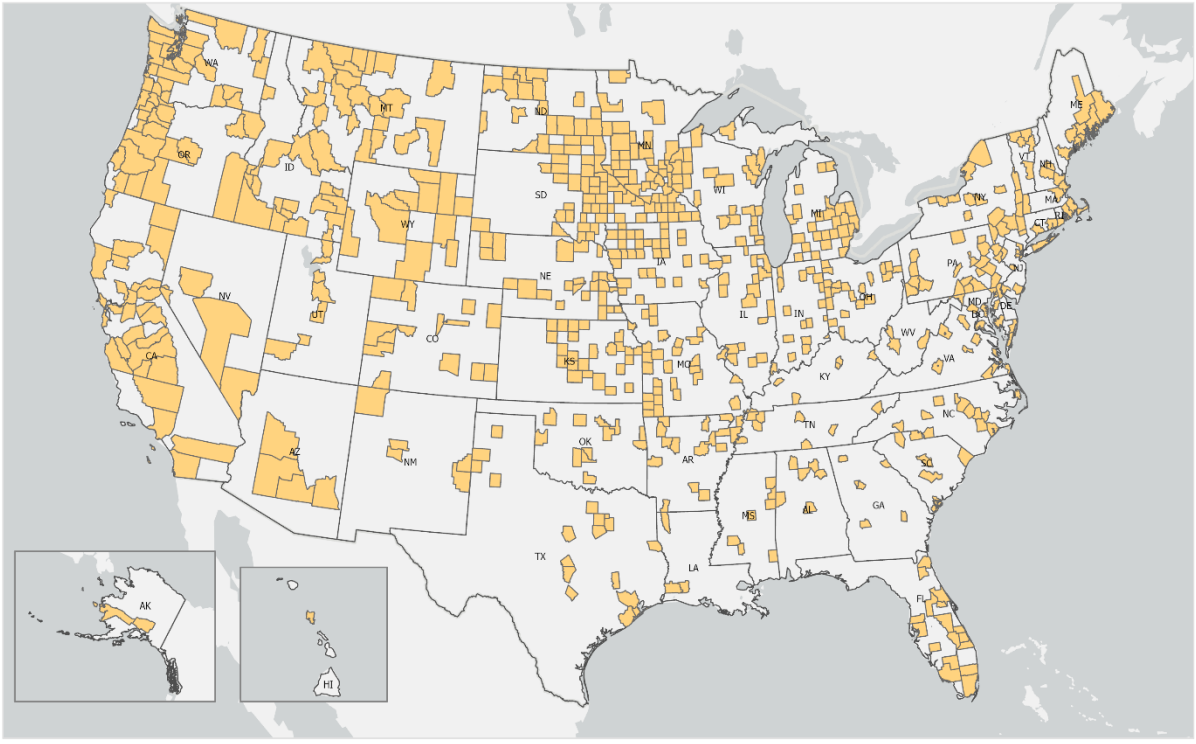
Status and Epidemiologic Analyses of HPAI-affected Poultry Flocks December 31, 2025 Interim Report



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ITEMS OF NOTE

A. Reporting Period: October 1, 2025, to December 31, 2025

- During the current reporting period, the event impacted 38 States, 245 premises, and over 6 million birds.
- Monthly cases consisted of 67 detections in October, 96 detections in November, and 82 detections in December. Although more than 20 States were impacted each month, Minnesota accounted for 22 percent (15 out of 67) of cases in October, while Indiana accounted for 55 percent (53 out of 96) and 27 percent (22 out of 82) of cases in November and December, respectively.
- Genotype D1.1 continues to predominate in both wildlife and domestic poultry during the current reporting period.
- During this reporting period, approximately one third of HPAI confirmations were associated with a large cluster of cases in Indiana; 90.4 percent (75 out of 83) of the cases in Indiana were attributed to common source or lateral transmission (CSLT).

B. Entire Event to Date: February 2022 to December 2025

- As of December 31, 2025, this HPAI event has impacted all 50 States and the territory of Puerto Rico, with a total of 1,985 premises infected and over 185 million birds affected.
- There have been at least 6 distinct Eurasian virus introductions (of the “A” genotypes) in North America during the current event, and over 150 genotypes have been described, to date.
- Between December 30, 2021, and December 31, 2025, wild bird surveillance has resulted in 17,879 detections of H5Nx HPAI in at least 197 species of wild birds across all North American flyways—8,662 detections in apparently healthy birds and 9,217 detections in sick or dead birds.
- Over the entire HPAI event, 67.3 percent (1,329 out of 1,947) of detections are attributed to independent introductions from wildlife sources and 31.6 percent (616 out of 1,947) of detections have been identified as having potential for CSLT.
- The percentage of annual detections attributed to CSLT has increased since the event started in 2022, accounting for 15.5 percent of detections in 2022 (110 out of 708), 20.1 percent (67 out of 333) in 2023, 43.3 percent (136 out of 314) in 2024, and 51.2 percent (303 out of 592) in 2025.
    - The increase in CSLT observed in 2024 was 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, followed by poultry-to-poultry transmission.
    - The increase in CSLT observed in 2025 was due to clusters of transmission in Indiana, Ohio, Pennsylvania, New York, Missouri, Minnesota, and California; more than 54 percent (164 out of 303) of 2025 detections attributed to CSLT occurred in Indiana and Ohio.

DESCRIPTION OF HPAI EVENT IN POULTRY

A. Reporting Period: October 1, 2025, to December 31, 2025

During the reporting period of October 1, 2025, to December 31, 2025, the National Veterinary Services Laboratories (NVSL; National Centers for Animal Health, Ames, Iowa) confirmed Eurasian clade 2.3.4.4b H5Nx highly pathogenic avian influenza (HPAI) in 38 out of 50 States and Puerto Rico, totaling 245 detections. The flock types affected include 101 commercial[1] poultry,[2] 53 backyard poultry,[3] and 91 backyard non-poultry.[4] These 101 poultry premises can be further divided to reflect the production types into 3 live bird market, 40 turkey, 4 table egg, 7 broiler, 46 duck, and 1 upland gamebird premises (**Figure 1**). The reporting period had no detections in goose or breeder (multiple bird species) premises. A table of impacted production types by species can be found in **Appendix Table A1**. Approximately 6.3 million birds have been affected, a lesser number when compared to the same month span in 2023 (20.9 million) and 2024 (29.6 million). The relative difference in the number of birds affected is attributed to fewer detections in larger table egg operations and increased detections in smaller backyard premises. Reporting period detections by flyway, State, and flock type are depicted in **Appendix Figure A1**.

