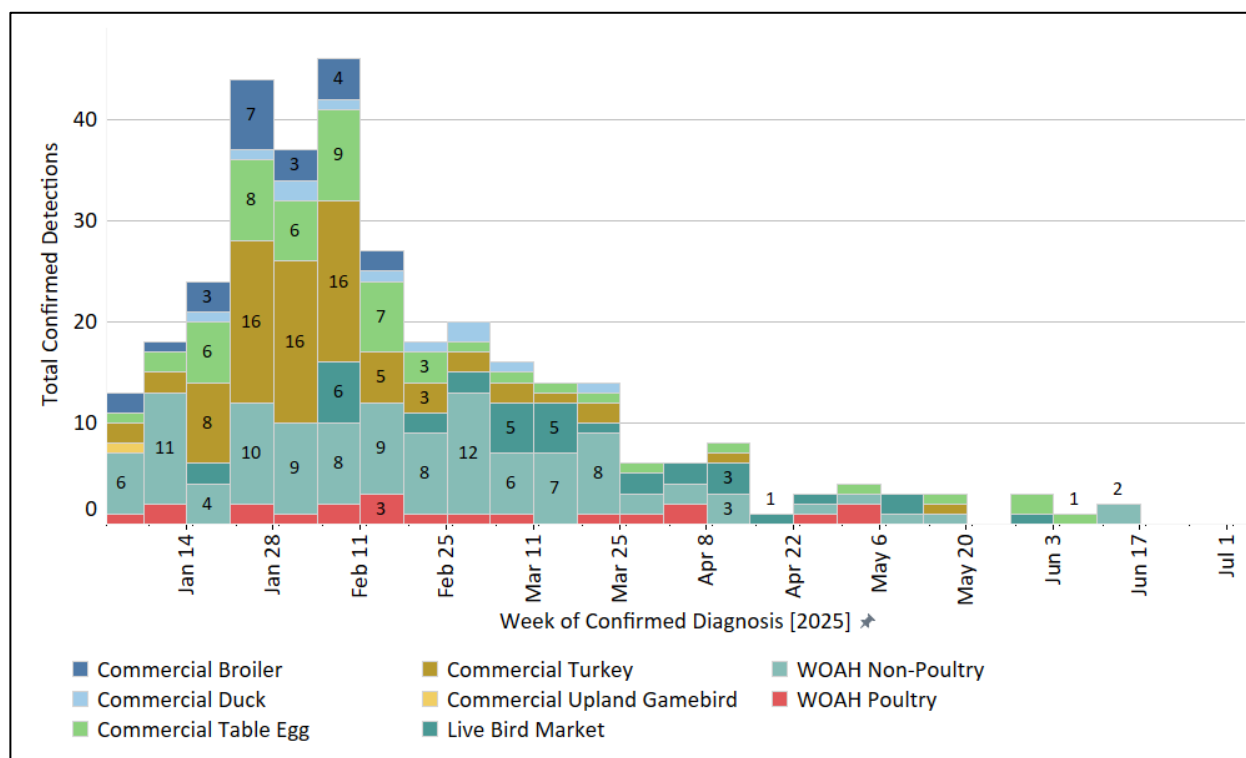


Figure 2. Weekly HPAI detections by premises type, from January 1, 2025 to June 30, 2025.

The current reporting period encompasses 14.6 percent of the entire event (6 out of 41 months). Detections during this period account for 16.3 percent (77 out of 473) of commercial turkey detections, 37.3 percent (53 out of 142) of commercial table egg detections, 63.6 percent (35 out of 55) of LBM detections, 24.4 percent (22 out of 90) of commercial broiler detections, 25.0 percent (11 out of 44) of all commercial duck detections, and 3.0 percent (1 out of 33) of all commercial upland gamebird detections since the beginning of the HPAI 2022 event. These detections represent a relative increase in cases among live bird market and commercial table egg, broiler, and duck premises when compared to the event prior to January 1, 2025. (**Figure 3**).

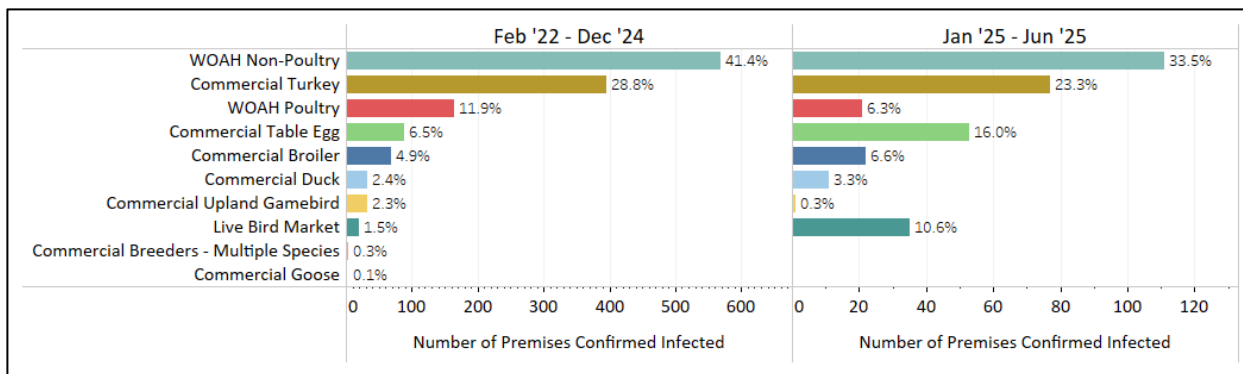


Figure 3. Number and relative percentage of confirmed infections by reportable commercial species type and reporting period.

When comparing temporal monthly trends by the event year, the total number of confirmed infections in January, February, and March 2025 were substantially higher than the totals observed in both 2023 and 2024. Compared to 2022, the first year of the event, an increase in detections was observed earlier in 2025, peaking in January, with subsequent monthly decline. The number of confirmed detections in April, May, June, and July followed similar temporal trends as in the last two years with total cases remaining low (Figure 4).

