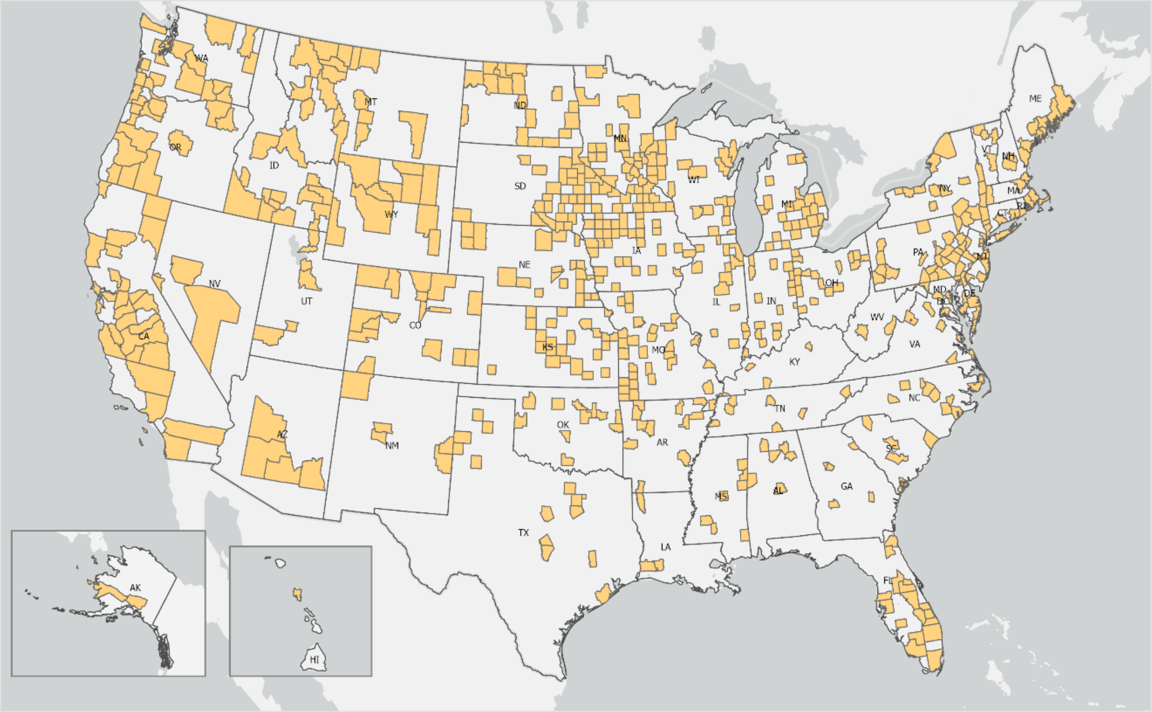
USDA Animal and Plant Health Inspection Service
U.S. DEPARTMENT OF AGRICULTURE

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



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For more information, contact:

Sarah Blasko
Acting Director, Center for Epidemiology and Animal Health
USDA–APHIS–Veterinary Services
Email: vs.ceah@usda.gov
Web: https://www.aphis.usda.gov/livestock-poultry-disease/epidemiology

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2150 Centre Avenue
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Email: vs.ceah@usda.gov
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ITEMS OF NOTE

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

- As of September 30, 2025, the 2022 HPAI event has impacted all 50 States and the territory of Puerto Rico, with a total of 1,741 premises infected and over 179 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 September 30, 2025, wild bird surveillance has resulted in 15,542 detections of H5Nx HPAI in at least 193 species of wild birds, with 7,469 detections in apparently healthy birds and 8,073 detections in sick or dead birds.
- Over the entire HPAI event, 70.4 percent (1,203 out of 1,710) of detections are attributed to independent wild bird introductions and 29.5 percent (505 out of 1,710) 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, 43.3 percent (136 out of 314) in 2024, and for the first nine months of 2025, 54.1 percent (192 out of 355).
- The increase in CSLT observed in 2024 is largely attributed to the B3.13 genotype, which was an initial spillover event into dairy cattle with subsequent transmission between dairy premises, and multiple transmission events into poultry premises, with subsequent poultry-to-poultry transmission.
- Between January 20, 2025, and September 30, 2025, the USDA biosecurity audit and assessment programs completed audits on 608 premises.

B. Reporting Period: July 1, 2025, to September 30, 2025

- During the current reporting period, the event has impacted 13 States and affected 33 premises and approximately 4 million birds.
- Monthly cases were the highest in September 2025 with 29 detections; only 4 detections occurred in July and August 2025.
- Genotype D1.1 continues to predominate in both wildlife and domestic poultry during the current reporting period.
- The reporting period has been defined by independent wild bird introductions into previously affected commercial turkey operations in North Dakota, Minnesota, and South Dakota.
- 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 September 2025

An event of highly pathogenic avian influenza (HPAI) in poultry in the United States has been ongoing since February 2022. As of September 30, 2025, the National Veterinary Services Laboratories (NVSL; National Centers for Animal Health, Ames, Iowa) have confirmed Eurasian clade 2.3.4.4b H5NX HPAI in 1,741 premises across all 50 States and Puerto Rico. The production types affected include 687 backyard[1] non-poultry,[2] 187 WOAH poultry[3] [backyard], and 866 WOAH poultry [commercial],[4] which can further be divided into 56 live bird markets (LBM), 494 turkey, 143 table egg, 90 broiler, 44 duck, 34 upland gamebird, 4 commercial breeders–multiple bird species premises, and 1 goose premises. Over 179 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 epidemiologic curve in **Figure 1** 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 production type is available in Appendix A (**Figure A1**).

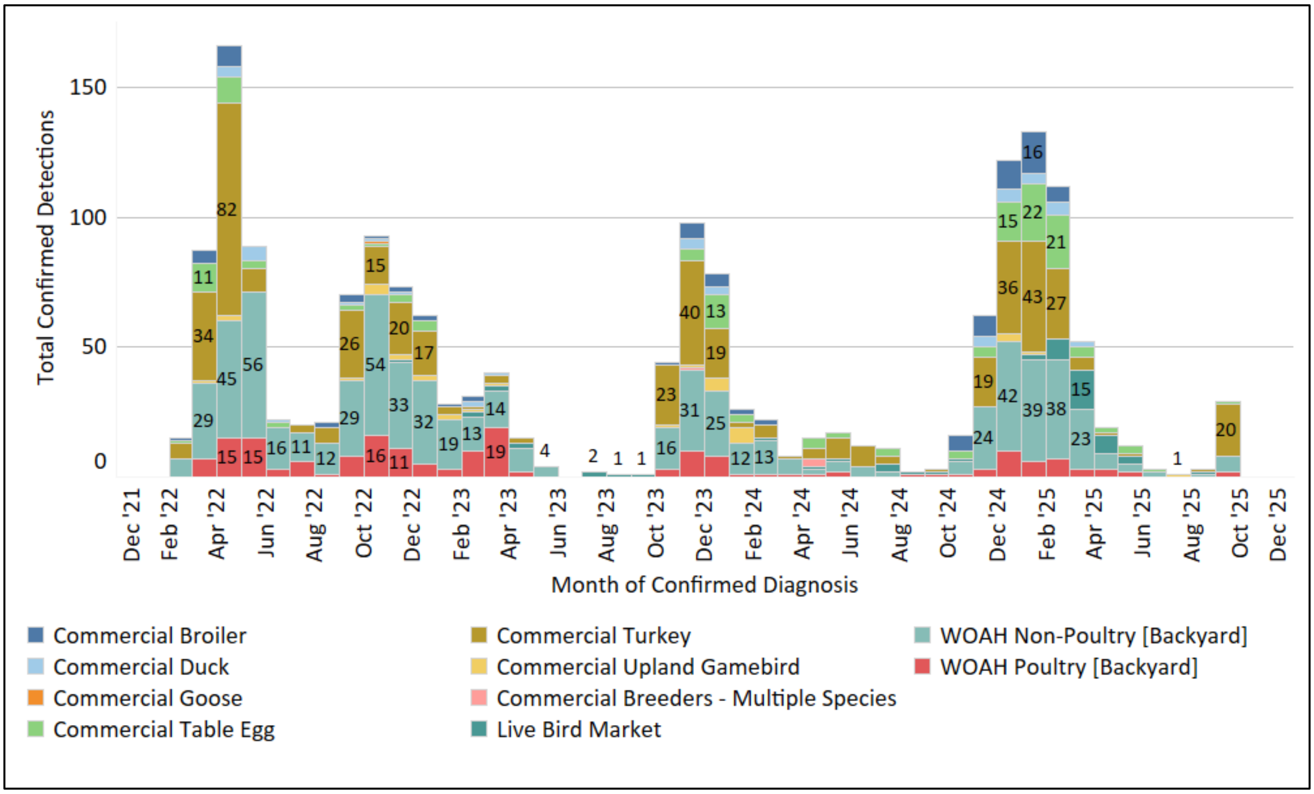

Figure 1. Monthly HPAI-confirmed detections by premises and type, as of September 30, 2025.

