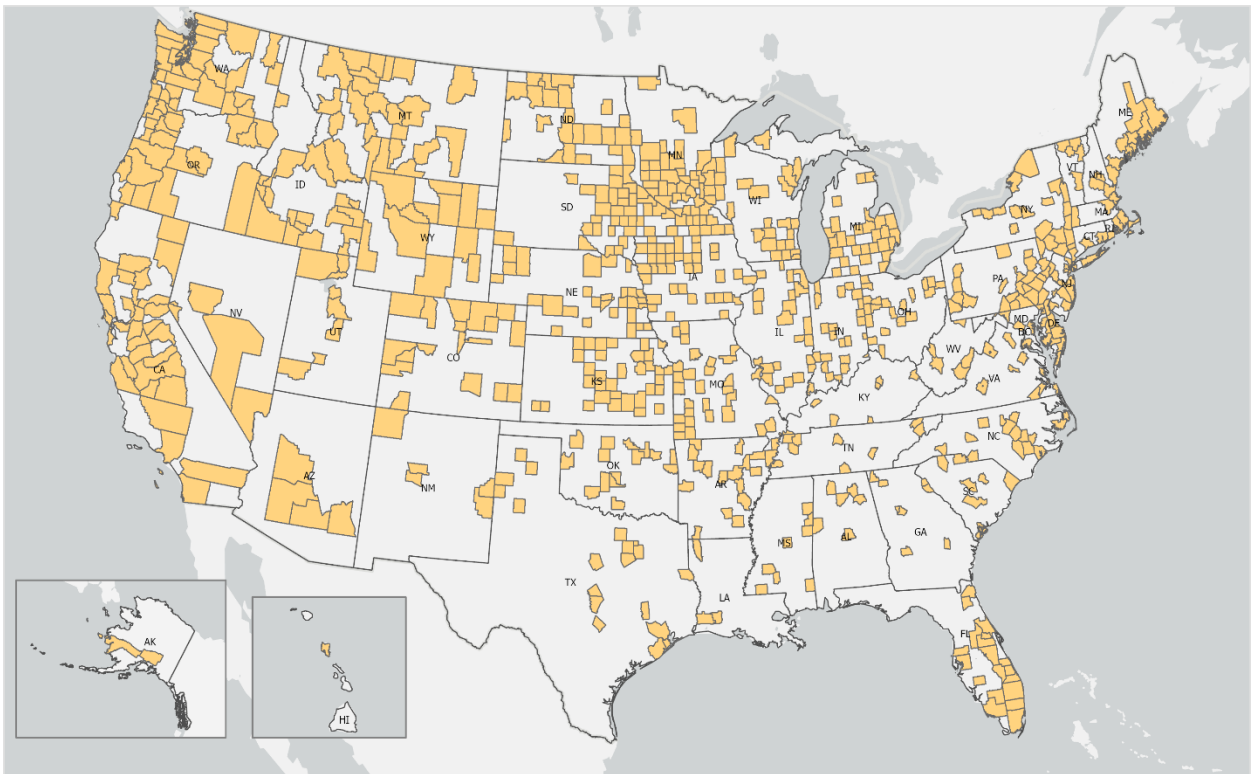




Status and Epidemiologic Analyses of HPAI-affected Poultry Flocks March 31, 2026 Interim Report



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ITEMS OF NOTE

A. **Reporting Period:** January 1, 2026, to March 31, 2026

- During the current reporting period, the event has impacted 37 States, 200 premises, and over 20 million birds.
- Monthly cases consisted of 62 detections in January 2026, 63 detections in February, and 75 detections in March.
- Genotype D1.1 continues to predominate in both wildlife and domestic poultry during the current reporting period.
- The reporting period has been defined by common source/lateral transmission clusters in Indiana and Pennsylvania, with smaller clusters in multiple other States.