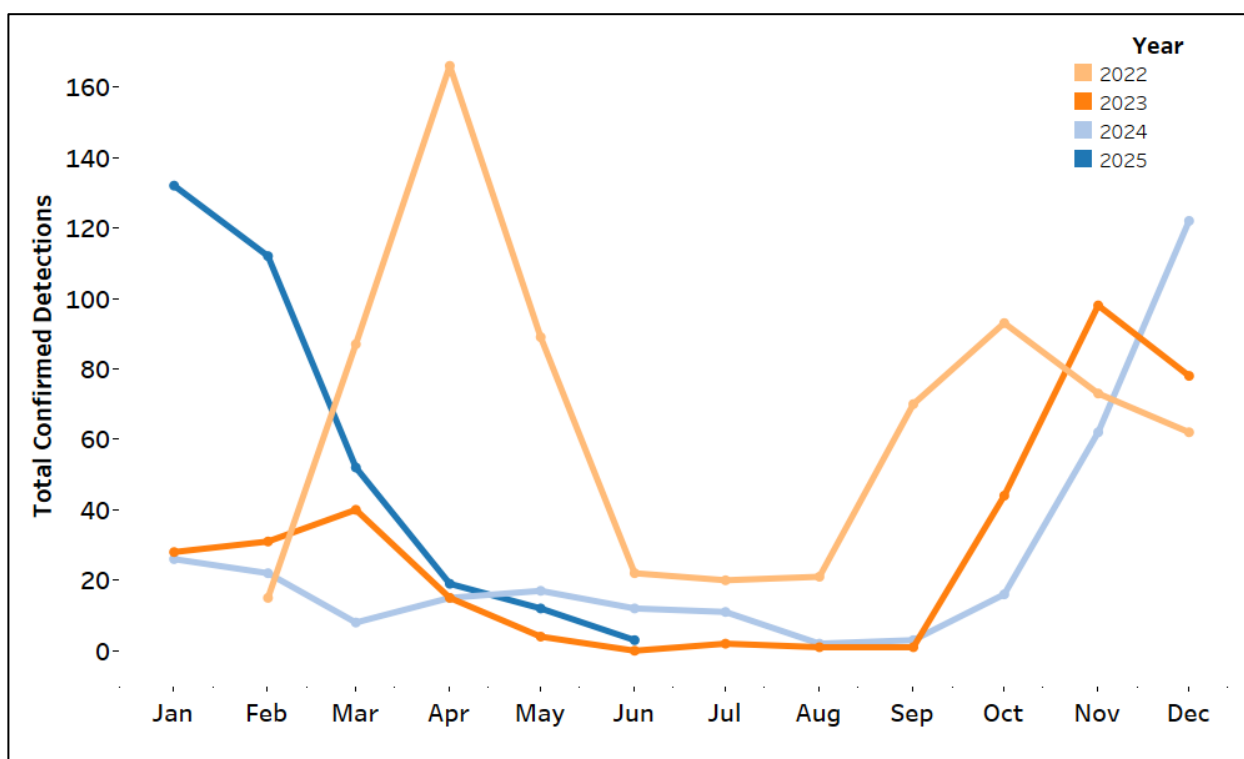


Figure 4. Epidemiological curves of infected premises count by month of confirmed diagnosis date, as of June 30, 2025.

DETECTIONS IN WILD BIRD AND MAMMALS

A. Wild Bird Surveillance Program

The United States conducts both active surveillance for HPAI in apparently healthy birds (primarily waterfowl) and passive surveillance in sick or dead wild birds (any species). Wild bird surveillance helps to understand how HPAI is distributed in the United States, detects the spread of HPAI to new areas of concern, provides a flexible surveillance framework that accounts for changing disease risks through time, and obtains sequence data to better understand HPAI transmission dynamics and spillover risk to poultry. Between December 30, 2021 and June 30, 2025, wild bird surveillance has resulted in 13,754 detections of H5Nx HPAI in wild birds across all four North American flyways (6,554 detections in apparently healthy birds; 7,200 detections in sick or dead birds; **Figure 5**).

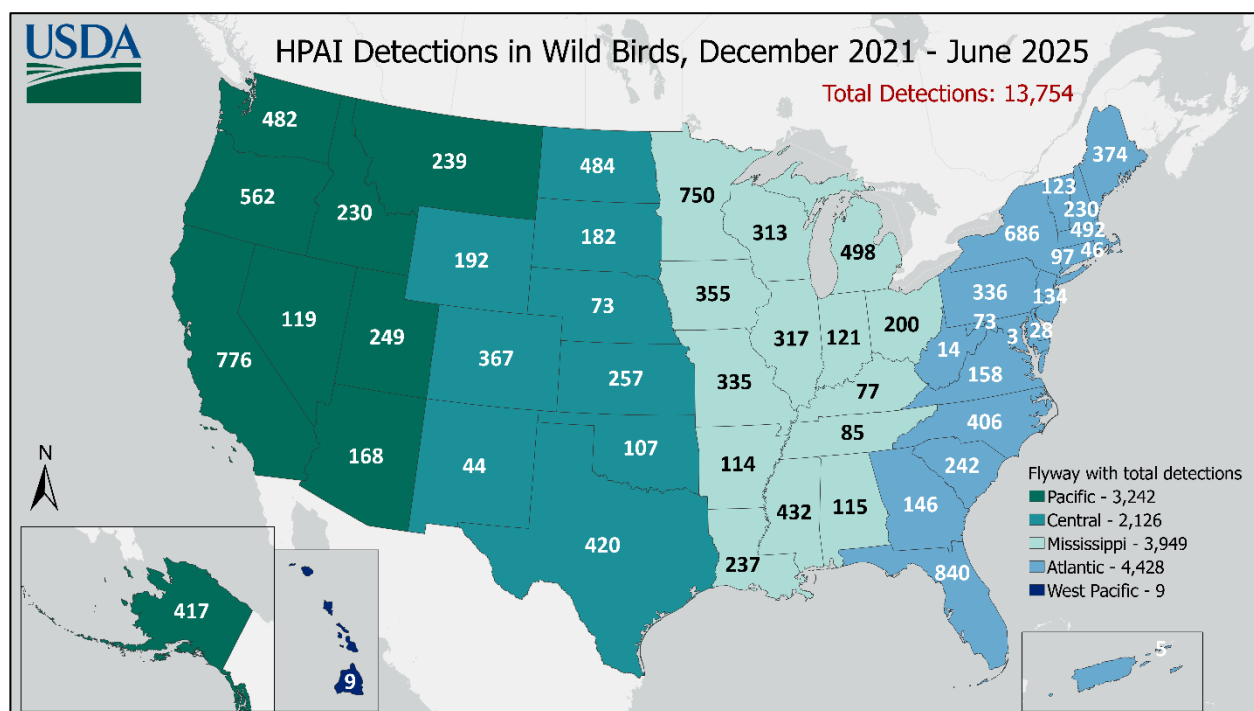


Figure 5. Number of HPAI detections in wild bird samples collected between December 30, 2021 and June 30, 2025. State totals include detections from both apparently healthy birds from active surveillance efforts and sick or dead birds from morbidity/mortality investigations.

Prevalence of HPAI H5Nx (i.e., the proportion of sampled individual birds testing positive for HPAI H5Nx) among apparently healthy wild birds appears to vary based on the time of year, with prevalence being the highest during the fall months and lowest during the spring and early summer (**Figure 6**). The fall 2024 to winter 2025 peak was observed later than the previous two years but subsided in the spring, as expected.