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[1] Premises with the [backyard] designation are those that do not meet the 9 C.F.R. 56.3(b)(1)(ii) definition for [commercial].

[2] Premises designated as WOAH non-poultry are those that do not meet the WOAH definition for poultry.

[3] WOAH poultry are defined 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."

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

B. **Reporting Period:** July 1, 2025, to September 30, 2025

During the current reporting period, a total of 33 detections occurred among 13 out of 50 States and Puerto Rico. NVSL-confirmed premises include 7 WOAH non-poultry [backyard], 2 WOAH poultry [backyard], and 24 WOAH poultry [commercial], which can be further divided into 1 LBM, 21 turkey, 1 table egg, and 1 upland gamebird premises (**Figure 2**). Approximately 5 million birds have been affected, a greater number when compared to the same month span in 2023 and 2024. Reporting period detections by flyway, State, and production type are depicted in **Figure A2**. The majority of confirmed detections occurred in South Dakota (11 out of 33) and Minnesota (8 out of 33), followed by North Dakota (3 out of 33) and Montana (2 out of 33). All other confirmed detections during the reporting period were single detections within the remaining nine States.

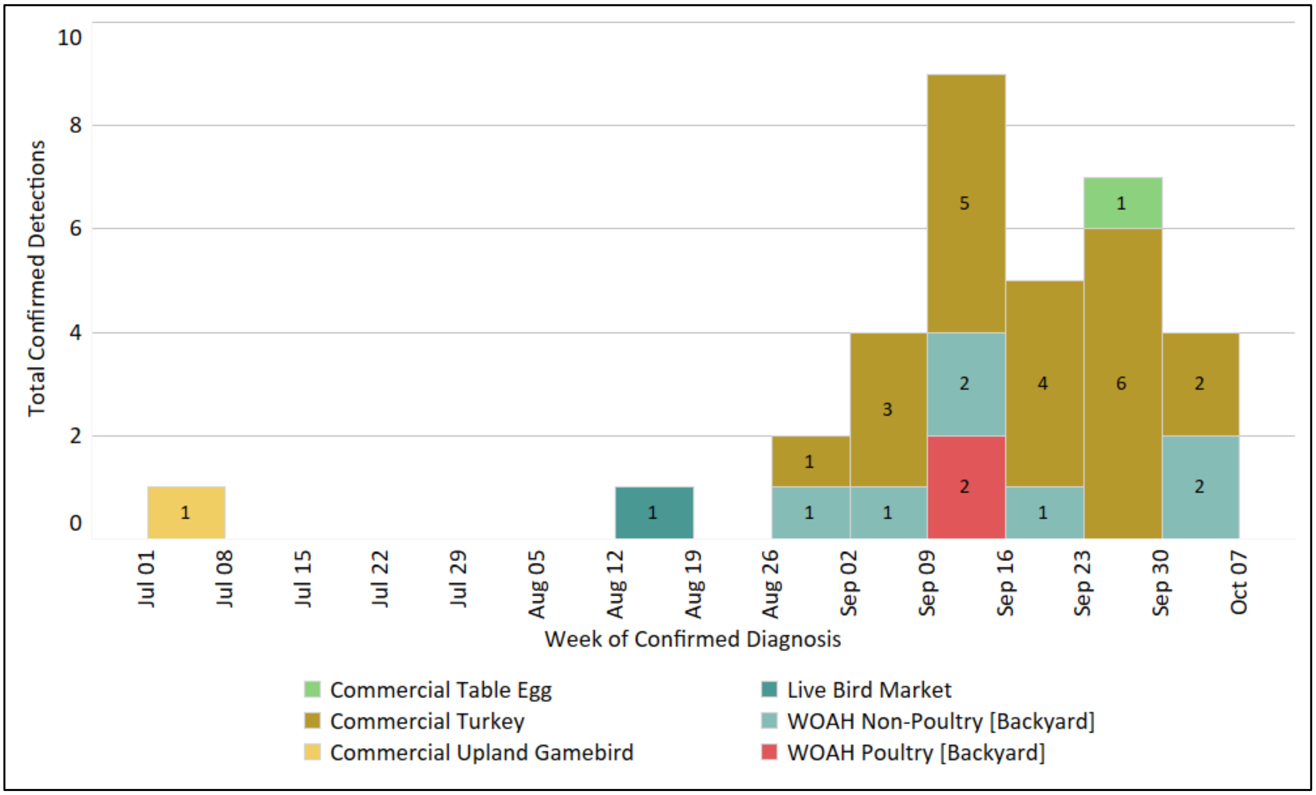


Figure 2. Weekly HPAI detections by premises type, from July 1, 2025, to September 30, 2025.

The current reporting period encompasses 6.8 percent of the entire event (3 out of 44 months). Detections during this period account for 4.25 percent (21 out of 494) of commercial turkey detections, 0.7 percent (1 out of 143) of commercial table egg detections, 1.8 percent (1 out of 56) of LBM detections, and 2.9 percent (1 out of 34) of all commercial upland gamebird detections since the beginning of the HPAI 2022 event (**Figure 3**).

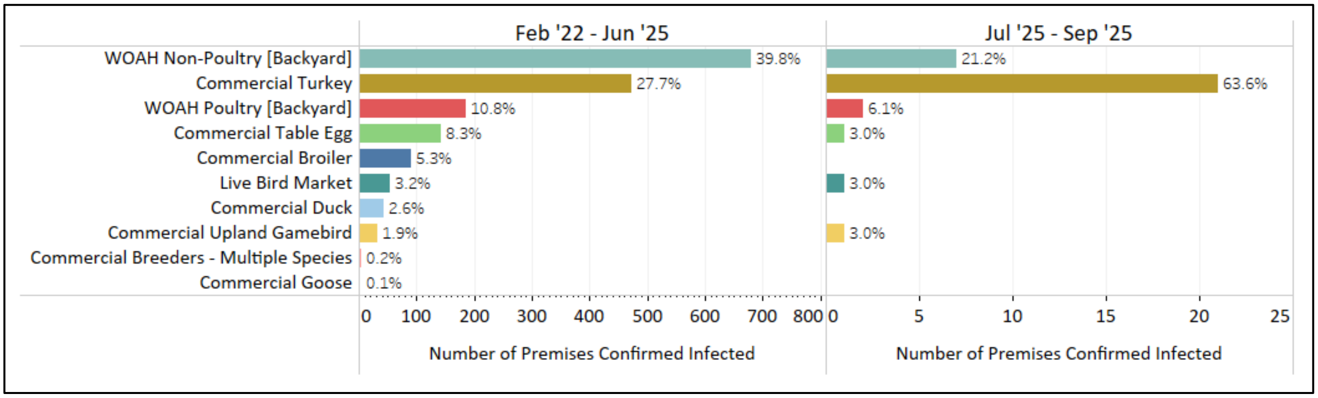


Figure 3. Number and relative percentage of confirmed infections by reportable production type and reporting period.

When comparing temporal monthly trends by the event year, the total number of confirmed infections in July and August 2025 were similar to trends observed in all years of the outbreak, with a reduction in cases over the summer months. September 2025 most closely mirrored the first year of the event, with an increase in cases starting earlier than in 2023 and 2024. However, the number of cases in September was less in 2025 than in 2022 (**Figure 4**).