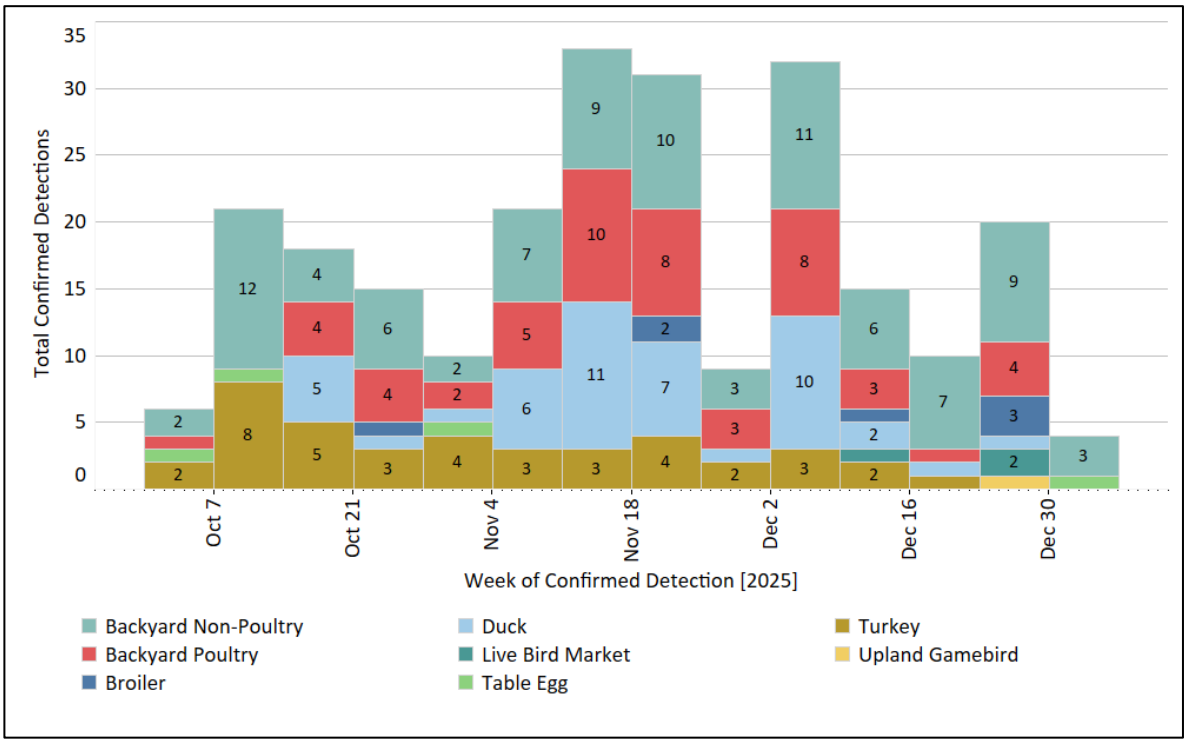

Figure 1. Weekly HPAI detections by flock type, from October 1, 2025, to December 31, 2025.

[1] Commercial premises are defined in 9 C.F.R. 56.3(b)(1)(ii).

[2] Poultry are defined by the World Organization for Animal Health (WOAH) as "all birds reared or kept in captivity for the production of any commercial *animal* products or for breeding for this purpose, fighting cocks used for any purpose, and all birds used for restocking supplies of game or for breeding for this purpose, until they are released from captivity."

[3] Backyard poultry refers to premises that do not meet the C.F.R. definition for commercial premises but meet the poultry definition, as defined by WOAH.

[4] Backyard non-poultry refers to premises that do not meet the C.F.R. definition for commercial premises and do not meet the definition for poultry, as defined by WOAH.

The current reporting period encompasses 6.4 percent of the entire event (3 out of 47 months). Production types that accounted for a greater percentage of detections in this period than across the entire event include duck (51.1 percent; 46 out of 90), backyard poultry (22.1 percent; 53 out of 240), backyard non-poultry (11.7 percent; 91 out of 778), turkey (7.5 percent; 40 out of 534), and broiler (7.2 percent; 7 out of 97). The relative percentage of detections by production type within the current reporting period compared with detections from February 2022 through September 2025 are seen in **Figure 2**.

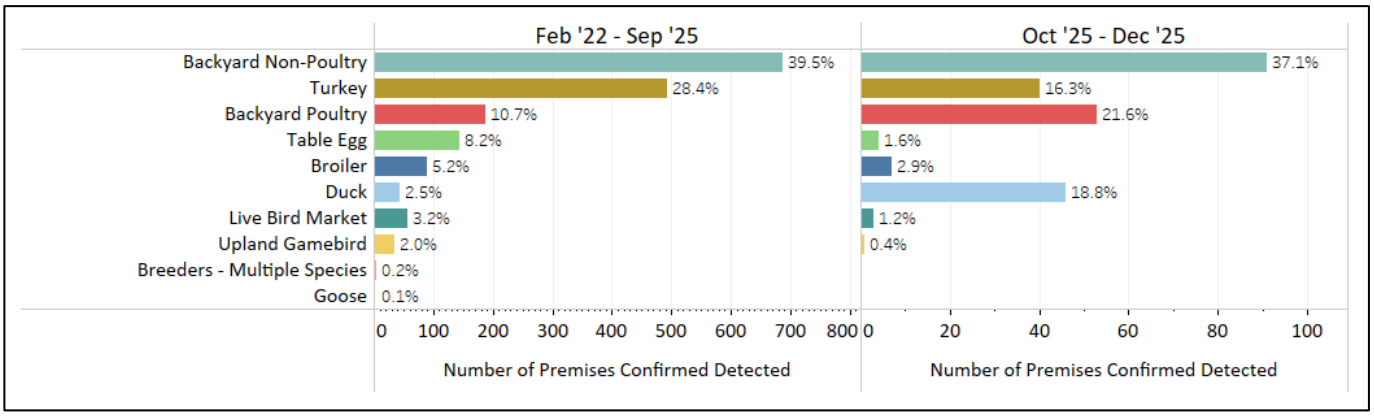

Figure 2. Number and relative percentage of confirmed detected premises by flock type, February 2022 to September 2025 compared to the reporting period.

When comparing chronological monthly trends by event year, the total number of confirmed detections within the current reporting period were similar to trends observed in 2023, with a peak in confirmed detections in November. In comparison, 2022 had a decline in total confirmed detections from October to December, and in 2024, there was a sharp increase in confirmed detections from October to December (**Figure 3**).

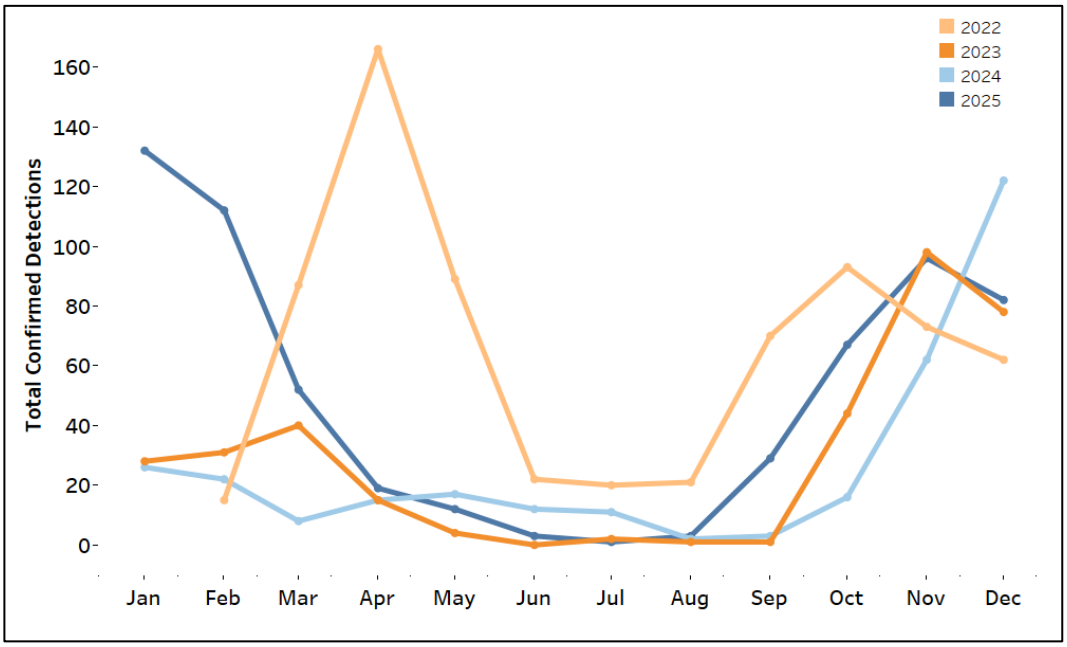

Figure 3. Yearly epidemiological curves of the total number of detections by month of confirmed detection, as of December 31, 2025.