HPAI detections in sick or dead birds occurred in the largest numbers during the first year of the event, likely due to the large number of immunologically naïve birds in North America when the virus was initially introduced. Detections in sick or dead birds have still been observed in the subsequent years of the event, but less than the first year and with seasonal peaks similar to those observed in apparently healthy wild birds (**Figure 7**).

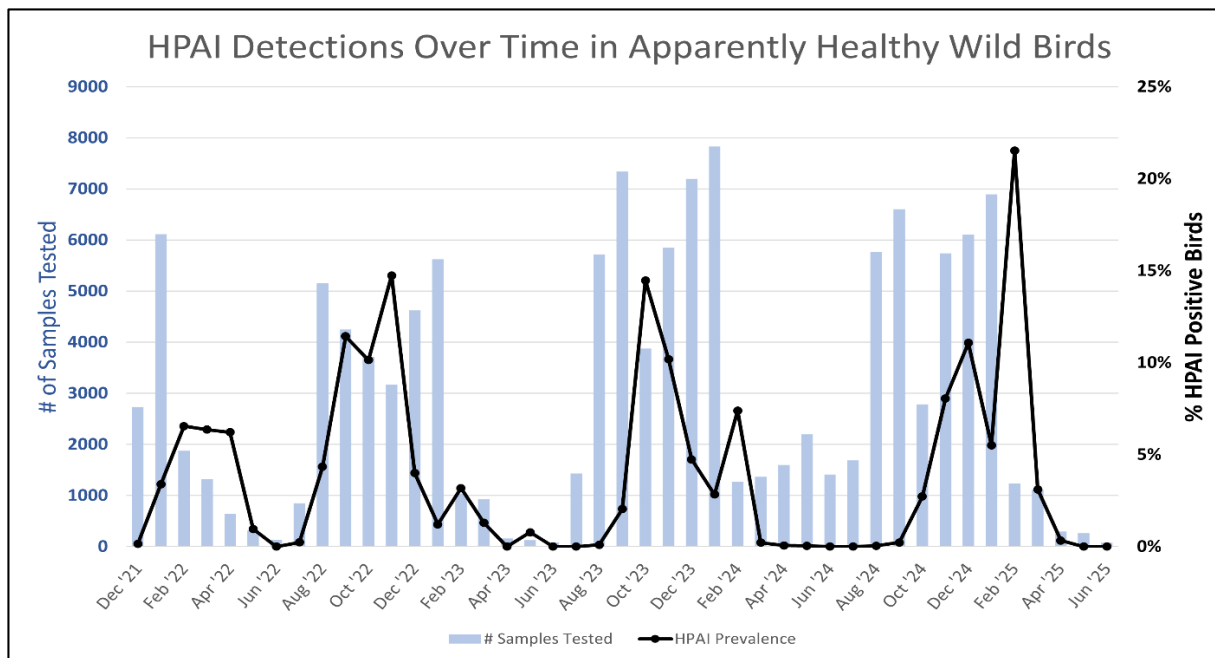


Figure 6. Monthly sampling effort (number collected; blue bars) and H5Nx HPAI prevalence (percentage of samples found to be HPAI H5Nx-positive; black line) in apparently healthy wild birds as part of the U.S. National Surveillance Plan for Highly Pathogenic Avian Influenza.

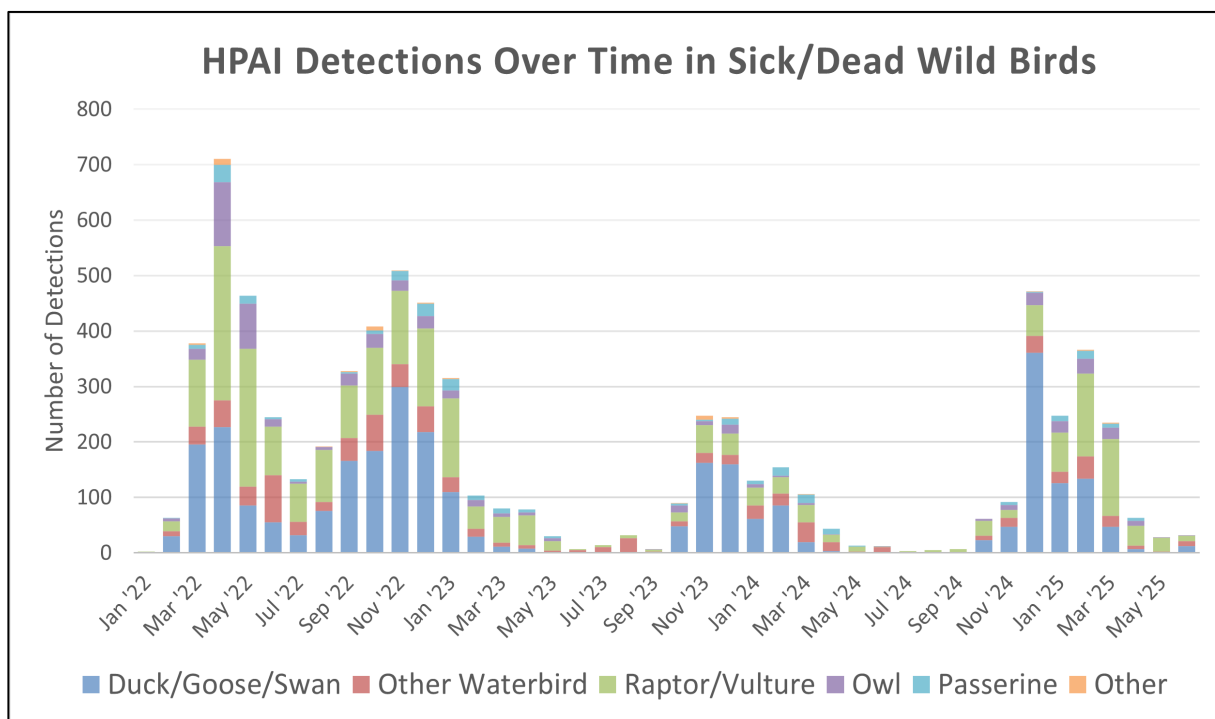


Figure 7. Stacked bar graph of the number of H5Nx HPAI detections in sick or dead wild birds sampled between December 30, 2021 and June 30, 2025. Different colors represent different functional groups of wild birds.

For additional information, see [Detections of Highly Pathogenic Avian Influenza in Wild Birds.](#)

B. Peri-domestic Wildlife Surveillance

Following the detections of H5N1 HPAI in dairy cattle in March 2024, USDA's Wildlife Services began conducting avian influenza surveillance in wild birds and mammals captured on infected dairy and poultry facilities. The goals of the program were to examine transmission dynamics between domestic animals and wildlife, assess changes in the virus over time, and compare apparent prevalence and virus strains detected on farms to those detected as part of routine wild bird surveillance efforts across the United States.