B. **Entire Event to Date:** February 2022 to March 2026

- As of March 31, 2026, the 2022 HPAI event has impacted all 50 States and the territory of Puerto Rico, with a total of 2,185 premises infected and over 205 million birds affected.
- 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.
- Between December 30, 2021, and March 31, 2026, wild bird surveillance resulted in 19,145 detections of H5Nx HPAI in at least 198 species of wild birds across all North American flyways (9,021 detections in apparently healthy birds; 10,124 detections in sick or dead birds).
- Over the entire HPAI event, 67.0 percent (1,437 out of 2,144) of detections are attributed to independent wild bird introductions (IND) and 33.0 percent (707 out of 2,144) of detections have been 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 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, 51.3 percent (304 out of 593) in 2025, and 44.4 percent (87 out of 196) in the first three months of 2026.
 - 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 and 2026 was due to different transmission clusters across several States—63.9 percent (250 out of 391) of 2025 and 2026 detections attributed to CSLT occurred in Indiana, Ohio, and Pennsylvania.

DESCRIPTION OF THE HPAI EVENT IN POULTRY

A. Reporting Period: January 1, 2026, to March 31, 2026

During the reporting period of January 1, 2026, to March 31, 2026, 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 37 out of 50 States, totaling 200 detections. The flock types affected include 93 commercial¹ poultry,² 30 backyard poultry,³ 59 backyard non-poultry⁴ and 18 live bird markets (LBM)⁵. The 93 commercial poultry premises can be further divided into production types: 23 turkey, 17 table egg, 15 broiler, 34 duck, and 4 upland gamebird premises (**Figure 1**). A table of impacted production types by flock type and species can be found in **Appendix Table 1**. Approximately 20.7 million birds have been affected—comparatively, this is greater than the number of impacted birds during the same month span in 2023 (0.8 million) and 2024 (2.4 million) but less than 2022 or 2025, when more than 37 million birds were impacted. More than 80 percent of the birds affected during the reporting period were table egg layers. Reporting period detections by flyway, State, and production type are depicted in **Appendix Figure 1**.

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

² Poultry are [defined](#) by the World Organisation 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 *Code of Federal Regulations* (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.

⁵ A live bird market is any facility that procures live poultry to hold or display for more than 24 hours and sells such poultry for onsite slaughter or offsite ritual use. From: Uniform Standards for Live Bird Marketing System, APHIS, 2024