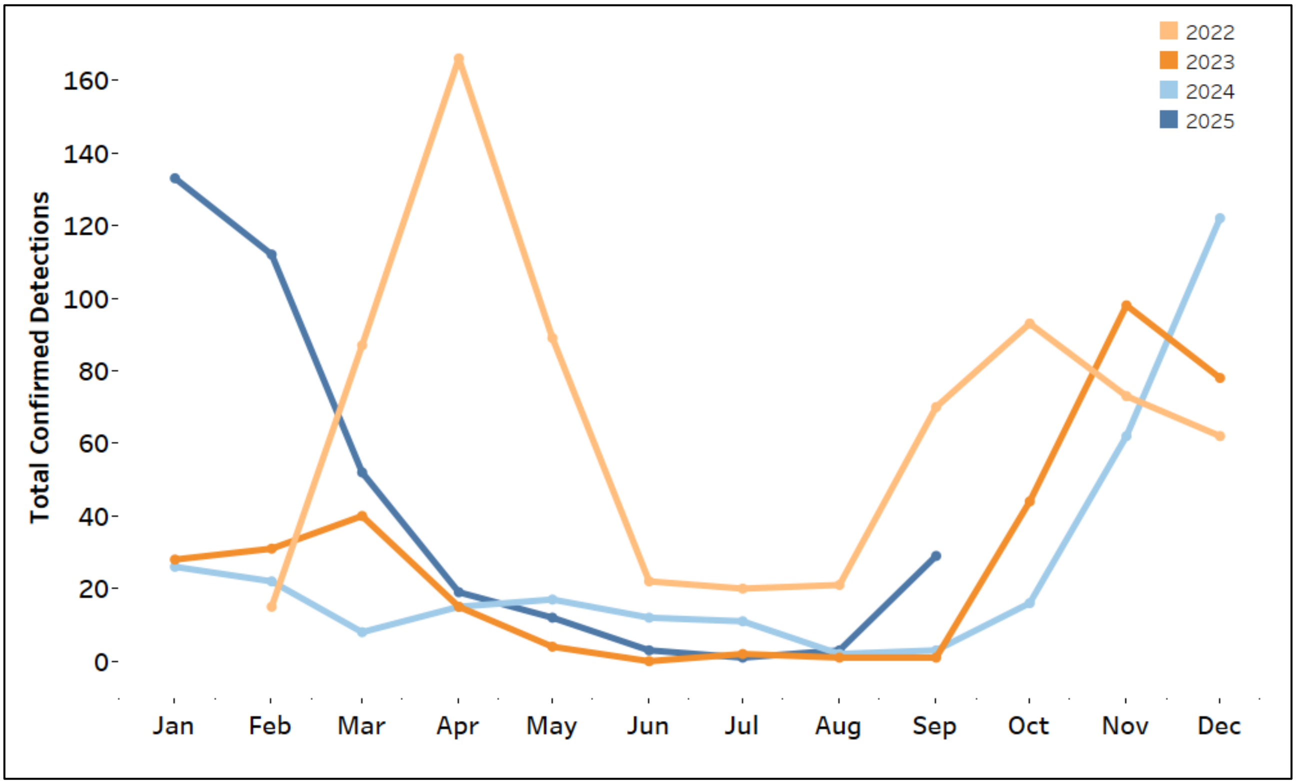


Figure 4. Epidemiologic curves of infected premises count by month of confirmed diagnosis date, as of September 30, 2025.

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 September 30, 2025, wild bird surveillance has resulted in 15,542 detections of H5Nx HPAI in at least 193 species of wild birds across all four North American flyways (7,469 detections in apparently healthy birds; 8,073 detections in sick or dead birds; **Figure 5**).

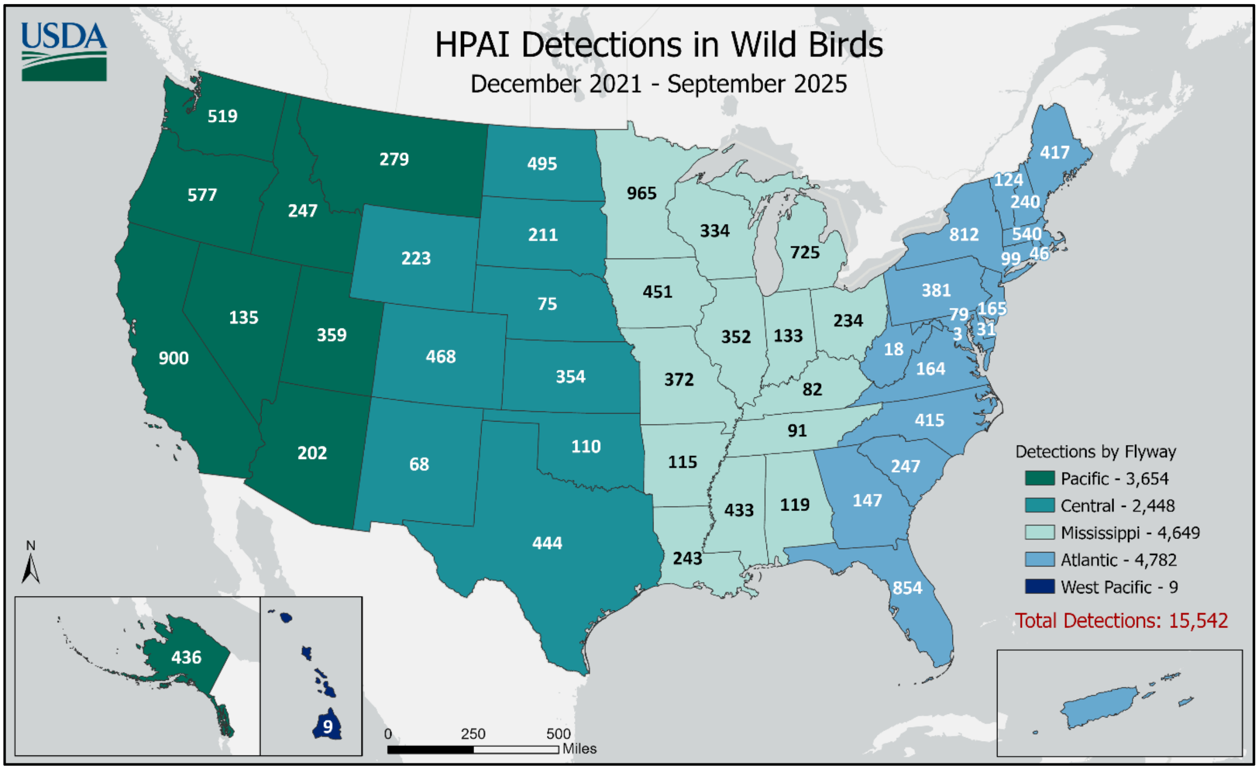


Figure 5. Number of HPAI detections in wild bird samples collected between December 30, 2021, and September 30, 2025. State totals include detections from both apparently healthy birds from active surveillance efforts and sick or dead birds from morbidity/mortality investigations.

Prevalence of H5Nx HPAI (i.e., the proportion of sampled individual birds testing positive for H5Nx HPAI) among apparently healthy wild birds varies 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 September 2025 was higher than the previous 2 years but comparable to September 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 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**).