Between April 1, 2024 and June 30, 2025, 10,950 samples were collected from 67 affected farms in 18 States, resulting in 434 detections of HPAI (**Figure 8**). The number of HPAI detections varied widely across farms, ranging from zero detections ($n = 35$ farms) to >30 detections ($n = 4$ farms). Investigations into the factors driving differences from farm to farm are ongoing.

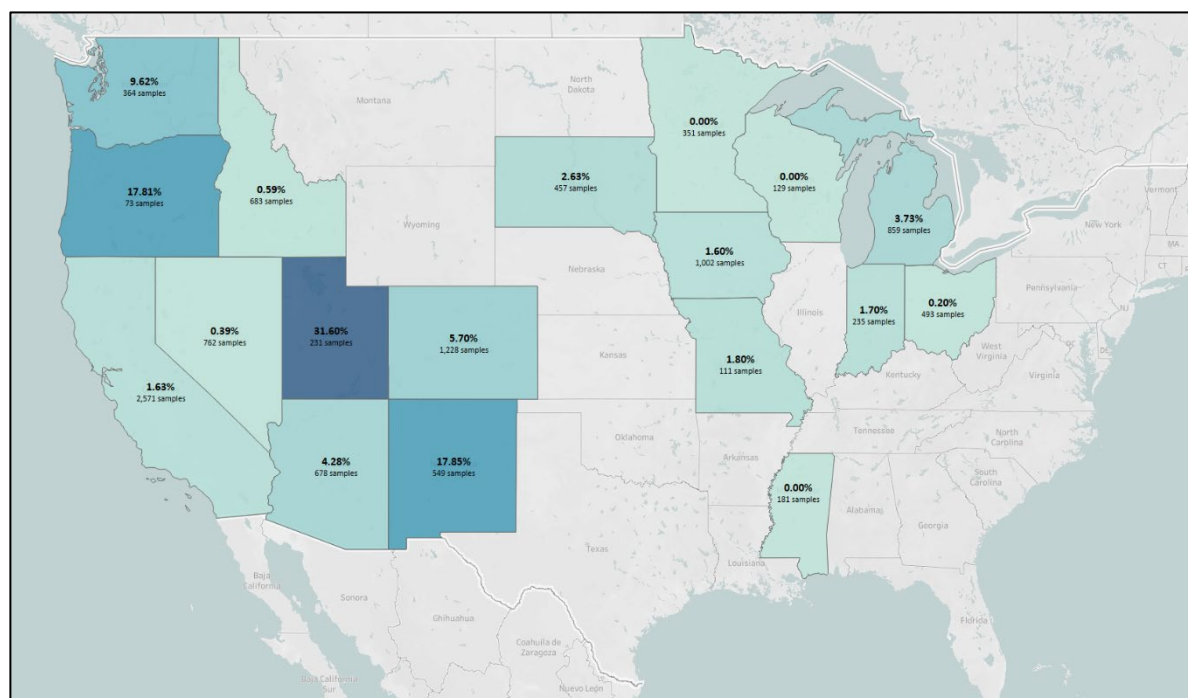


Figure 8. Peri-domestic wildlife surveillance efforts for HPAI from April 1, 2024 to June 30, 2025. Sampling of both wild birds and mammals occurred on HPAI-affected dairy and poultry farms in the States colored in blue. Darker colored states indicate higher apparent prevalence of HPAI in the wildlife sampled on the farms.

C. HPAI Detection in Mammals

Although HPAI primarily affects wild birds and poultry, these viruses can be occasionally transmitted to mammals. A rising number of HPAI cases have been reported in several terrestrial and aquatic mammalian animals across the United States (**Figure 9**). In some cases, infection may cause illness, including severe disease and death. As of June 30, 2025, there have been 644 HPAI detections in at least 44 wild or captive wild mammal species in 40 States since the start of the HPAI event. The majority of HPAI detections in mammals have been from sick or dead animals, although recent surveillance of peri-domestic wildlife found in and around HPAI-positive farms has resulted in detections of HPAI in apparently healthy wild mammals.

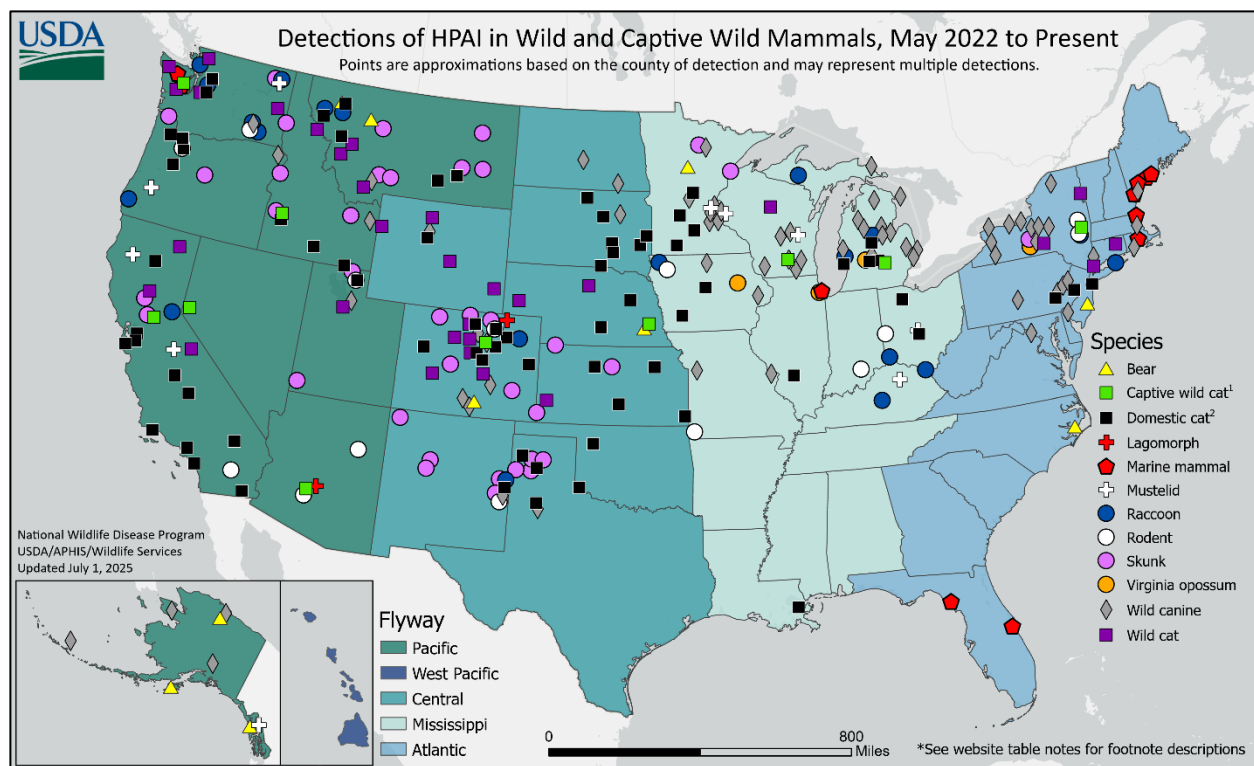


Figure 9. Detections of HPAI virus in wild mammals and captive wild mammals in the United States as of June 30, 2025. The map shows detections in both sick/dead mammals as well as apparently healthy mammals collected on HPAI-infected farms as part of peri-domestic wildlife surveillance efforts.