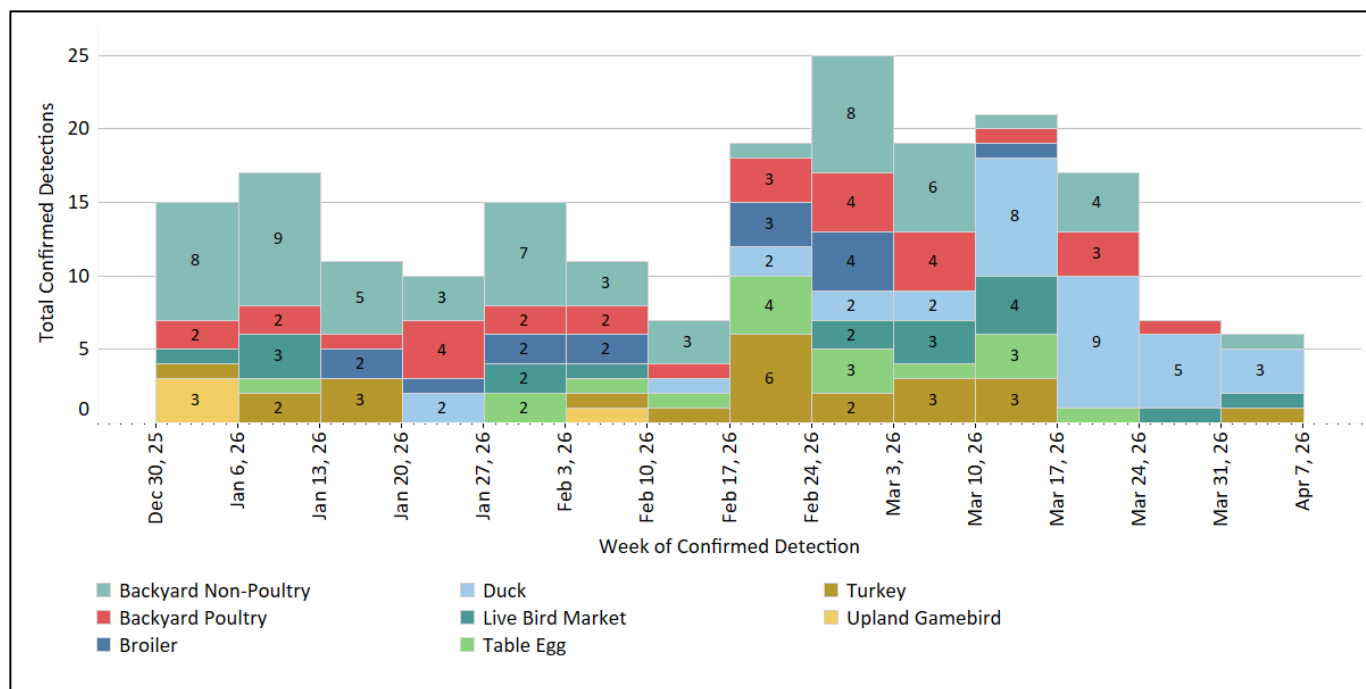


Figure 1. Weekly HPAI detections by production type, from January 1, 2026, to March 31, 2026.

The current reporting period encompasses 6.0 percent of the entire event (3 out of 50 months). Production types that accounted for a greater percentage of detections in this period than across the entire event include duck (27.4 percent; 34 out of 124), LBM (23.4 percent; 18 out of 77), broiler (13.4 percent; 15 out of 112), backyard poultry (11.1 percent; 30 out of 270), table egg (10.4 percent; 17 out of 164), upland gamebird (10.3 percent; 4 out of 39), and backyard non-poultry (7.1 percent; 59 out of 837). **Figure 2** illustrates the relative percentage of detections by production type within the current reporting period compared with detections from February 2022 through December 2025.

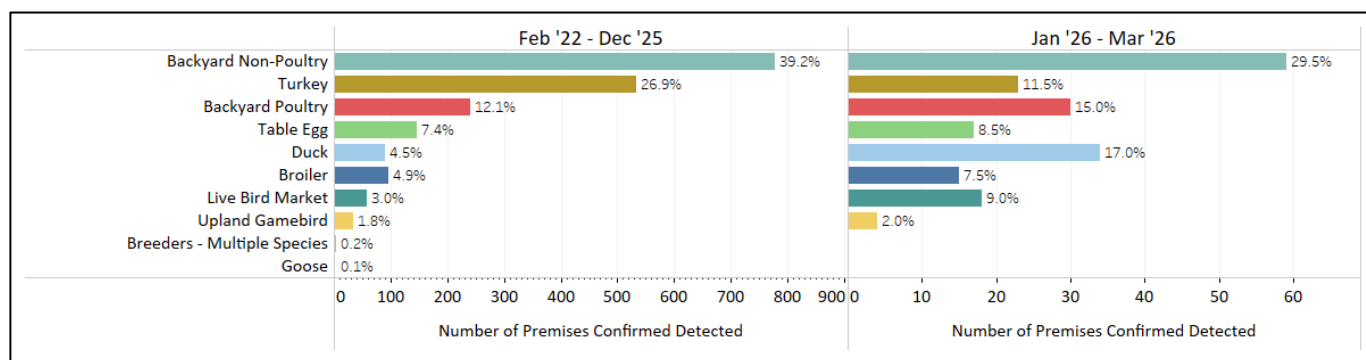


Figure 2. Number and relative percentage of confirmed detected premises by production type, February 2022 to December 2025 compared to the reporting period.

During the reporting period, there was a slight increase in the monthly totals of confirmed detections. Examining trends for the months of January, February, and March in previous years, 2022 had a sharp increase in total detections, 2023 followed a similar trend to 2026 but had half the number of detections, 2024 had a slight decrease, and 2025 had a sharp decrease (**Figure 3**).