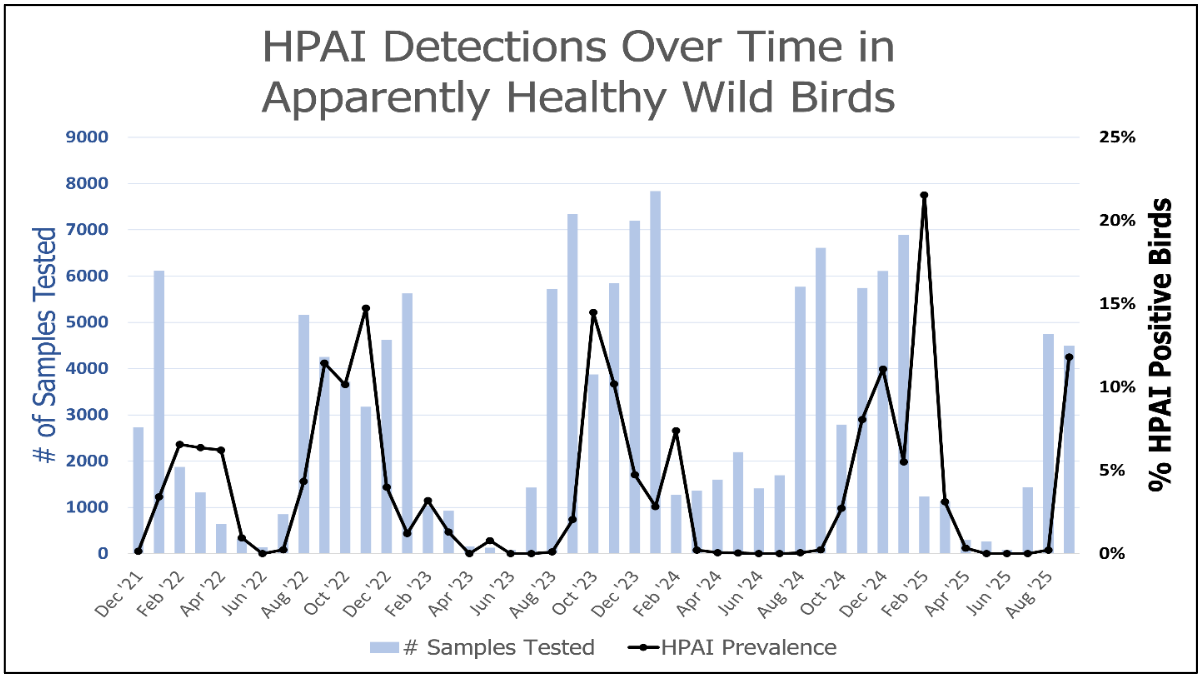


Figure 6. Monthly sampling effort (number collected; blue bars) and H5Nx HPAI prevalence (percentage of samples found to be H5Nx HPAI-positive; black line) in apparently healthy wild birds as part of the U.S. National Surveillance Plan for Highly Pathogenic Avian Influenza.

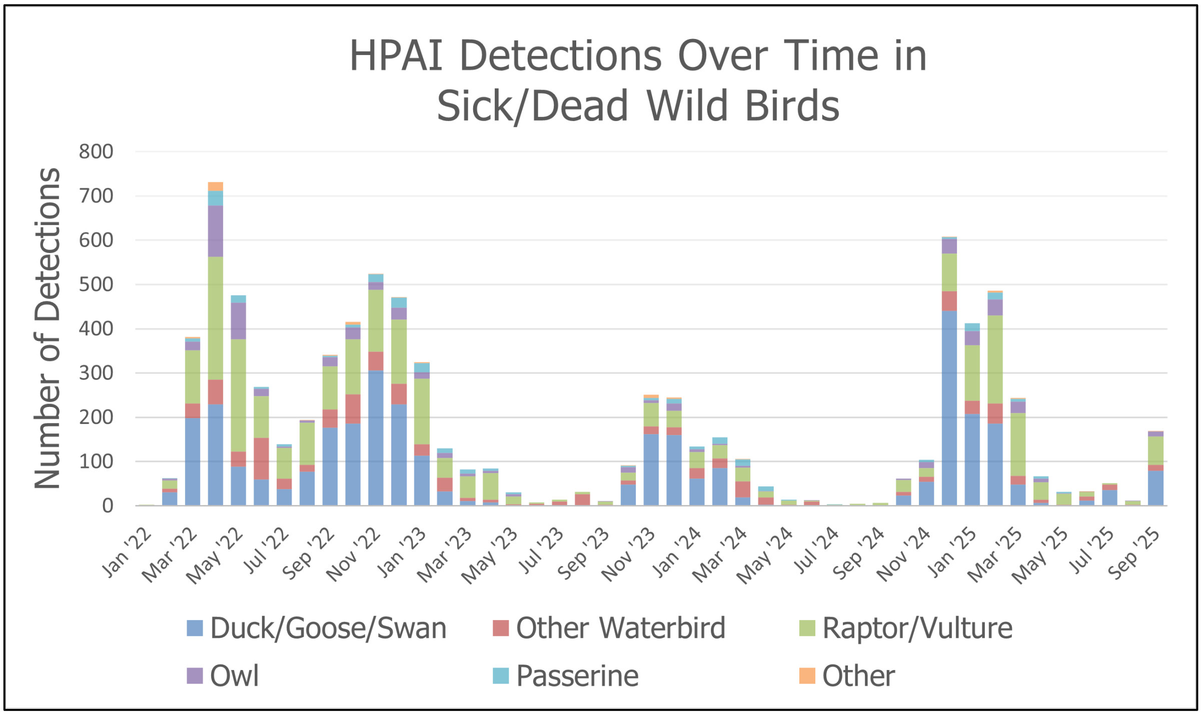


Figure 7. Stacked bar graph of the number of H5Nx HPAI detections in sick or dead wild birds sampled between December 30, 2021, and September 30, 2025. Different colors represent different functional groups of wild birds.

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 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 September 30, 2025, 11,539 samples were collected from 71 affected farms in 18 States, resulting in 437 detections of HPAI (**Figure 8**). The number of HPAI detections varied widely across farms, ranging from zero detections (n = 36 farms) to >30 detections (n = 4 farms). Investigations into the factors driving differences from farm to farm are ongoing.

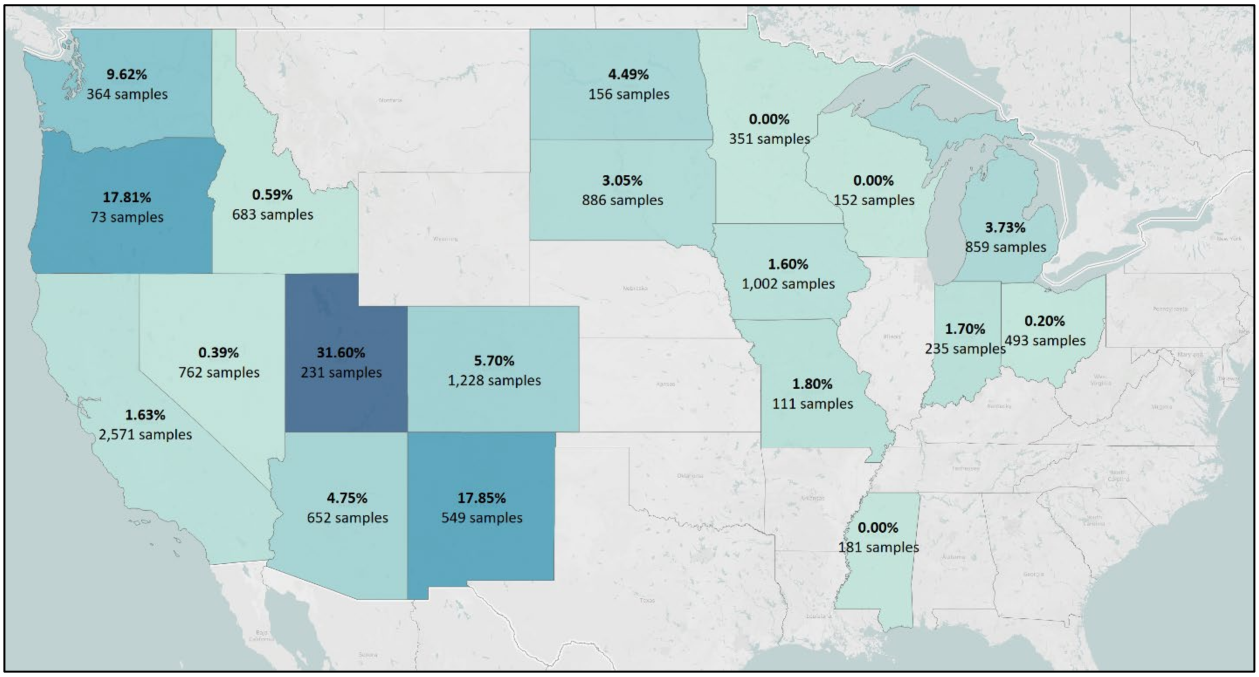


Figure 8. Peri-domestic wildlife surveillance efforts for HPAI from April 1, 2024, to September 30, 2025. Sampling of both wild birds and mammals occurred on HPAI-affected dairy and poultry farms in the States, shown in blue. Darker colored states indicate higher apparent prevalence of HPAI in the wildlife 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 September 30, 2025, there have been 652 HPAI detections in at least 45 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.