PHYLOGENETICS

A. Background

The NVSL is the national confirmatory laboratory for influenza A virus in animals and conducts genomic sequencing on suspect samples submitted from infected poultry or livestock premises, wildlife surveillance samples, as well as other animal and related samples. Ongoing phylogenetic analysis allows virus monitoring for naturally occurring changes over time and across populations. The data pipeline for influenza A includes several bioinformatics tools, including [IRMA](#), [GenoFLU](#), and [vSNP](#), as well as evaluation for potential mutations of interest. High-quality raw genetic data are uploaded to the National Center for Biotechnology Information (NCBI) Sequence Read Archive, with consensus genomes assembled and submitted to NCBI GenBank, as appropriate.

B. Distribution of GenoFLU Genotypes

Genotype is determined by GenoFLU ([GitHub - USDA-VS/GenoFLU: Influenza data pipeline to automate genotyping assignment](#)) which was developed by the NVSL to better track genotypic diversity of the HPAI H5Nx goose/Guangdong clade 2.3.4.4b viruses as they reassort with wild-bird origin low pathogenicity influenza viruses. The “A” genotypes represent fully Eurasian H5Nx clade 2.3.4.4b viruses; “B” genotypes are reassortants of genotype A1 viruses with North American wild bird-origin viruses; “C” genotypes are reassortants of A2 viruses; and “D” genotypes are reassortants of A3 viruses. There have been at least 6 distinct introductions of Eurasian viruses (“A” genotypes) in North America during the current event, and over 100 genotypes have been described, to date.

Prior to March 2024, the genotype distribution of HPAI detections in poultry closely followed that of wild bird detections (**Figure 10**). However, following an initial spillover event of genotype B3.13 from wildlife to dairy cattle in late fall 2023, with spread and detection in March 2024, dairy-to-poultry spillover was established as a new route of virus introduction into poultry. There have been no detections of genotype B3.13 in migratory waterfowl since March 2024; however, detections in peri-domestic avian and mammalian species on and near affected dairies have been reported in addition to detections in peri-domestic species sampled on affected premises by Wildlife Services. Genotype B3.13 was detected on four commercial and four WOA non-poultry premises in California (seven premises) and Idaho (one premises) during this reporting period.

Genotype D1.1 has vastly predominated in both wildlife and domestic poultry during the current reporting period (**Figure 10**). First detected in September 2024, genotype D1.1 is a reassortant of the A3 virus introduced via the Pacific flyway and first detected in Alaska early in 2022. Circulation of genotype A3 remained limited to the Pacific flyway until late fall and winter of 2024, when A3 and the “D” genotypes expanded eastward, affecting wild birds, poultry, and wild mammals across all four migratory flyways.

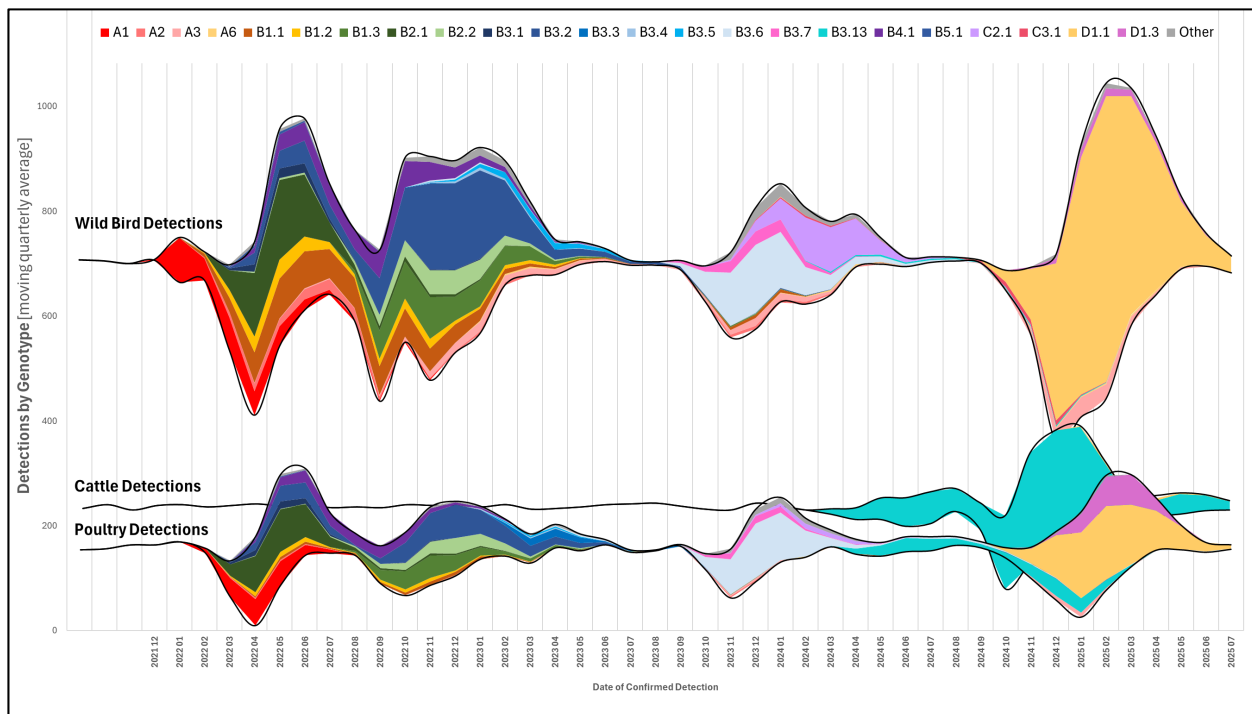


Figure 10. Genotype distribution of wild bird (top), dairy cattle (middle), and poultry detections (bottom), represented as moving quarterly averages normalized to detections in each animal category, for the total 2022 HPAI event as of June 30, 2025.

SPILLOVER AND TRANSMISSION EVENTS

A. Entire Event to Date: February 2022 to June 2025

Partnering the phylogenetic analysis with epidemiological investigation data strengthens the ability to interpret how the virus was introduced and to evaluate onward spread, where applicable. Phylogenetic analysis provides information on the evolution of the virus over time by comparing changes in the genome via single nucleic polymorphisms (SNPs), as well as comparison to other recent detections across the country in domestic and wild species. Such analyses are used to distinguish independent introduction of wild bird-origin virus (IND; e.g., spillover event) from common source exposure or lateral transmission events (CSLT). Common source exposure may be suspected where several premises have highly-related sequences within a short period of time and in the absence of other epidemiologic links. It is critical to consider the available epidemiologic data where analysis supports the potential for lateral transmission. Evidence for lateral transmission implies that transmission occurred from one premises to another and epidemiologic investigations are needed. A table of introduction type (IND versus CSLT) by month and year is available in **Table A1**. Phylogenetic analysis was available for 1,677 out of 1,707 detections.