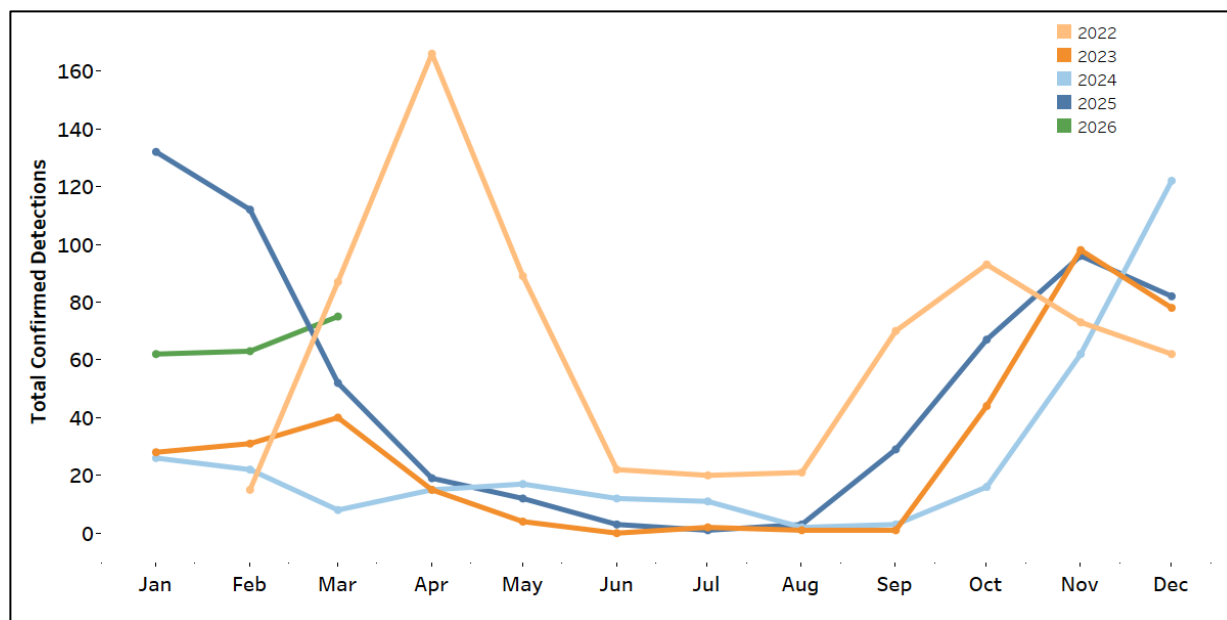


Figure 3. Yearly epidemiological curves of the total number of detections by month of confirmed detection, as of March 31, 2026.

B. Entire Event to Date: February 2022 to March 2026

This event of HPAI in poultry in the United States has been ongoing since February 2022, resulting in 2,185 affected premises across all 50 States and Puerto Rico. NVSL-confirmed premises include 1,001 commercial poultry, 270 backyard poultry, 837 backyard non-poultry, and 77 LBM. The 1,001 commercial poultry can further be divided into 557 turkey, 164 table egg, 112 broiler, 124 duck, 39 upland gamebird, 4 breeder (multiple bird species), and 1 goose premises. Over 205 million birds have been affected since the start of the event, varying annually from nearly 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 for overall detections by flyway, State, and production type is available in **Appendix Figure 2**.