B. **Entire Event to Date:** February 2022 to December 2025

This HPAI poultry event has been ongoing in the United States since February 2022, resulting in 1,985 affected premises across all 50 States and Puerto Rico. NVSL-confirmed premises include 967 commercial poultry, 240 backyard poultry, and 778 backyard non-poultry. The 967 commercial poultry premises can further be divided into 59 live bird market, 534 turkey, 147 table egg, 97 broiler, 90 duck, 35 upland gamebird, 4 breeder (multiple bird species), and 1 goose premises. Over 185 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 4** shows the most prominent peaks occurred during the spring and fall months, which align with typical wild bird migratory seasons. A figure of overall detections by flyway, State, and flock type is available in **Appendix Figure A2**.

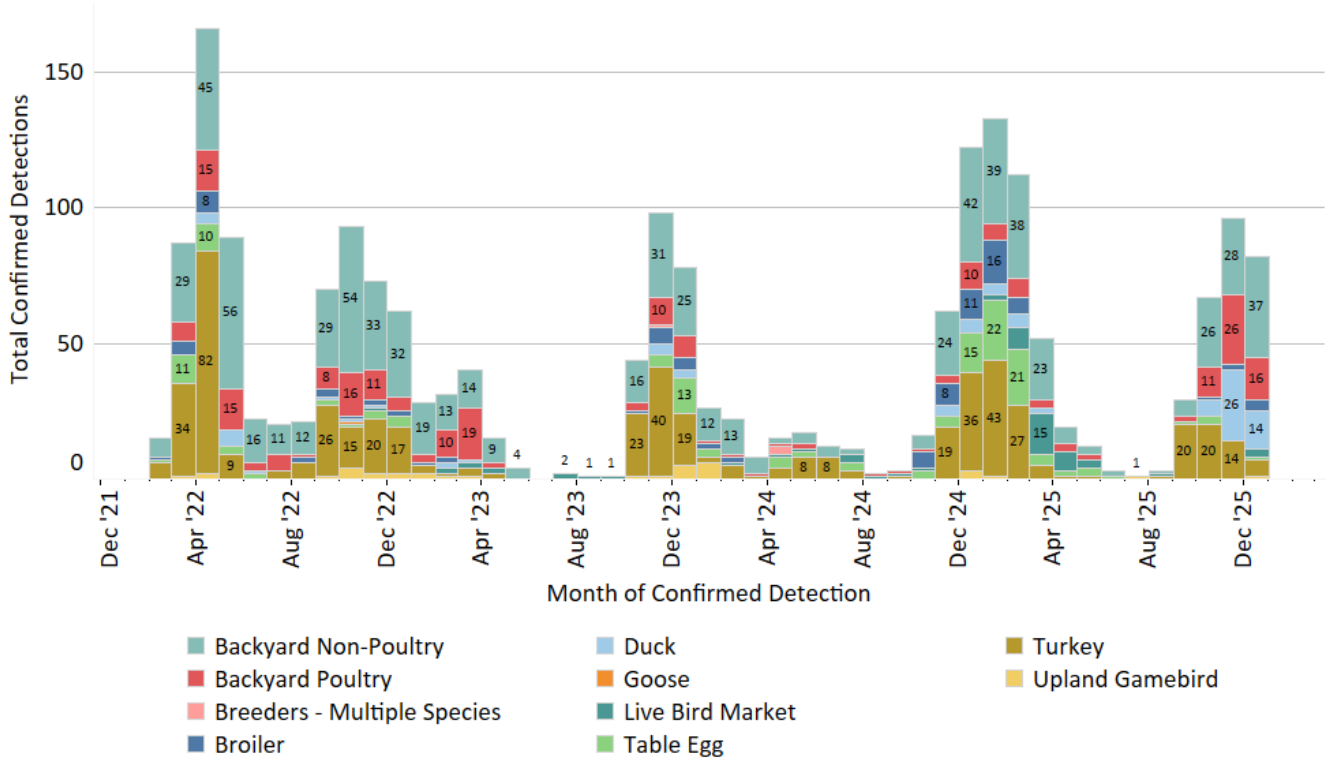

Figure 4. Monthly HPAI confirmed detections by flock type, as of December 31, 2025.

DETECTIONS IN WILD BIRD AND MAMMALS

A. Wild Bird Surveillance Program

The United States conducts both active surveillance for HPAI in apparently healthy wild birds (primarily waterfowl) and passive surveillance in sick or dead wild birds (any species, including birds from zoos and other captive animal facilities). 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 December 31, 2025, wild bird surveillance has resulted in 17,879 detections of H5Nx HPAI in at least 197 species of wild birds across all North American flyways (8,662 detections in apparently healthy birds; 9,217 detections in sick or dead birds; **Figure 5**).

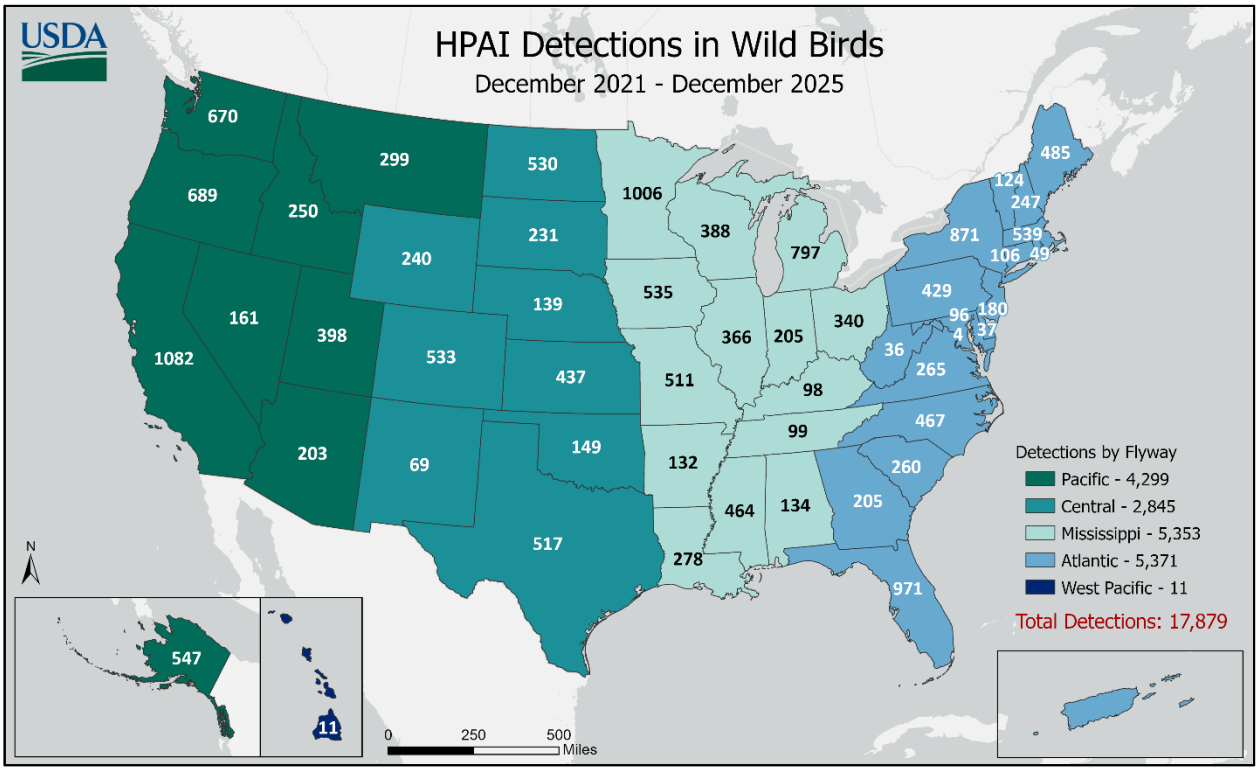

Figure 5. Number of HPAI detections in wild bird samples collected between December 30, 2021, and September 30, 2025. State totals include detections from apparently healthy wild birds from active surveillance efforts and sick or dead birds from morbidity/mortality investigations (including captive wild birds from zoos and other captive animal facilities).

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**). Prevalence in fall of 2025 peaked sooner than the previous two years but was comparable to fall of 2022. Such differences from year to year are expected, due to changing environmental conditions and duck migratory patterns across years.