Overall, 70.2 percent (1,178 out of 1,677) of detections are attributed to independent wild bird introductions. The percentage of IND detections by migratory flyway were as follows: 17.6 percent (207 out of 1,178) in the Atlantic flyway, 32 percent (377 out of 1,178) in the Mississippi flyway, 26.8 percent (316 out of 1,178) in the Central flyway, and 23.6 percent (278 out of 1,178) in the Pacific flyway.

The occurrence and frequency of independent wild bird introductions increases the risk for subsequent transmission to additional poultry premises (e.g., common source or lateral transmission). Overall, 29.8 percent (499 out of 1,677) of detections have been attributed to common source or lateral transmission; however, it is important to note 21.8 percent (109 out of 499) of CSLT detections were of the B3.13 genotype, which reflects multiple transmission events from infected dairy premises to poultry premises, and some poultry-to-poultry premises transmission. With the B3.13 transmission events excluded, 75.1 percent (1,178 out of 1,568) of detections were IND, while 24.9 percent (390 out of 1,568) of detections were CSLT.

While CSLT overall reflects a smaller subset of detections, the percentage of cases attributed to CSLT has continued to increase throughout the HPAI 2022 event—15.5 percent in 2022 (110 out of 708), 20.4 percent (68 out of 333) in 2023, 43.3 percent (136 out of 314) in 2024, and for the first six months of 2025, 57.4 percent (185 out of 322) (**Figure 11**). The increase in CSLT observed in 2024 is largely attributed to the B3.13 genotype, which accounted for 74.2 percent (101 out of 136) of detections; 4.3 percent (8 out of 185) of CSLT detections in 2025 were B3.13. Events leading to increased CSLT observed in the first six months of 2025 and are detailed below for the current reporting period.

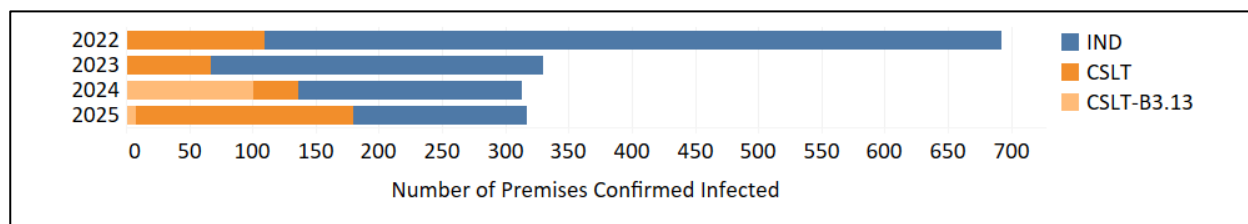


Figure 11. Number of poultry premises confirmed infected over the total 2022 HPAI event separated by year and potential route of introduction.

B. Reporting Period: January 2025 – June 2025

Between January and June 2025, there were 137 independent wild bird introductions; this is lower than the 317 cases between January and June 2022, but higher than the 81 cases in 2023 and 41 cases in 2024 between January and June. The 137 detections were spread across migratory flyways as follows: 43.8 percent (60 out of 137) in the Atlantic flyway, 24.8 percent (34 out of 137) in the Mississippi flyway, 18.3 percent (25 out of 137) in the Central flyway, and 13.1 percent (18 out of 137) in the Pacific flyway.

Independent wild bird introductions mainly occurred among WOAH non-poultry [backyard] (94 out of 137) and WOAH poultry [backyard] (12 out of 137) premises. Twenty-six WOAH poultry [commercial] detections were attributed to IND introductions, consisting of 10 broiler, 7 turkey, 6 table egg, 2 duck, and 1 upland gamebird premises. The remaining five IND detections occurred in WOAH poultry [LBM] premises.

In addition to an increase in the number of IND introductions, an increase in CSLT was also observed, with 185 CSLT detections between January and June 2025. Compared to the same month span in past years of the event, this is greater than the 57 detections in 2022, 29 detections in 2023, and 17 detections in 2024.

During the reporting period, CSLT introductions mainly occurred among WOAH poultry [commercial] premises (134 out of 185). Split by commercial sector, CSLT was attributed to 70 turkey, 46 table egg, 11 broiler, and 7 duck premises. The remaining introductions occurred in the WOAH poultry [LBM] (27 out of 185), WOAH non-poultry (16 out of 185), and WOAH poultry [backyard] (8 out of 185) premises (**Figure 12**).

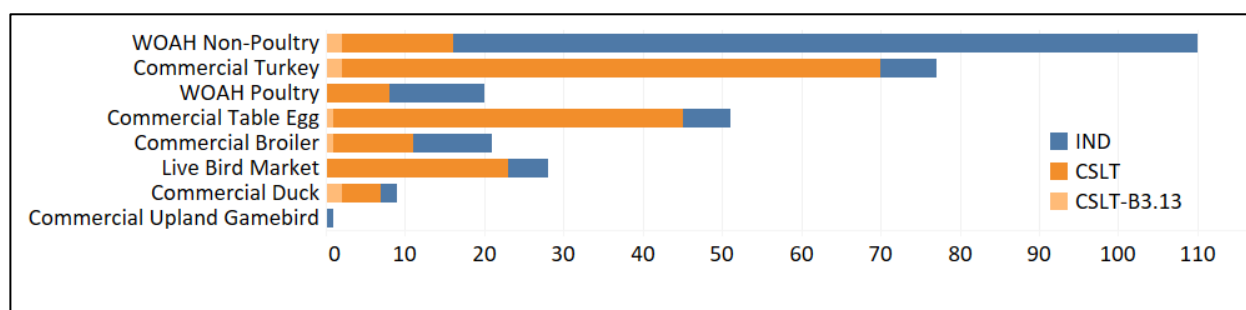


Figure 12. Number of poultry premises confirmed infected between January 2025 and June 2025 separated by production type and potential route of introduction.

Among the CSLT introductions, 81.6 percent (151 out of 185) were attributed to large clusters observed in Missouri; Ohio and Indiana; New Jersey, New York, and Pennsylvania; and Arizona. The remaining occurrences of CSLT were spread across 15 States. Thirteen States had genotype D1.1 CSLT events with

clusters containing three or less premises; two States, California and Idaho, had genotype B3.13 CSLT detections (total of eight premises) associated with potential transmission from dairy premises with subsequent spread among poultry premises (**Figure 13**).