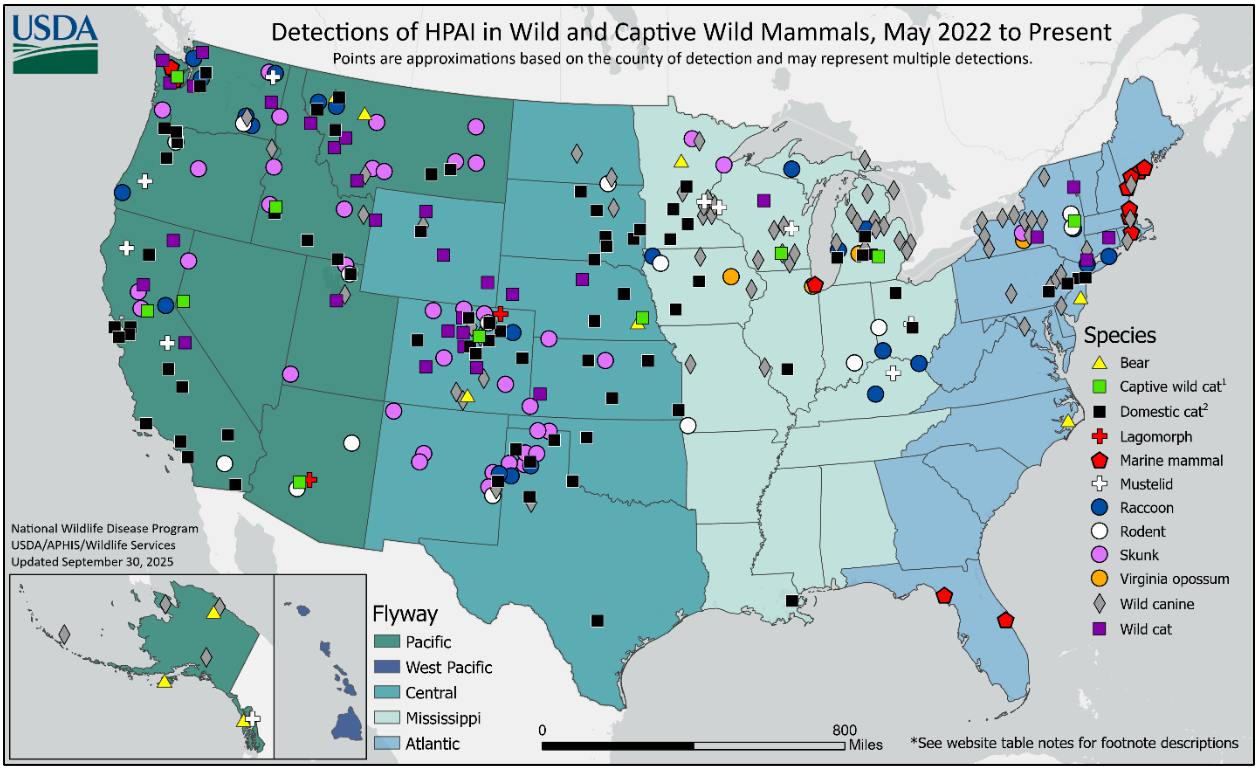


Figure 9. Detections of HPAI virus in wild mammals and captive wild mammals in the United States as of September 30, 2025. The map shows detections in both sick/dead mammals, as well as apparently healthy mammals collected on HPAI-infected farms as part of peri-domestic wildlife surveillance efforts.

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, and 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.

The distribution of genotypes affecting poultry, as well as spillovers into other species, typically mirrors contemporary virus found in the wild migratory bird flyways (**Figure 10**). During early 2025, there were two new spillovers into dairy cattle in Nevada (confirmed in January 2025) and Arizona (confirmed in February 2025). These two genotype D1.1 dairy events are each distinct spillovers that have since resolved, are unrelated to the ongoing genotype B3.13 event in dairy cattle identified in March 2024 and had limited transmission and did not cross State lines. Following an initial spillover event of genotype B3.13 from wildlife to dairy cattle in late fall 2023, subsequent dairy-to-poultry spillover was established as a new route of virus introduction into poultry. 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 peri-domestic avian and mammalian species on and near affected dairies have been reported in addition to detections in peri-domestic species sampled on B3.13-affected premises by Wildlife Services. Genotype B3.13 was detected in a single LBM premises in California during this reporting period.

Genotype D1.1 continues to predominate in wildlife and in 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. The D1 genotype continues to evolve with new genotypes (D1.5 and D1.6 [AM N2]) identified during this reporting period.

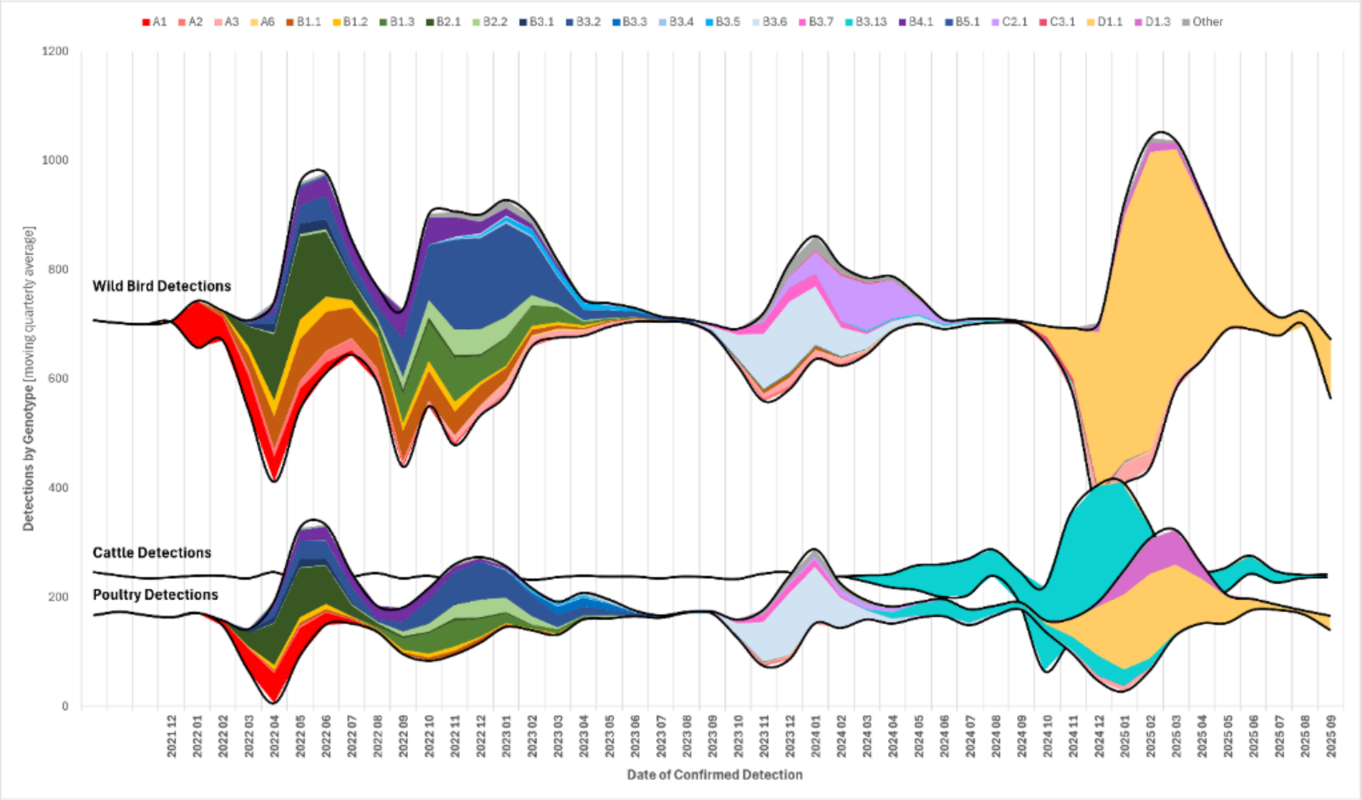


Figure 10. Genotype distribution over time of wild bird (top; n = 8209), dairy cattle (middle; n = 932), and poultry detections (bottom; n = 1731), represented as moving quarterly averages normalized to detections in each animal category, as of September 30, 2025. Data for poultry and dairy represent a single sequence for each affected premises.

SPILLOVER AND TRANSMISSION EVENTS

A. **Entire Event to Date:** February 2022 to September 2025

Partnering the phylogenetic analysis with epidemiologic 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; i.e., 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 1,710 out of 1,740 detections.