HPAI detections in sick or dead wild 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 wild 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**).

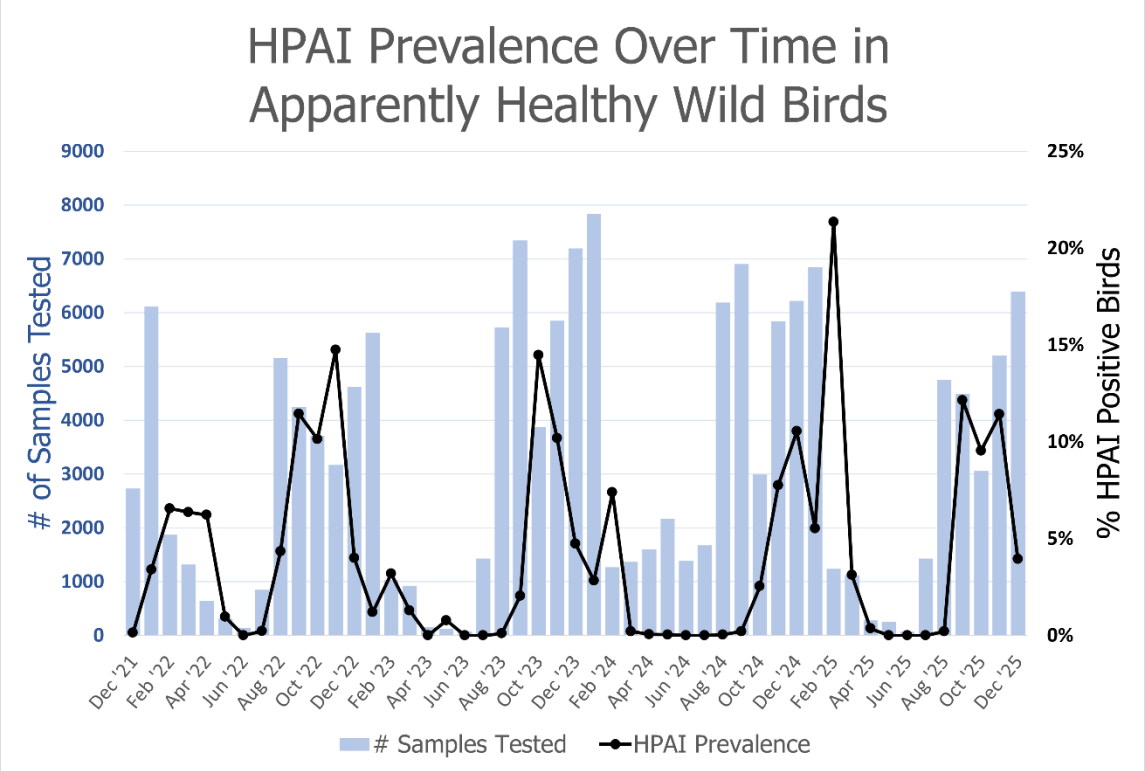

Figure 6. Monthly sampling effort (number collected; blue bars) and H5Nx HPAI prevalence (percentage of samples found to be HPAI H5Nx-positive; black line) in apparently healthy wild birds as part of USDA's National Surveillance Plan for Highly Pathogenic Avian Influenza.

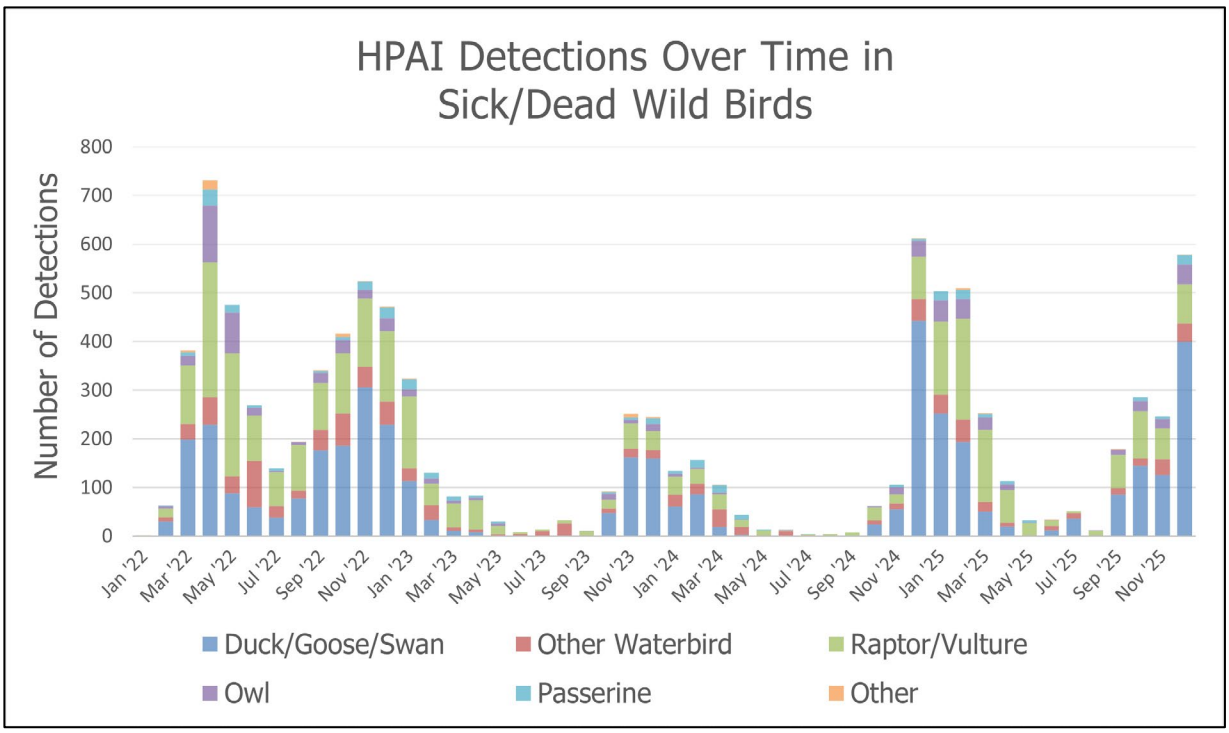

Figure 7. Stacked bar graph of the number of H5Nx HPAI detections in sick or dead wild birds sampled between January 1, 2022, and December 31, 2025. The various colors represent different functional groups of wild birds.

For additional information, see Detections of Highly Pathogenic Avian Influenza in Wild Birds.

B. Peridomestic 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 operations. The goals of the program are 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 December 31, 2025, 12,059 samples were collected from 70 affected farms in 20 States, resulting in 477 detections of HPAI (**Figure 8**). The number of HPAI detections varied widely across farms, ranging from zero detections (n = 38 farms) to >30 detections (n = 5 farms). Investigations into the factors driving differences from farm to farm are ongoing.