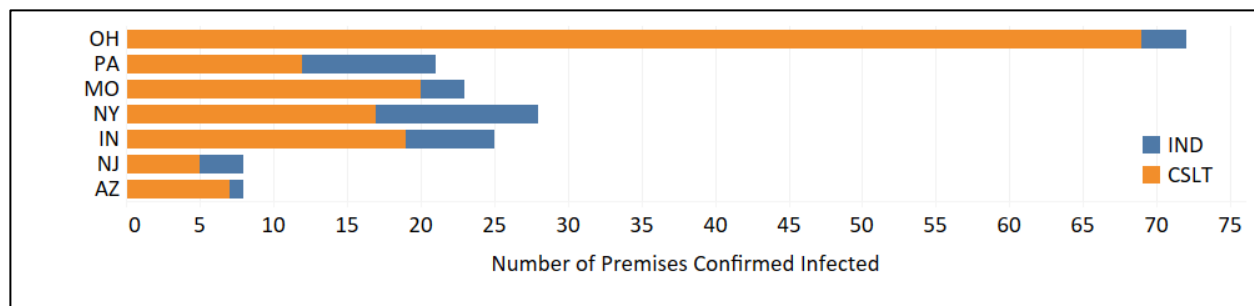


Figure 13. Potential sources of introduction for states with large clusters of common source or lateral transmission for this reporting period.

Missouri: January 2025 – February 2025

Between January and February 2025, a large transmission event of genotype D1.1 occurred in Missouri and impacted 20 WOAHP poultry [commercial] poultry operations. Impacted commercial species include 14 turkey, 4 broiler, and 2 table egg layer premises. While the premises cluster together phylogenetically, separate production types and geographical separation suggest this cluster could have a multifactorial cause, such as contribution from a common source of infection (e.g., wild birds with high viral load in the area), in addition to direct or indirect lateral spread between premises. Within commercial species groups, shared company affiliation was an observed risk factor.

Ohio and Indiana: January 2025 – March 2025

Between January and March 2025, a large, sustained transmission event of genotype D1.3 was observed among 88 poultry premises in Ohio and Indiana. This event included 46 commercial turkey, 34 commercial table egg, 4 commercial duck, 3 WOAHP non-poultry [backyard], and 1 WOAHP poultry premises. These detections accounted for 64.2 percent (34 out of 53) of all table egg and 59.7 percent (46 out of 77) of all commercial turkey premises in the United States impacted during the current reporting period.

Phylogenetic analysis indicates that this event originated from a single independent introduction of a wild bird-origin virus. The lack of D1.3 sequences in wildlife, and subsequent phylogenomic homogeneity of the poultry sequences, suggests this transmission event was sustained by premises-to-premises transmission. Veterinary Services Field Epidemiologic Investigation Services team (FEIS) conducted an in-depth analysis of this cluster, with a focus on 72 cases occurring in Ohio. Their investigation did not identify any direct animal movements during the 28-day reference period prior to detection on infected premises, indicating reported animal movement was not a factor in spread. Spatial proximity to infected premises, a known risk factor for HPAI spread, was evident in this transmission cluster, with infected premises often located in overlapping control areas of other infected premises. Other potential risk factors include sharing of equipment, employees living in community housing, visitors, location near a body of water, and shared company ownership.

New York, New Jersey, and Pennsylvania: February 2025 – April 2025

Between February and April 2025, another large transmission event of genotype D1.1 was observed in the northeastern United States, impacting 38 premises in New York (21 out of 38), New Jersey (5 out of 38), and Pennsylvania (12 out of 38). This transmission cluster included 27 WOAHPoultry [LBM], 5 WOAHPoultry [backyard], 1 WOAHPoultry non-poultry, and 5 WOAHPoultry [commercial] premises (2 broiler, 1 duck, 1 table egg, and 1 turkey). The WOAHPoultry [LBM] detections account for 77 percent (27 out of 35) of LBM detections during the current reporting period. In most instances, specific movements associated with disease transmission were not identified; however, the frequent movement of birds to and from LBM operations is a reoccurring risk factor identified throughout the HPAI 2022 event.

Arizona: May 2025 – June 2025

Between May and June 2025, Arizona had a cluster containing four WOAHPoultry [commercial] table egg premises and one WOAHPoultry non-poultry premises infected with the D1.1 genotype. While these premises were linked to a D1.1 spillover event in dairy cattle in Arizona, phylogenetic analysis suggests an initial transmission from a dairy herd into a poultry premises, with subsequent transmission among poultry premises. Identified risk factors for lateral transmission include spatial proximity, shared company affiliation, and possible sharing of feed trucks between operations.