Overall, 70.4 percent (1,203 out of 1,710) of detections are attributed to independent wild bird introductions. The percentage of IND detections by migratory flyway were as follows: 17.6 percent (212 out of 1,203) in the Atlantic flyway, 31.7 percent (381 out of 1,203) in the Mississippi flyway, 27.4 percent (330 out of 1,203) in the Central flyway, and 23.3 percent (280 out of 1,203) in the Pacific flyway.

The occurrence and frequency of independent wild bird introductions increase the risk for subsequent transmission to additional poultry premises (i.e., common source or lateral transmission). Overall, 29.5 percent (505 out of 1,710) of detections have been attributed to common source or lateral transmission; however, it is important to note that 21.8 percent (110 out of 505) 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 both June 2025 and August 2025. With the B3.13 transmission events excluded, 75.2 percent (1,203 out of 1,600) of detections were IND, and 24.7 percent (395 out of 1,600) 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 current HPAI event—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 for the first nine months of 2025, 54.1 percent (192 out of 355) (**Figure 11; Table A1**). 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; 4.7 percent (9 out of 192) of CSLT detections in 2025 were B3.13. Although 2025 had an overall increase in the number of cases attributed to CSLT, only 4.2 percent (8 out of 192) of CSLT cases occurred within the July through September 2025 reporting period.

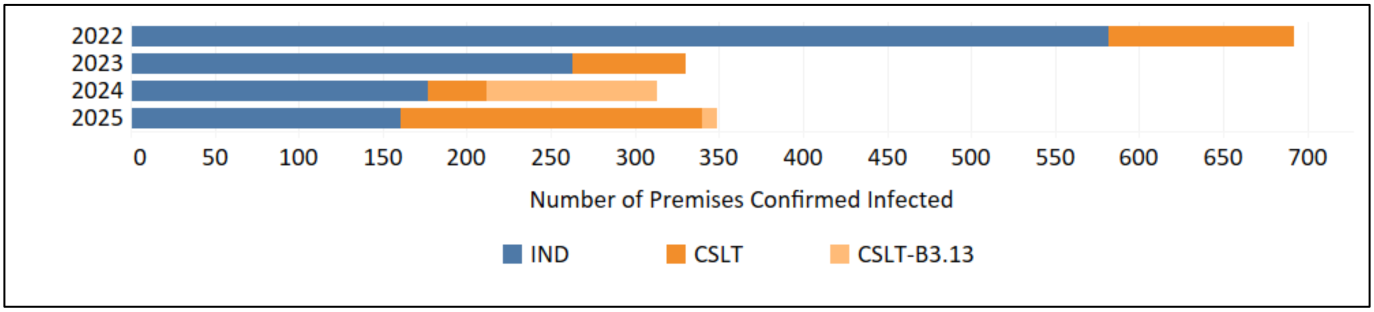


Figure 11. Number of poultry premises confirmed infected over the total HPAI event separated by year and potential route of introduction.

B. **Reporting Period**: July 1, 2025, to September 30, 2025

Between July and September 2025, there were 25 independent wild bird introductions; this is lower than the 90 cases during the same time period in 2022, but higher than the 1 case in 2023 and 2 cases in 2024. The 25 detections were spread across migratory flyways as follows: 20.0 percent (5 out of 25) in the Atlantic flyway, 16.0 percent (4 out of 25) in the Mississippi flyway, 56.0 percent (14 out of 25) in the Central flyway, and 8.0 percent (2 out of 25) in the Pacific flyway.

Independent wild bird introductions occurred in 7 WOAH non-poultry [backyard], 2 WOAH poultry [backyard], and 16 WOAH poultry [commercial] premises, which can be further divided into 14 turkey, 1 table egg, and 1 upland gamebird premises. The current reporting period saw an increase in all production types compared to 2023 and 2024 and a relative increase in the number of commercial IND detections (64 percent; 16 out of 25) compared to 2022, where only 32 percent (30 out of 93) were commercial farms. During the months of July, August, and September 2022, independent wild bird introductions occurred in 47 WOAH non-poultry [backyard], 15 WOAH poultry [backyard], and 28 WOAH poultry [commercial] premises, which can be further divided into 24 turkey, 2 table egg, 1 upland gamebird, and 1 duck premises. Independent wild bird introductions in 2023 consisted of two WOAH poultry [commercial] premises, specifically two LBM premises, while independent introductions in 2024 consisted of one WOAH poultry [backyard] premises.

During the reporting period, CSLT introductions mostly occurred among commercial turkey (7 out of 8) operations. Minnesota accounted for six of the seven detections, while the other detection occurred in Utah. The remaining CSLT introduction occurred in a California LBM and is associated with the B3.13 genotype (**Figure 12**).

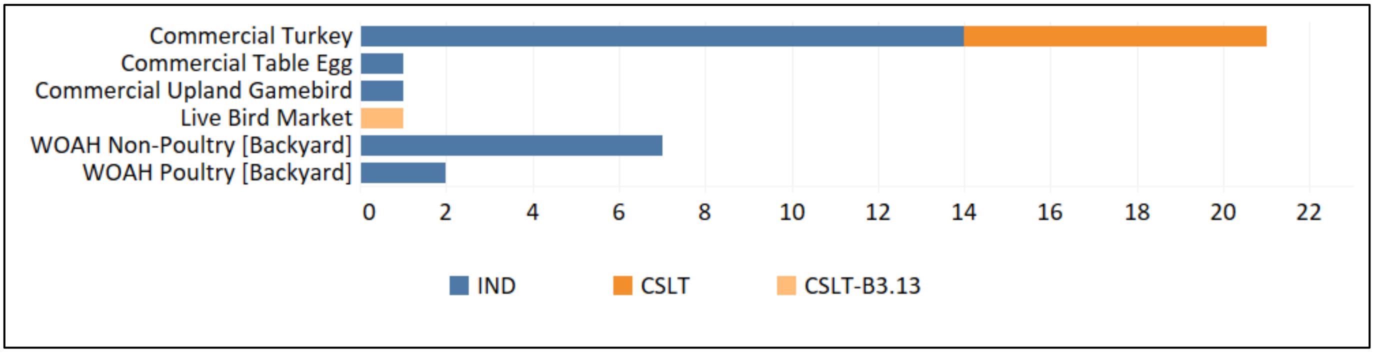


Figure 12. Number of poultry premises confirmed infected between July 2025 and September 2025, separated by production type and potential route of introduction.

DETECTIONS AMONG PREVIOUSLY AFFECTED PREMISES

A. **Entire Event to Date:** February 2022 to September 2025

There have been 1,740 confirmed detections, with 149 occurrences of virus reintroduction into previously infected premises. Virus reintroduction is the infection of a premises previously infected with a different virus strain. These reintroductions occurred on 102 premises spread across 18 States; 32 premises had more than 2 confirmed detections of HPAI. The majority of virus reintroductions have occurred in South Dakota (49 percent; 73 out of 149) and Minnesota (18.1 percent; 27 out of 149). The relative differences in the number of confirmed detections and unique premises per State in **Figure 13** reflect the number of premises with viral reintroductions. The viral reintroductions have predominately occurred on WOAH poultry [commercial] premises, which included turkey (73.2 percent; 109 out of 149) and table egg (12.8 percent; 19 out of 149) premises (**Figure 14**). Examining potential sources of introduction, 68.9 percent (104 out of 149) of reintroductions are associated with IND, while 27.8 percent (42 out of 149) were CSLT; phylogenetic data was not available for 2 percent (3 out of 149) of reintroductions.