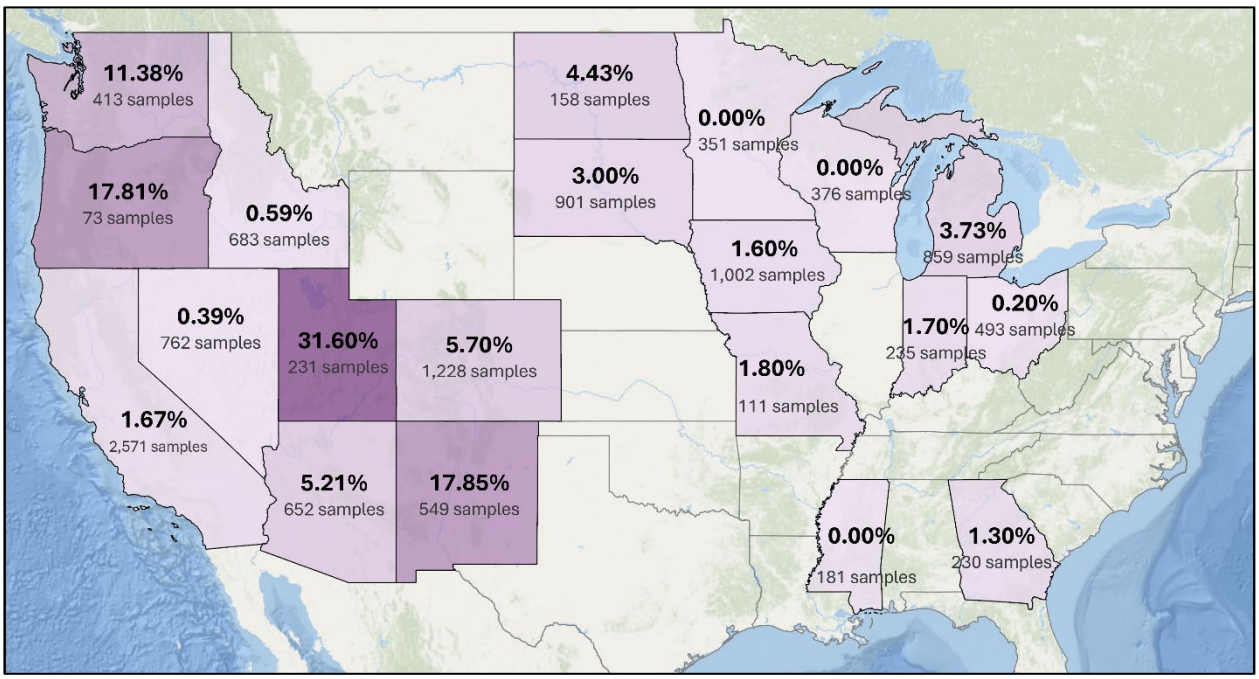

Figure 8. Peridomestic wildlife surveillance efforts for HPAI from April 1, 2024, to December 31, 2025. Sampling of both wild birds and mammals occurred on HPAI-affected dairy and poultry farms in the States colored purple. The progression of light purple to dark purple indicates the increasing prevalence 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 December 31, 2025, there have been 699 HPAI detections in at least 46 wild or captive wild mammal species in 42 States since the start of the HPAI event. The majority of HPAI detections in wild mammals have been from sick or dead animals, although recent surveillance of peridomestic wildlife found in and around HPAI-positive farms has resulted in detections of HPAI in apparently healthy wild mammals.

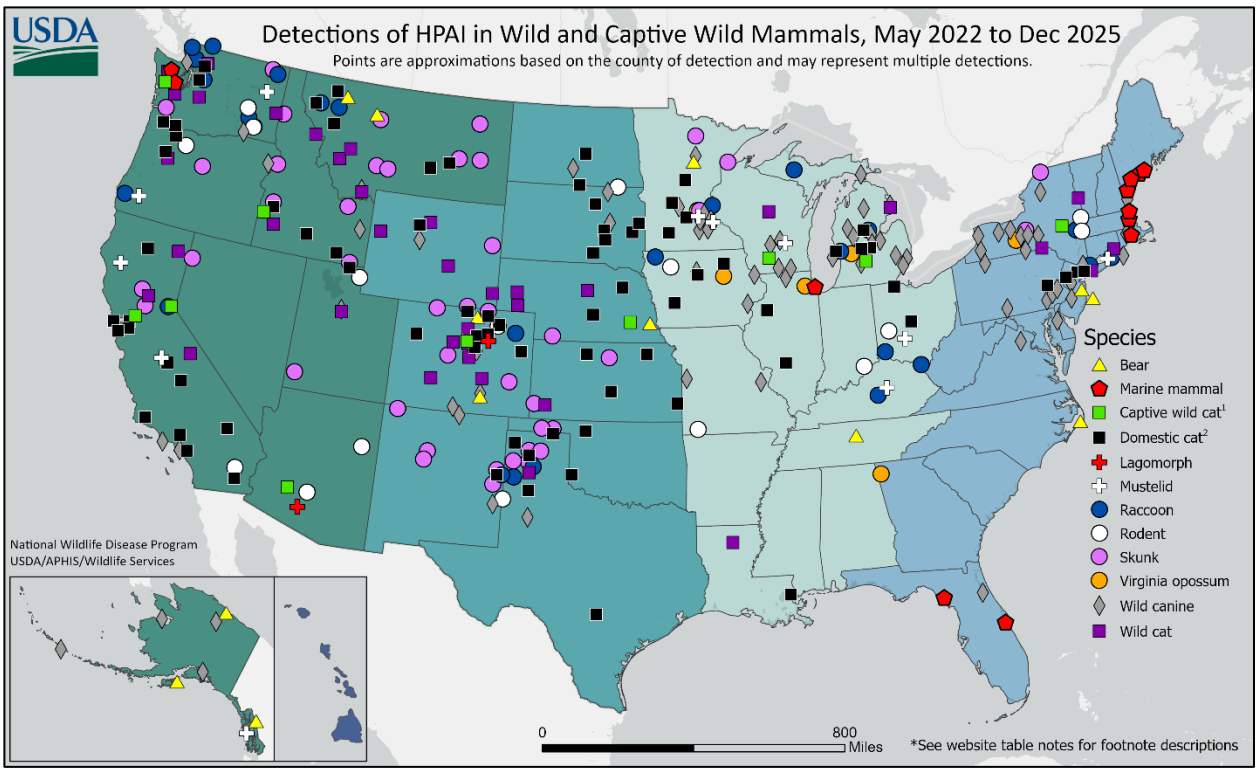

Figure 9. Detections of HPAI virus in wild and captive wild mammals in the United States, as of December 31, 2025. The map shows detections in both sick or dead mammals, as well as apparently healthy mammals collected on HPAI-infected farms as part of peridomestic wildlife surveillance efforts.

For additional information, see Detections of Highly Pathogenic Avian Influenza in Mammals.

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 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 150 genotypes have been described, to date.

The distribution of genotypes affecting poultry, as well as spillovers into other species, typically mirrors contemporary viruses found in the wild migratory bird flyways (**Figure 10**). During December 2025, another spillover event into a single dairy cattle herd in Wisconsin was identified as genotype D1.1, which was unrelated to the prior D1.1 dairy events in Arizona and Nevada, and unrelated to the ongoing genotype B3.13 event in dairy cattle identified in March 2024. Genotype B3.13 remains unique in that transmission is dairy to dairy, with no evidence to support dissemination by migratory wild waterfowl. There have been no detections of genotype B3.13 in migratory waterfowl since March 2024; however, detections in peridomestic avian and mammalian species on and near affected dairies have been reported, in addition to detections in peridomestic species sampled on B3.13-affected premises by Wildlife Services.

Genotype D1.1 continues to predominate in wildlife and in domestic poultry during the current reporting period. 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. The A3 reassortant genotypes continue to evolve, with several new genotypes (D1.7 to D1.11) identified during this reporting period.