APPENDIX A

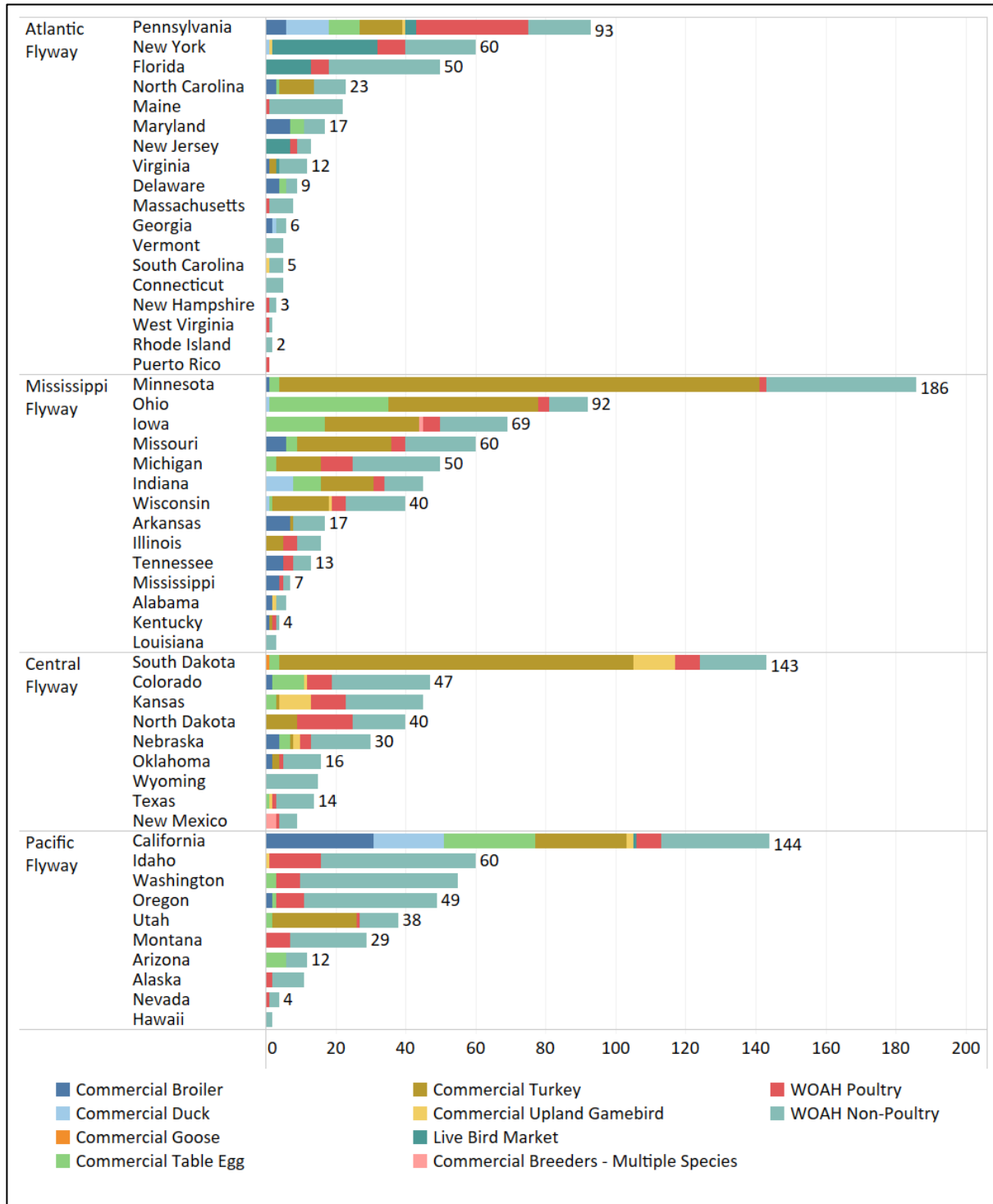


Figure A1. Detections of highly pathogenic avian influenza by migratory flyway, State, and commercial species between February 8, 2022 and June 30, 2025.

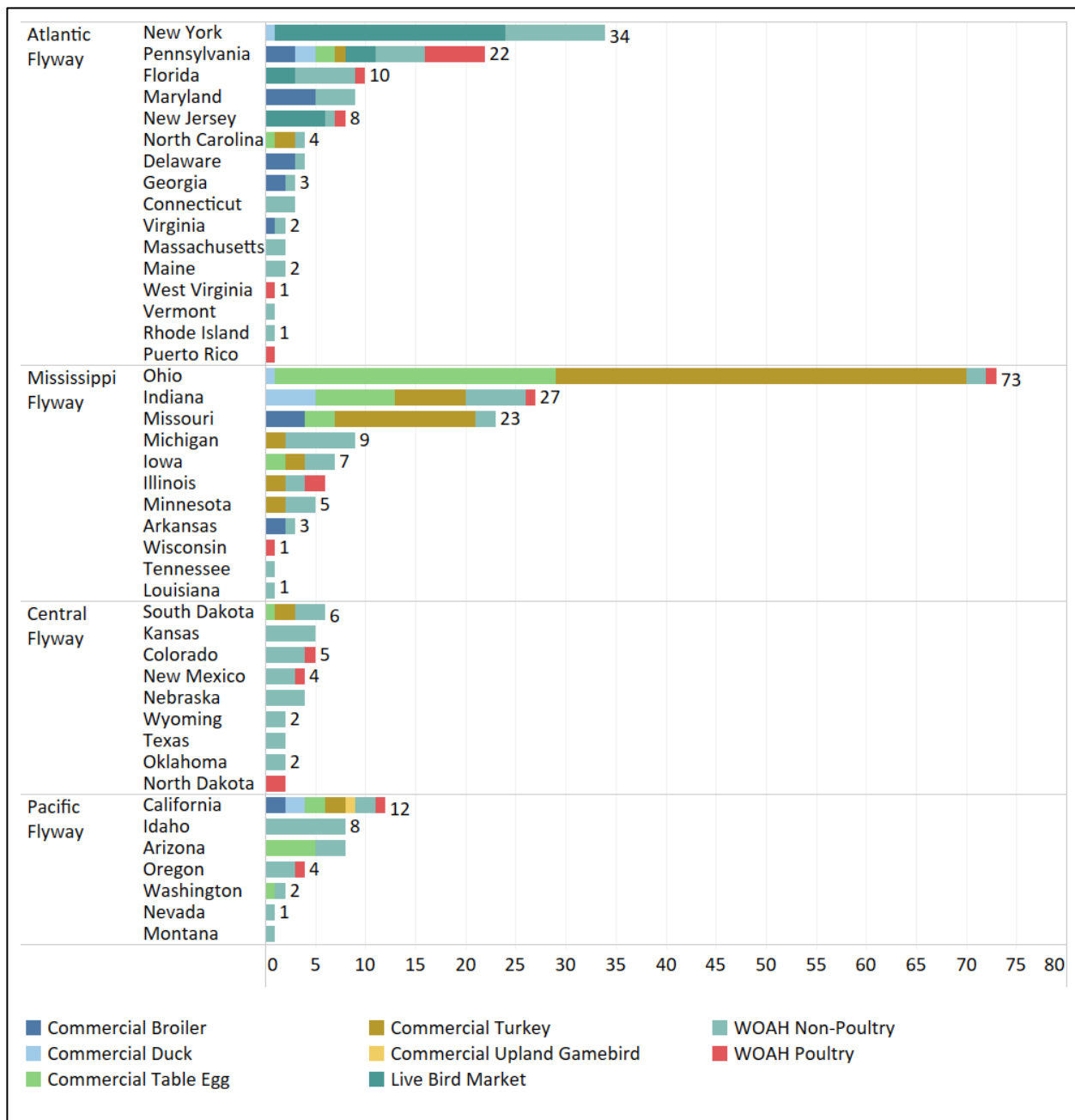


Figure A2. Confirmed detections between January 31, 2025 and June 30, 2025, by flyway, State, and production types.

Table A1. Number of confirmed detections by year, month, and source of introduction. Color intensity reflects the relative number of cases attributed to each source of introduction for the combined year and month to indicate the relative sources of transmission for that month.

		Confirmed Diagnosis												Grand Total
		Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	
2022	CSLT		2	4	35	13	3	1	4	14	12	12	10	110
	IND		13	82	129	74	19	19	16	55	79	60	52	598
	Total		15	86	164	87	22	20	20	69	91	72	62	708
2023	CSLT	2	7	17	3			2	1		4	10	22	68
	IND	25	24	17	11	4				1	40	87	56	265
	Total	27	31	34	14	4		2	1	1	44	97	78	333
2024	CSLT	12	5	2	13	14	12	11	1	2	9	24	31	136
	IND	14	16	6	2	3			1	1	7	38	90	178
	Total	26	21	8	15	17	12	11	2	3	16	62	121	314
2025	CSLT	70	69	30	8	5	3							185
	IND	61	40	20	9	7								137
	Total	131	109	50	17	12	3							322
Grand Total		184	176	178	210	120	37	33	23	73	151	231	261	1,677