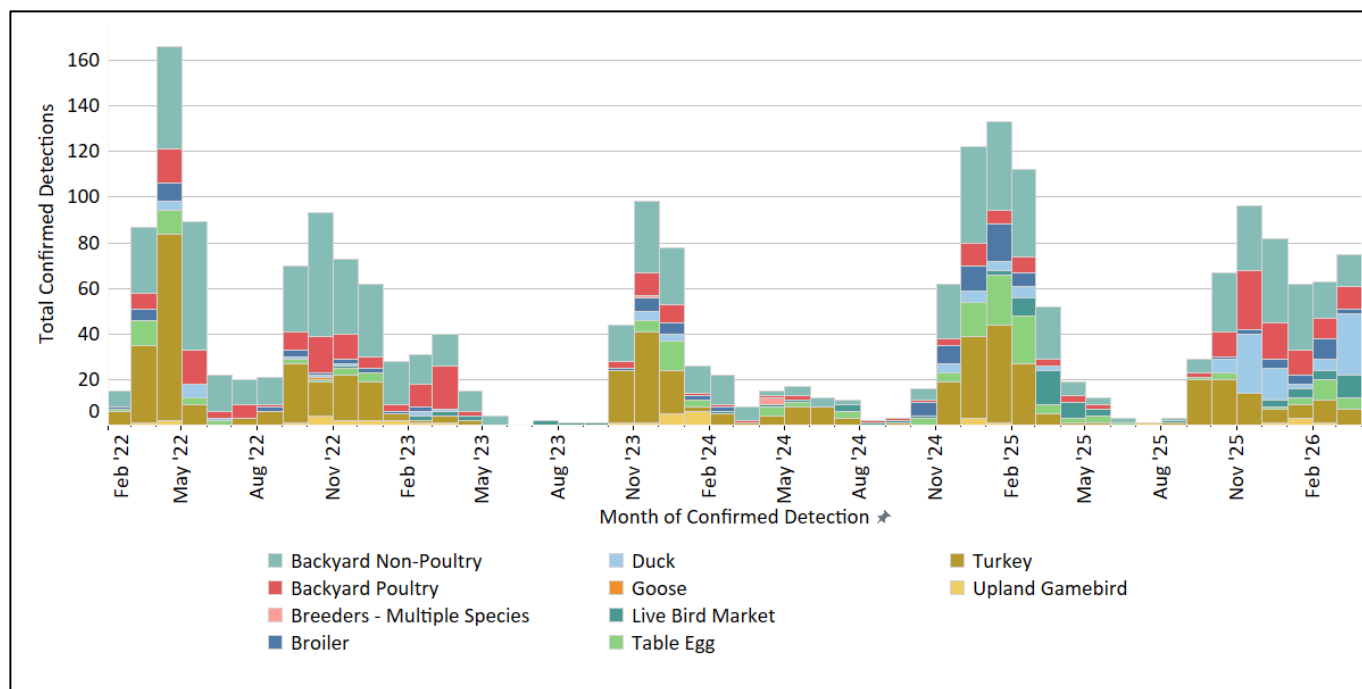


Figure 4. Monthly HPAI confirmed detections by production type, as of March 31, 2026.

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, 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 March 31, 2026, wild bird surveillance has resulted in 19,145 detections of H5Nx HPAI in at least 198 species of wild birds across all North American flyways (9,021 detections in apparently healthy birds; 10,124 detections in sick or dead birds; **Figure 5**).

Prevalence of HPAI H5Nx (i.e., the proportion of sampled individual birds testing positive for HPAI H5Nx) among apparently healthy wild birds varies by 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.