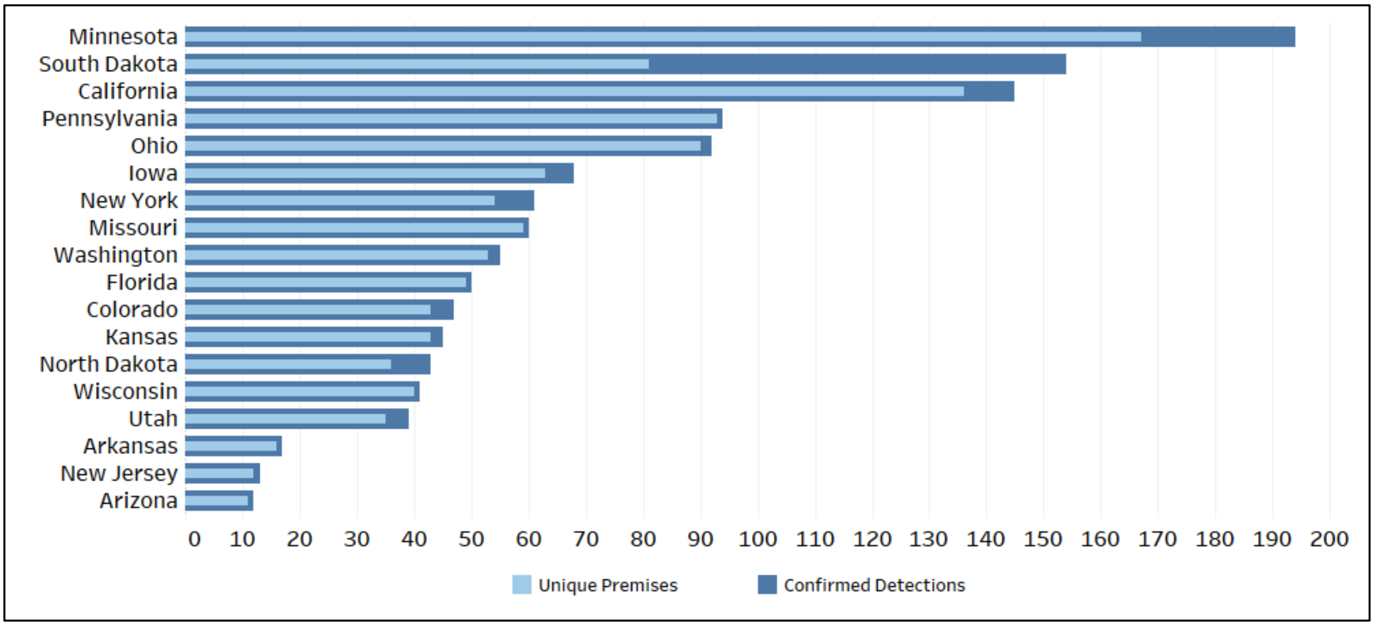


Figure 13. Bar graph displaying the overall numbers of NVSL-confirmed HPAI detections and unique premises infected for States with HPAI viral reintroductions during the entire outbreak.

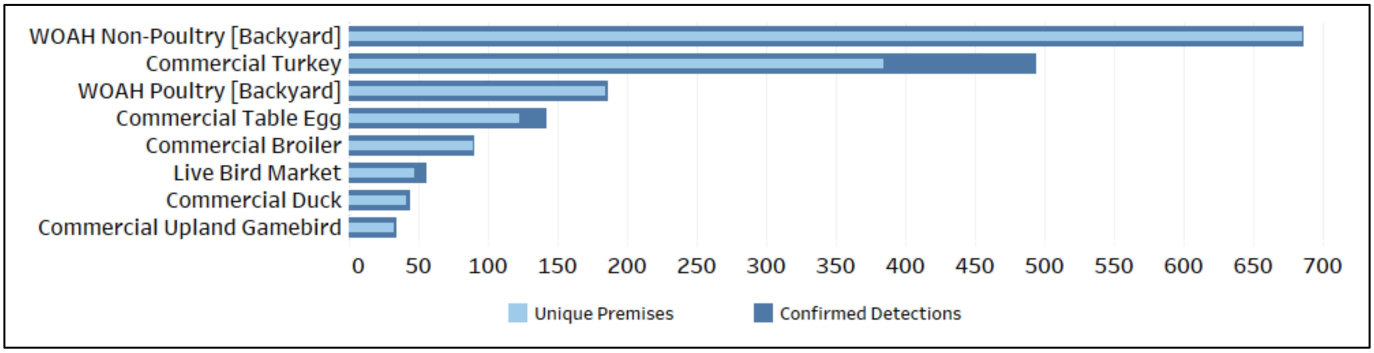


Figure 14. Bar graph displaying the overall numbers of NVSL-confirmed HPAI detections and unique premises infected by production type during the entire outbreak.

B. **Reporting Period:** July 1, 2025, to September 30, 2025

During the current reporting period, 20 of the 33 confirmed detections reflect virus reintroductions into previously infected premises. The reintroductions occurred in 11 premises in South Dakota, 6 premises in Minnesota, 2 premises in North Dakota, and 1 premises in Wisconsin. These reintroductions occurred among 1 WOAH poultry [backyard] and 19 WOAH poultry [commercial] premises, which included 18 turkey and 1 table egg premises. Among these 20 reintroductions, 75 percent (15 out of 20) detections were attributed to IND introductions; the remaining 5 detections were CSLT introductions among WOAH poultry [commercial] turkey premises in Minnesota. Since the outbreak began, these 20 premises have been infected a total of 64 times (**Figure 15**), with 55 out of the 64 detections attributed to independent wild bird introduction. The remaining nine CSLT detections occurred among WOAH poultry [commercial] turkey premises in Minnesota.

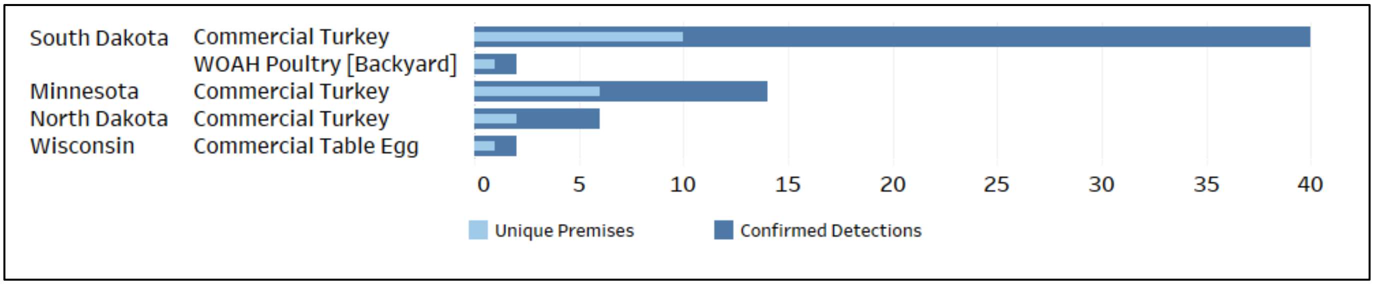


Figure 15. Bar graph displaying the overall numbers of NVSL-confirmed HPAI detections and unique premises infected by State and production type for States with reintroductions during the reporting period.

North Dakota and South Dakota

Given the repeated infections, Veterinary Services epidemiologists conducted an epidemiologic investigation at the request of South Dakota and North Dakota Area Veterinarians in Charge and State Animal Health Officials to evaluate the repeated HPAI detections in meat turkey operations since 2022. Onsite and virtual Veterinary Services personnel conducted site visits, interviews, and assessed current and historical data. During field visits, operations appeared to be consistently well-managed with biosecurity mitigations that meet industry standards. No epidemiologic links among these premises were identified and human-mediated lateral spread was not suspected. Since the start of the outbreak, all reintroductions in North Dakota have been IND and 95.9 percent (70 out of 73) of reintroductions in South Dakota have also been IND. Geographic location within a major waterfowl migratory flyway, proximity to waterfowl habitat, and industry standard curtain-sided barn infrastructure may create a higher risk of exposure to wildlife than operations in other geographic areas of the United States. Studies to gather data on species-specific migratory patterns in this region, evaluation of routes of virus entry into turkey barns, and investigation of turkey premises in the region that have never been infected may reveal more information to help these regional producers reduce their risk of HPAI infection.

Wisconsin

The table egg layer premises that experienced a virus reintroduction during the report period was previously infected in the spring of 2022, which was also attributed to an IND introduction. Epidemiologic interviews were conducted following both detections and indicated the presence of migratory waterfowl and waterbirds. In addition, the premises is in close proximity to both a river and a creek, with a local wildlife area nearby, which may reflect increased environmental pressure.