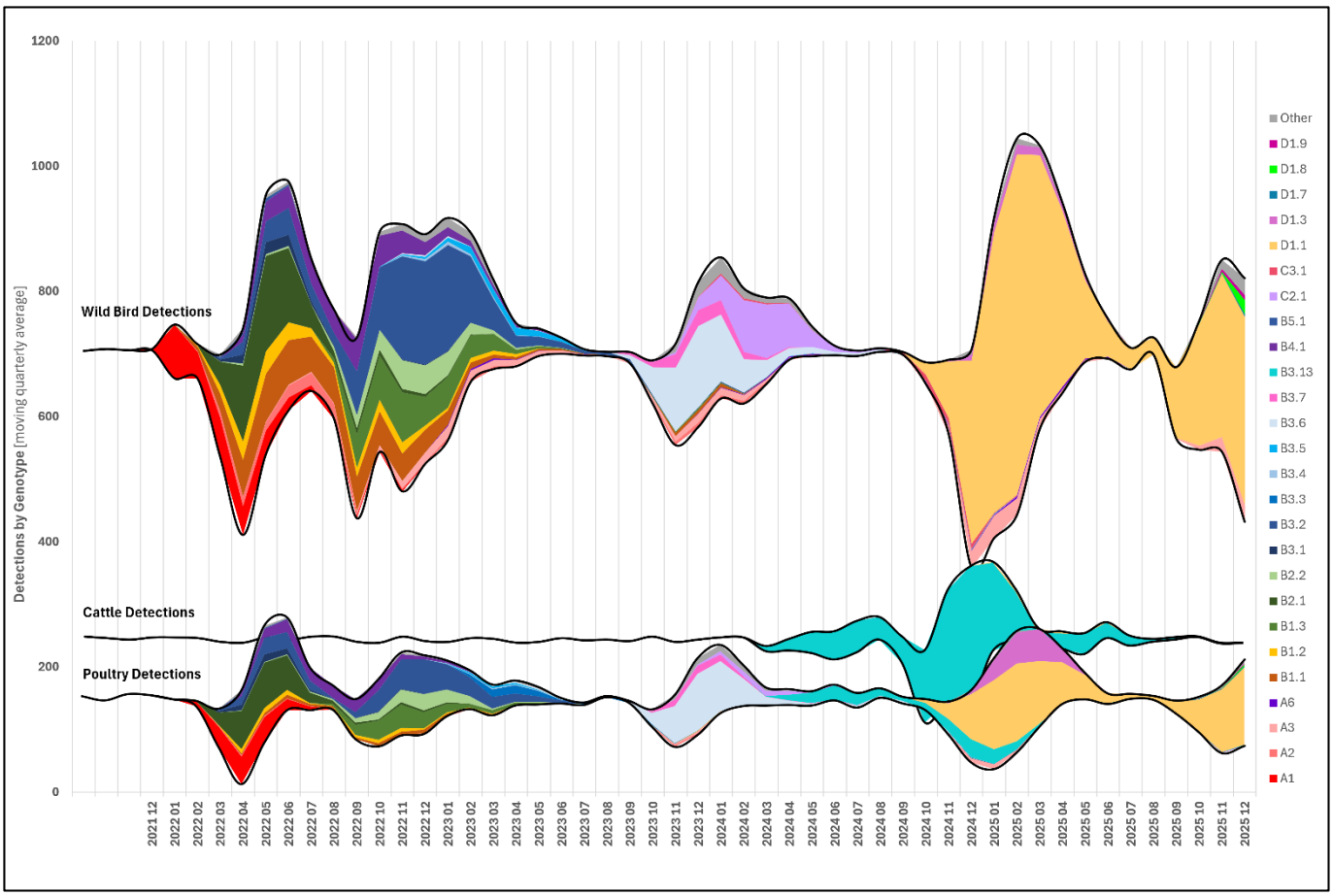

Figure 10. Genotype distribution over time of wild bird (top; n=9392), dairy cattle (middle; n=934), and poultry detections (bottom; n=1980), represented as moving quarterly averages, as of December 31, 2025. Data for poultry and dairy represent a single sequence for each affected premises and where a high-quality sequence was obtained.

SPILLOVER AND TRANSMISSION EVENTS

A. Reporting Period: October 1, 2025, to December 31, 2025

Partnering the phylogenetic analysis with epidemiologic investigation data strengthens the ability to interpret how the virus was introduced and to assess onward spread, where applicable. Phylogenetic analysis provides information on the evolution of the virus over time by comparing changes in the genome via single nucleotide 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 (CSLT) events.

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. During the reporting period, phylogenetic analysis was available for 237 out of 245 detections. A table of introduction type (IND versus CSLT) by month and year is available in **Appendix Table A2**.

Between October and December 2025, there were 126 independent introductions from wildlife sources. This is lower than the number of IND introductions for the same period (October to December) in previous years: 191 in 2022, 183 in 2023, and 135 in 2024. In contrast, the 111 detections attributed to CSLT from October and December 2025 were considerably greater than the 34 detections between October and December in 2022, the 36 detections in 2023, and the 64 detections in 2024; this was largely due to a cluster of cases in Indiana (75 out of 111)

Of the 111 cases of CSLT between October and December 2025, 69 were commercial poultry, 38 backyard poultry, and 4 backyard non-poultry. The 69 commercial poultry can be further divided into 2 live bird market, 21 turkey, 1 table egg, 2 broiler, and 43 duck premises (**Figure 11**). The predominant flock types for CSLT during the reporting period were duck (43 out of 111), backyard poultry (38 out of 111), and turkey (21 out of 111). Turkey was also a predominant flock type impacted by CSLT during October to December in previous years of this event: 2022, 64.7 percent (22 out of 34); 2023, 47.2 percent (17 out of 36); 2024, 32.8 percent (21 out of 64).

During the reporting period, 42 out of 43 CSLT infections in ducks and 31 out of 38 backyard poultry CSLT infections occurred in Indiana.

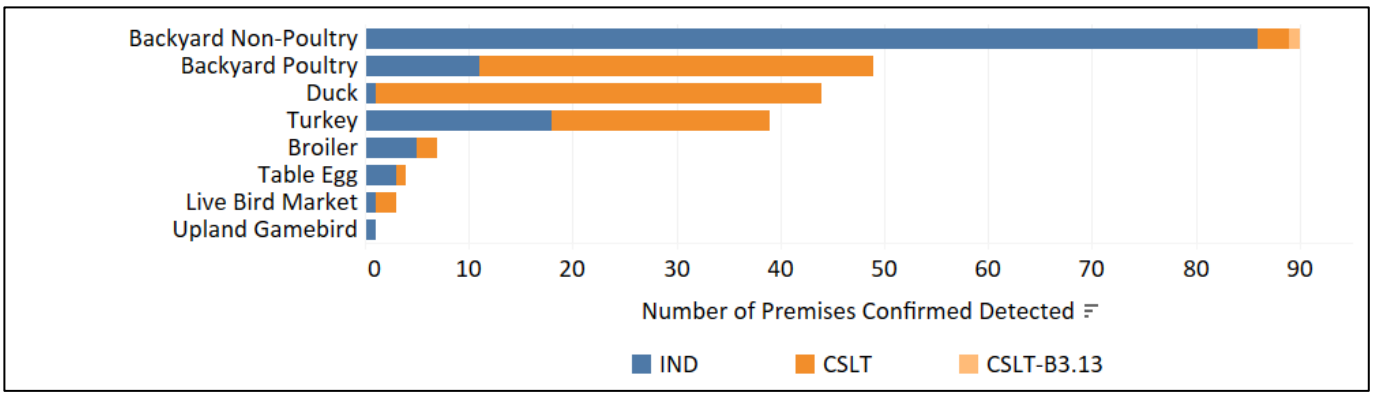

Figure 11. Number of premises confirmed detected between October 2025 and December 2025, by flock type and potential route of introduction. IND, independent introduction. CSLT, common source or lateral transmission.

B. **Entire Event to Date:** February 2022 to December 2025

Over the course of the entire event to date, phylogenetic analysis was available for 1,947 out of 1,985 detections. Overall, 68.2 percent (1,329 out of 1,947) of detections are attributed to independent introductions. The percentage of IND detections split by migratory flyway were as follows: 17.3 percent (230 out of 1,329) in the Atlantic flyway, 31.8 percent (423 out of 1,329) in the Mississippi flyway, 27.3 percent (363 out of 1,329) in the Central flyway, and 23.6 percent (313 out of 1,329) in the Pacific flyway.

The occurrence and frequency of independent introductions increase the risk for subsequent transmission to additional poultry premises (i.e., CSLT). During this event, 31.6 percent (616 out of 1,947) of detections have been attributed to CSLT; however, it is important to note 18.0 percent (111 out of 616) 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. These transmission events predominately occurred between March 2024 and February 2025, with single poultry detections of B3.13 in June 2025, August 2025, and November 2025. With the B3.13 transmission events excluded, 72.4 percent (1,329 out of 1,836) of detections were IND, while 27.5 percent (505 out of 1,836) of detections were CSLT.