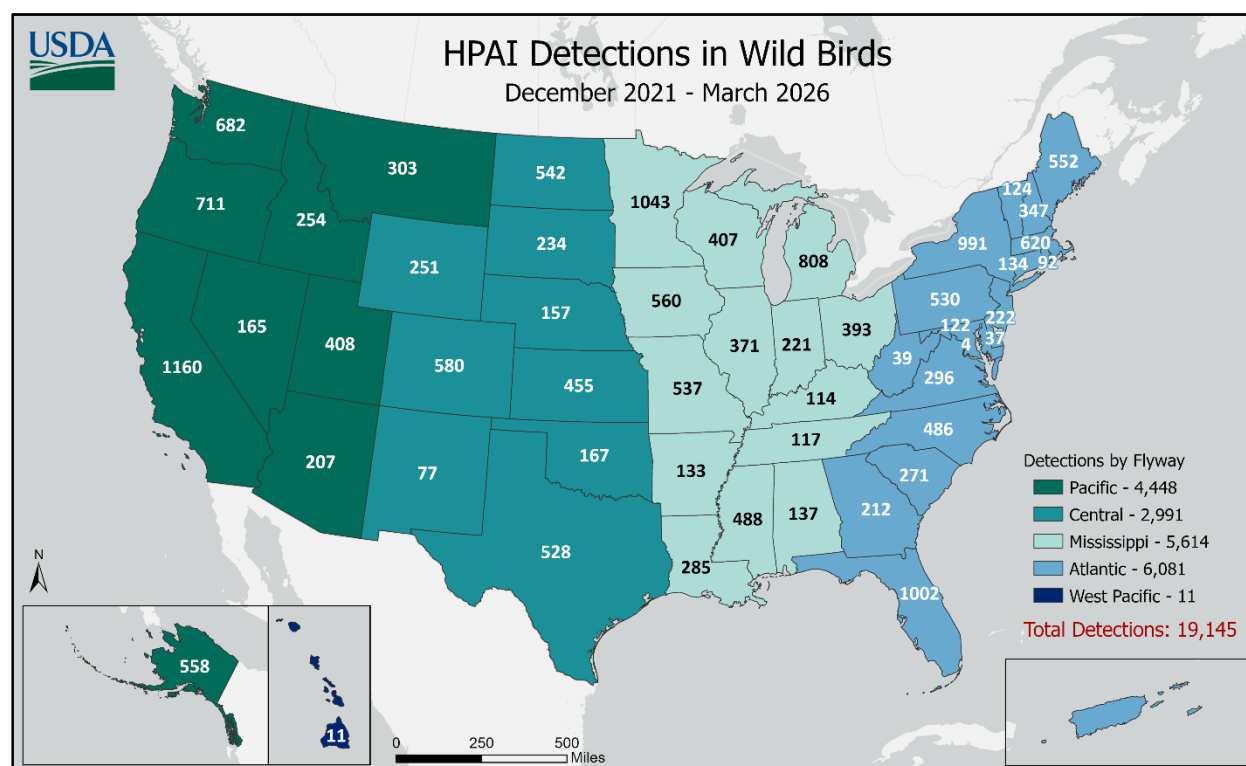


Figure 5. Number of HPAI detections in wild bird samples collected between December 30, 2021, and March 31, 2026. State totals include detections from apparently healthy wild birds from active surveillance efforts and sick or dead birds from morbidity/mortality investigations (including captive wild birds from zoos and other captive animal facilities).

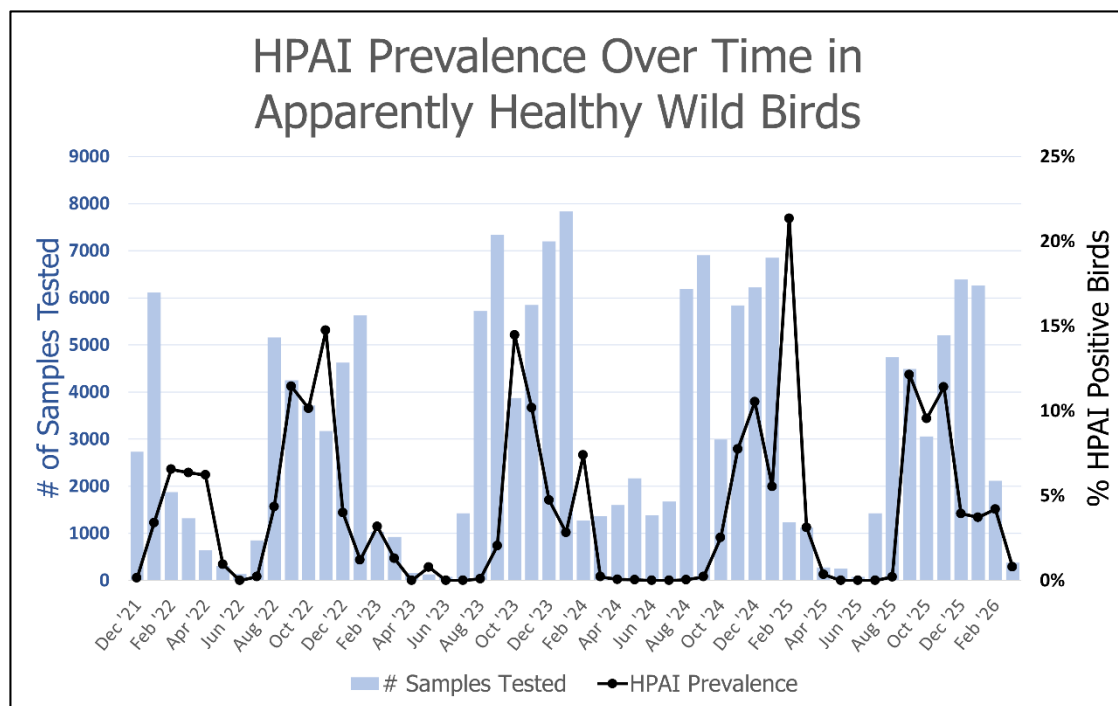


Figure 6. Monthly sampling effort (number collected; blue bars) and H5Nx HPAI prevalence (percentage of samples found to be HPAI H5Nx-positive; black line) in apparently healthy wild birds as part of the U.S. National Surveillance Plan for Highly Pathogenic Avian Influenza.