APPENDIX A

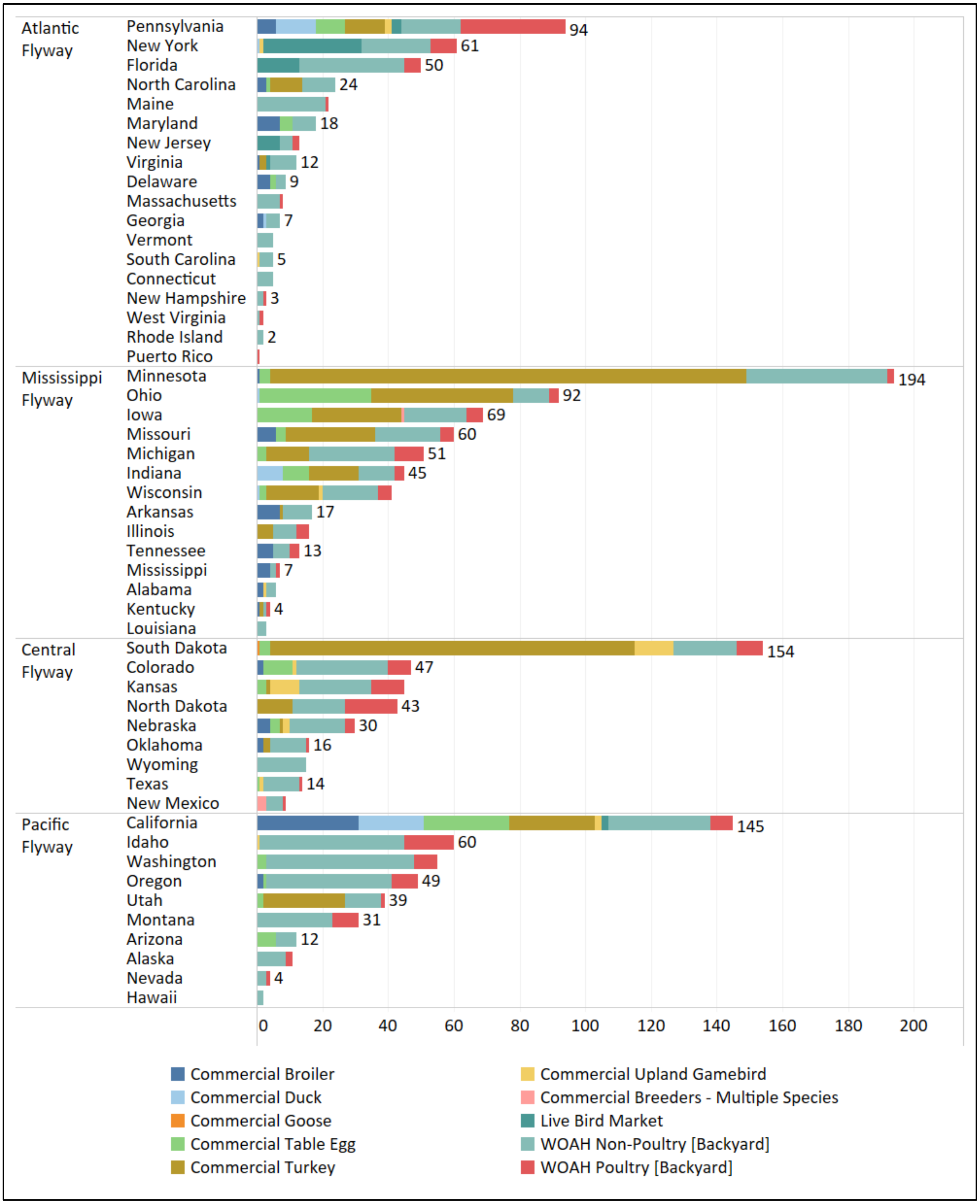


Figure A1. Detections of HPAI by migratory flyway, State, and premises type between February 8, 2022, and September 30, 2025.

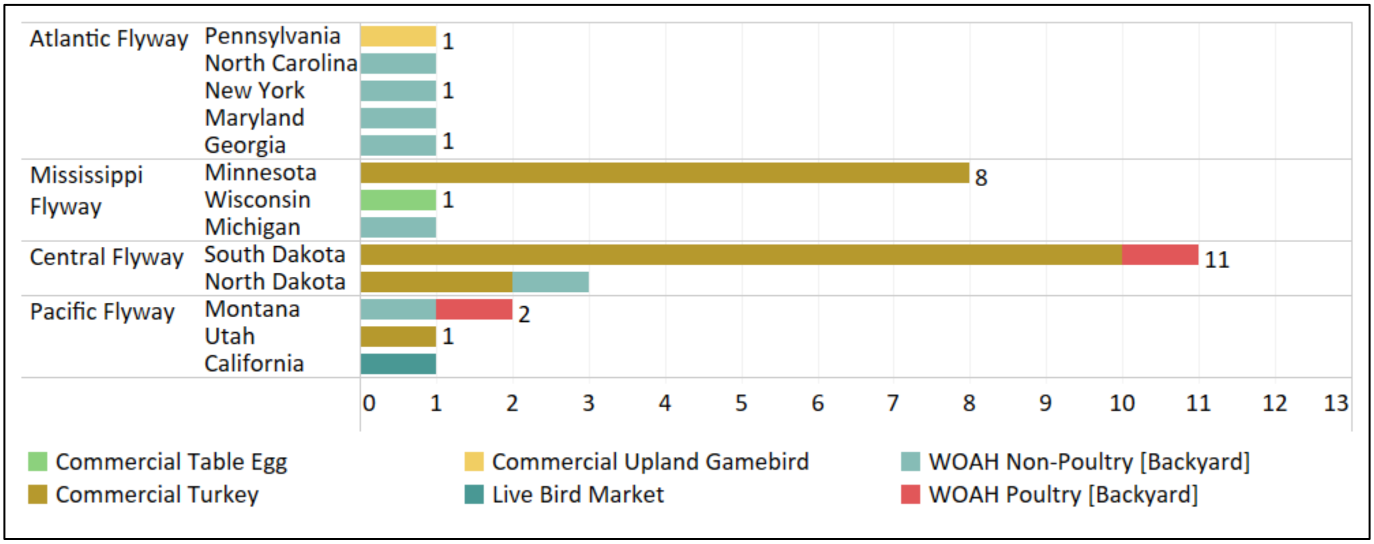
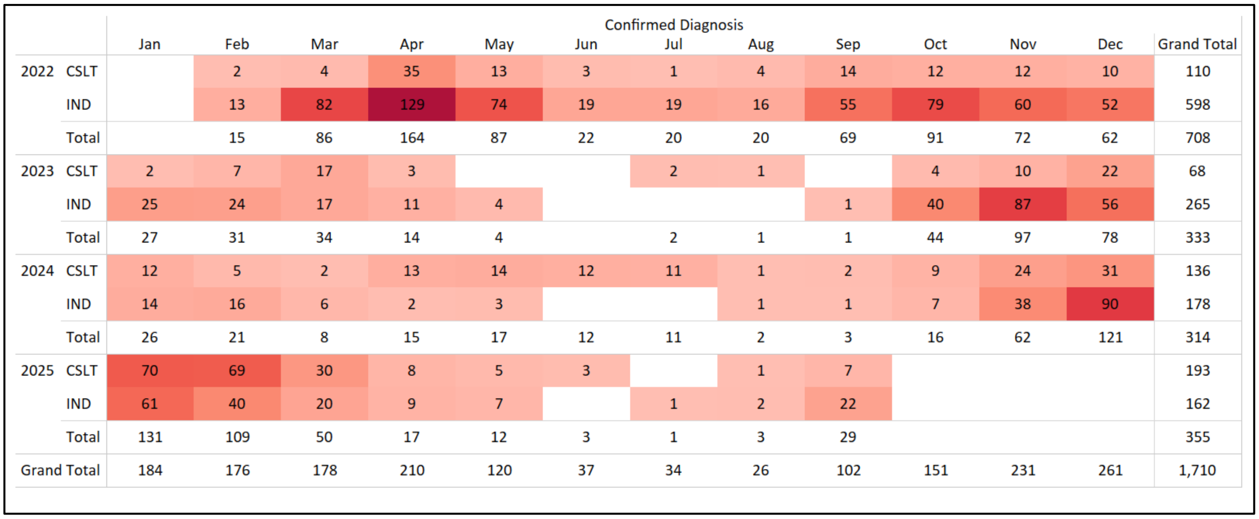


Figure A2. Confirmed HPAI detections between July 31, 2025, and September 30, 2025, by flyway, State, and production types.

Table A1. Number of confirmed HPAI detections by year, month, and source of introduction. Color intensity reflects the relative number of cases.



		Confirmed Diagnosis												
		Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Grand Total
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		1	7				193
	IND	61	40	20	9	7		1	2	22				162
	Total	131	109	50	17	12	3	1	3	29				355
Grand Total		184	176	178	210	120	37	34	26	102	151	231	261	1,710