Although CSLT reflects a smaller subset of detections in the entire HPAI event overall, the percentage of detections attributed to CSLT has continued to increase over time—15.5 percent in 2022 (110 out of 708), 20.1 percent (67 out of 333) in 2023, 43.3 percent (136 out of 314) in 2024, and 51.2 percent (303 out of 592) in 2025 (**Figure 12; Appendix Table A2**). The increase in CSLT observed in 2024 was largely attributed to the B3.13 genotype, which accounted for 74.2 percent (101 out of 136) of detections. Of the detections attributed to CSLT in 2025, only 3.3 percent (10 out of 303) were B3.13, significantly lower than in 2024. A large percentage of the CSLT detections in 2025, 36.6 percent (111 out of 303), occurred within the October through December 2025 reporting period, and predominately occurred in Indiana.

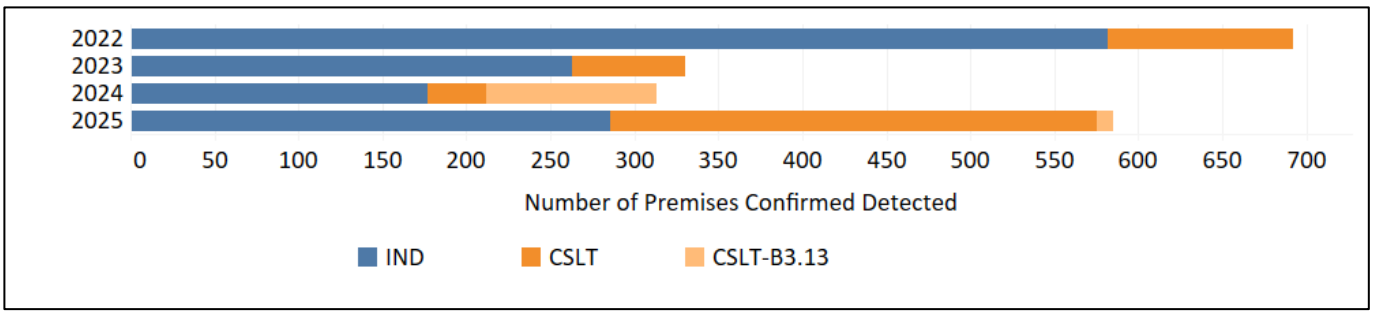

Figure 12. Number of premises confirmed detected over the entire HPAI event, by year and potential route of introduction (IND = independent introduction; CSLT = common source or lateral transmission).

STATE-SPECIFIC HPAI DETECTIONS: OCTOBER 1, 2025, TO DECEMBER 31, 2025

The majority of confirmed detections during the reporting period of October 1, 2025, to December 31, 2025, occurred in Indiana (83 out of 243), followed by Minnesota (18 out of 243), Michigan (12 out of 243), Washington (12 out of 243), and Oregon (10 out of 243). All other confirmed detections during the reporting period occurred in 33 States with fewer than 10 detections each.

Indiana had the largest percentage of infections for a single State during the reporting period, with 34.2 percent (83 out of 243) of confirmed detections. Among these detections, 55.4 percent (46 out of 83) occurred in commercial poultry, which included 44 duck and 2 broiler premises; 42.2 percent (35 out of 83) occurred in backyard poultry; and 2.4 percent (2 out of 83) of detections occurred in backyard non-poultry. The vast majority of detections, 90.4 percent (75 out of 83), were attributed to CSLT of the D1.1 genotype.

Indiana has had a total of 128 confirmed detections since the beginning of the HPAI event. Most of these detections occurred in 2025 (85.9 percent; 110 out of 128), with a higher concentration during the current report period (64.8 percent; 83 out of 128). The detections in Indiana were spatially grouped in 2025, with a large cluster of detections during the reporting period in LaGrange County (66 out of 83 detections) and Elkhart County (13 out of 83 detections) in the northeast region of the State. Impacted premises were in close spatial proximity and frequently shared company and community affiliations. During the spring of 2025, another cluster of detections occurred in the eastern part of the State bordering Ohio, which experienced a concurrent series of detections.

Minnesota and Michigan also each had a greater proportion of detections in turkey premises than other types during the reporting period. Michigan had 66.6 percent (8 out of 12) of detections in commercial poultry, specifically turkey premises, and 33.3 percent (4 out of 12) of detections in backyard non-poultry; 6 of the 8 confirmed detections in turkey premises were attributed to CSLT. Minnesota had 72.2 percent (13 out of 18) of detections in commercial poultry, specifically turkey premises, and 27.8 percent (5 out of 18) of detections occurring in backyard non-poultry; 7 of the 13 confirmed detections in turkey premises were attributed to CSLT.

Detections in Washington during the reporting period consisted of mostly backyard non-poultry (9 out of 12), with other detections in backyard poultry (2 out of 12) and commercial poultry (1 out of 12). This remains consistent with detections in Washington over the course of the entire event, with 54 out of 67 detections in backyard non-poultry, 9 out of 67 detections in backyard poultry, and 4 out of 67 detections in commercial poultry. All the commercial poultry detections in Washington have occurred on table egg premises.

All detections in Oregon during the reporting period (10 out of 10) were backyard non-poultry detections. This remained consistent with Oregon detections over the course of the entire event, with the majority of confirmed detections (48 out of 59) in backyard non-poultry, with other detections occurring in backyard poultry (8 out of 59) and commercial poultry (3 out of 59), which can be further broken down into 1 table egg and 2 broiler premises.

APPENDIX A

Table A1. Number of confirmed detections between October 1, 2025, and December 31, 2025, by flock type, commercial species, and production type.

Flock Type	Species	Production Type	Confirmed Detections
Backyard Non-Poultry		WOAH Non-Poultry	91
Backyard Poultry		WOAH Poultry	53
Commercial Poultry	Broiler	Commercial Broiler Breeder	1
		Commercial Broiler Breeder Pullets	1
		Commercial Broiler Production	5
	Duck	Commercial Duck Breeder	14
		Commercial Duck Meat Bird	32
	Live Bird Market	Live Bird Market	3
	Table Egg	Commercial Table Egg Layer	3
		Commercial Table Egg Pullets	1
	Turkey	Commercial Breeder Operation	1
		Commercial Turkey Breeder Hens	6
		Commercial Turkey Breeder Replacement Hens	2
		Commercial Turkey Meat Bird	31
	Upland Gamebird	Commercial Raised for Release Upland Game Bird	1

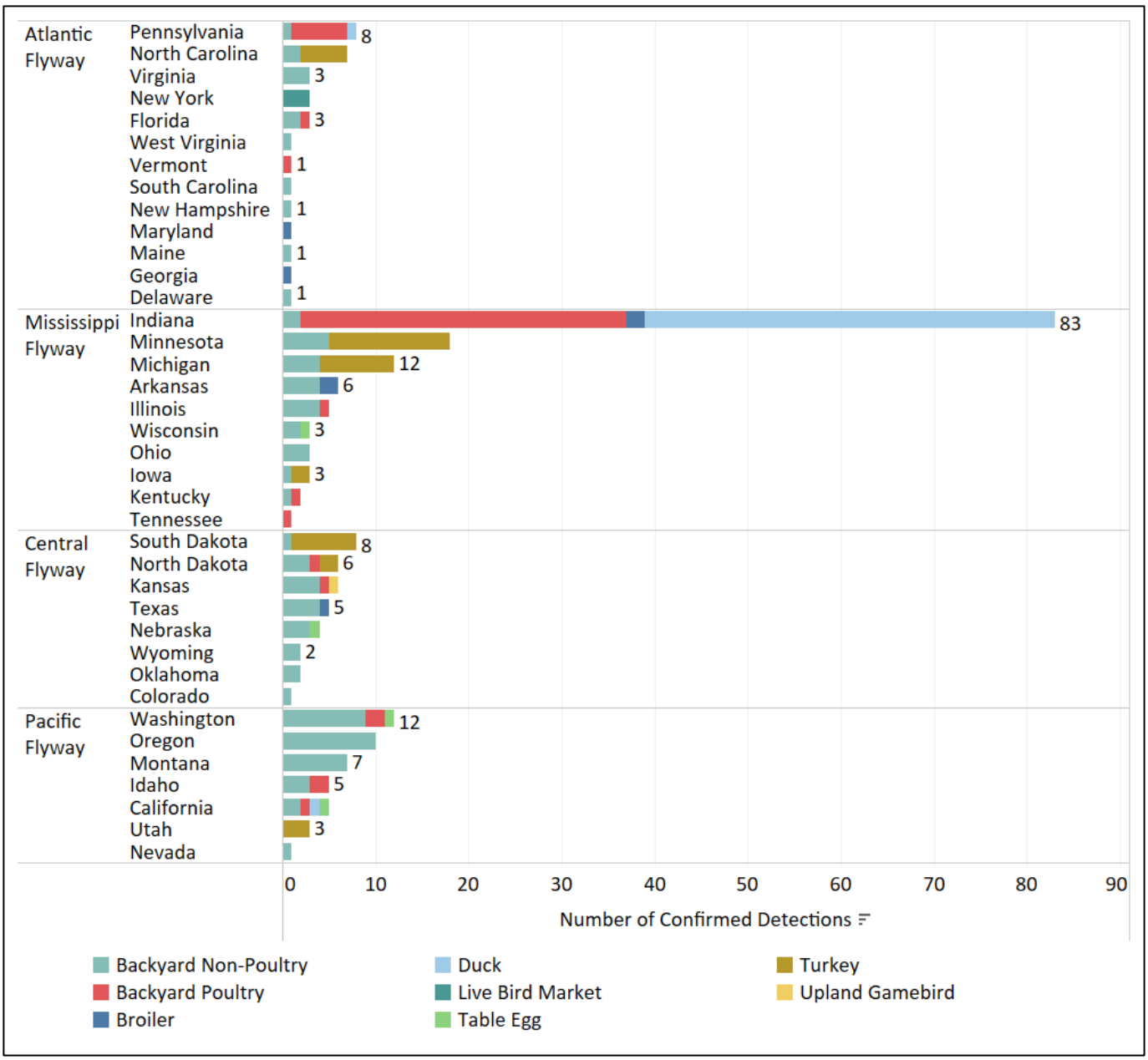

Figure A1. Numbers of confirmed detections between October 1, 2025, and December 31, 2025, by flyway, State, and flock type.

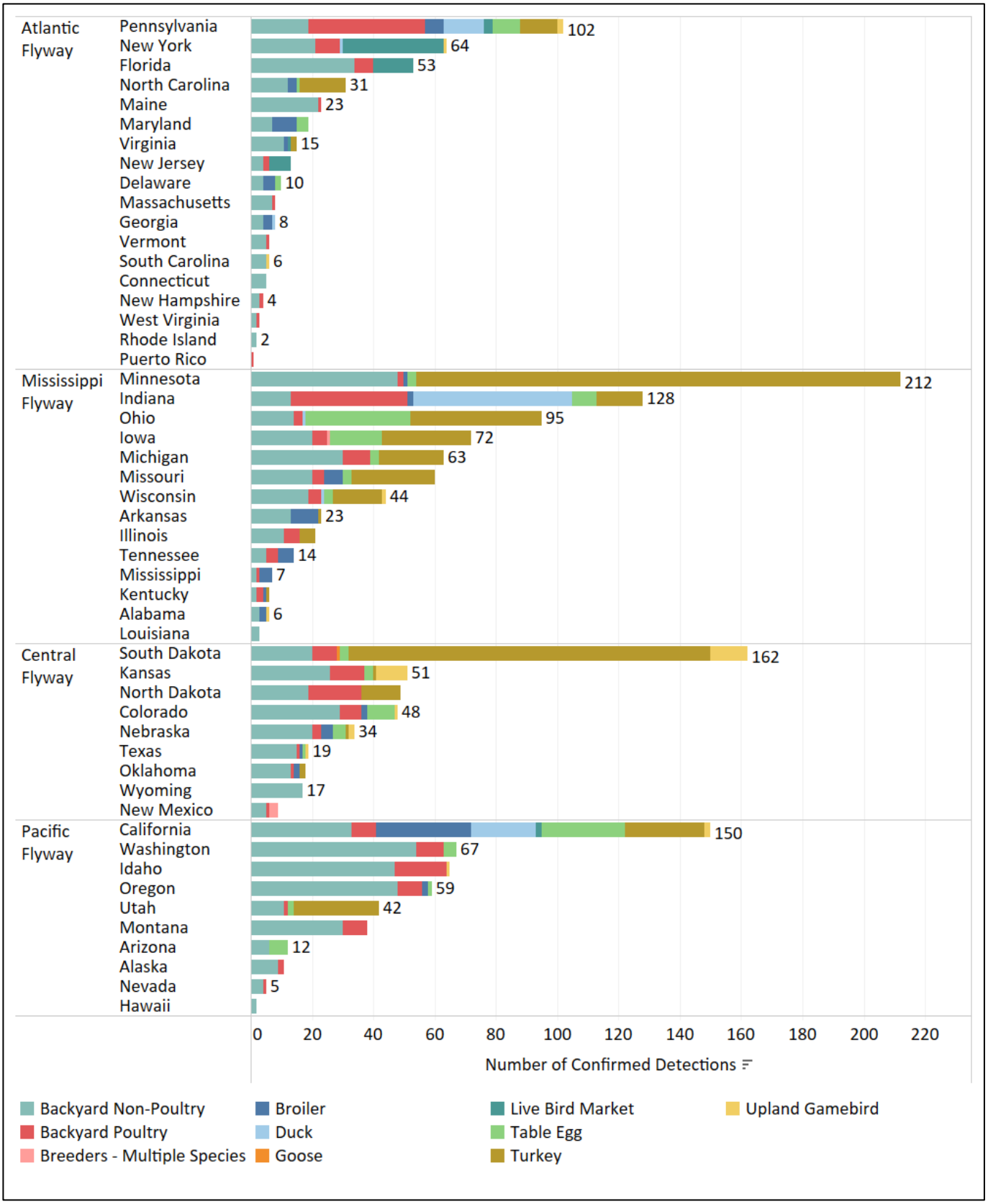

Figure A2. Numbers of confirmed detections by migratory flyway, State, and flock type between February 8, 2022, and December 31, 2025.

Table A2. Number of confirmed detections by year, month, and source of introduction. Color intensity reflects the relative number of detections attributed to each source of introduction by month for each year of the outbreak.

		Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
	CSLT		2	4	35	13	3	1	4	14	12	12	10
2022	IND		13	82	129	74	19	19	16	55	79	60	52
	Total		15	86	164	87	22	20	20	69	91	72	62
	CSLT	2	7	17	3	0	0	2	1	0	4	10	22
2023	IND	25	24	17	11	4	0	0	0	1	40	87	56
	Total	27	31	34	14	4	0	2	1	1	44	97	78
	CSLT	12	5	2	13	14	12	11	1	2	9	24	31
2024	IND	14	16	6	2	3	0	0	1	1	7	38	90
	Total	26	21	8	15	17	12	11	2	3	16	62	121
	CSLT	70	69	30	8	5	3	0	1	7	27	61	23
2025	IND	61	40	20	9	7	0	1	2	22	38	32	56
	Total	131	109	50	17	12	3	1	3	29	65	93	79

CSLT: Common Source Exposure or Lateral Transmission Events
IND: Independent Introduction of Wildlife-Origin Virus (e.g., spillover event)