Initial screening of sick or dead birds occurs at State or regional laboratories, and only positive samples are sent to the NVSL for confirmatory testing. Because the USDA does not receive information on the total number of samples tested—including negative results—there is no denominator available to calculate disease prevalence. As a result, the USDA reports only the number of confirmed cases from sick or dead birds, rather than prevalence over time. 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 like those observed in apparently healthy wild birds (**Figure 7**).

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

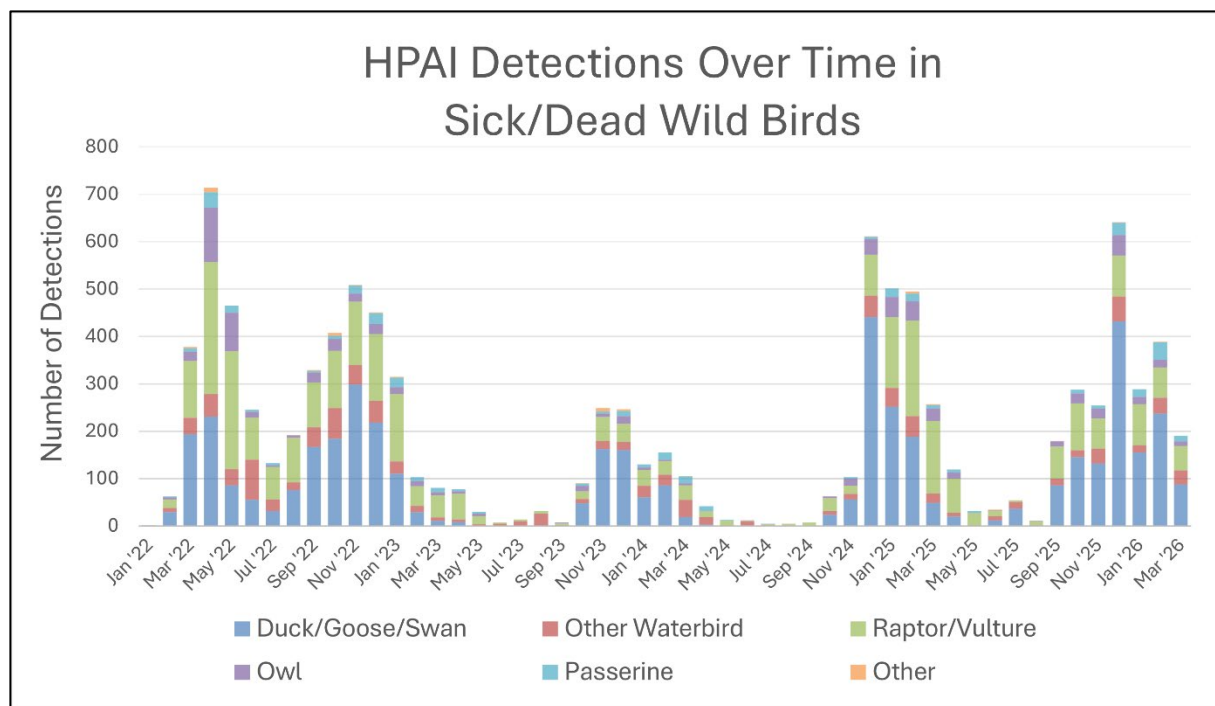


Figure 7. Stacked bar graph of the number of H5Nx HPAI detections in sick or dead wild birds sampled between January 1, 2022, and March 31, 2026. Different colors represent different functional groups of wild birds.

B. Peridomestic Wildlife Surveillance

Following the detections of H5N1 HPAI in dairy cattle in March 2024, the 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 March 31, 2026, 12,892 samples were collected from 83 affected farms in 20 States, resulting in 507 detections of HPAI (**Figure 8**). The number of HPAI detections varied widely across farms, ranging from zero detections ($n = 41$ farms) to ≥ 30 detections ($n = 5$ farms). Investigations into the factors driving differences from farm to farm are ongoing.

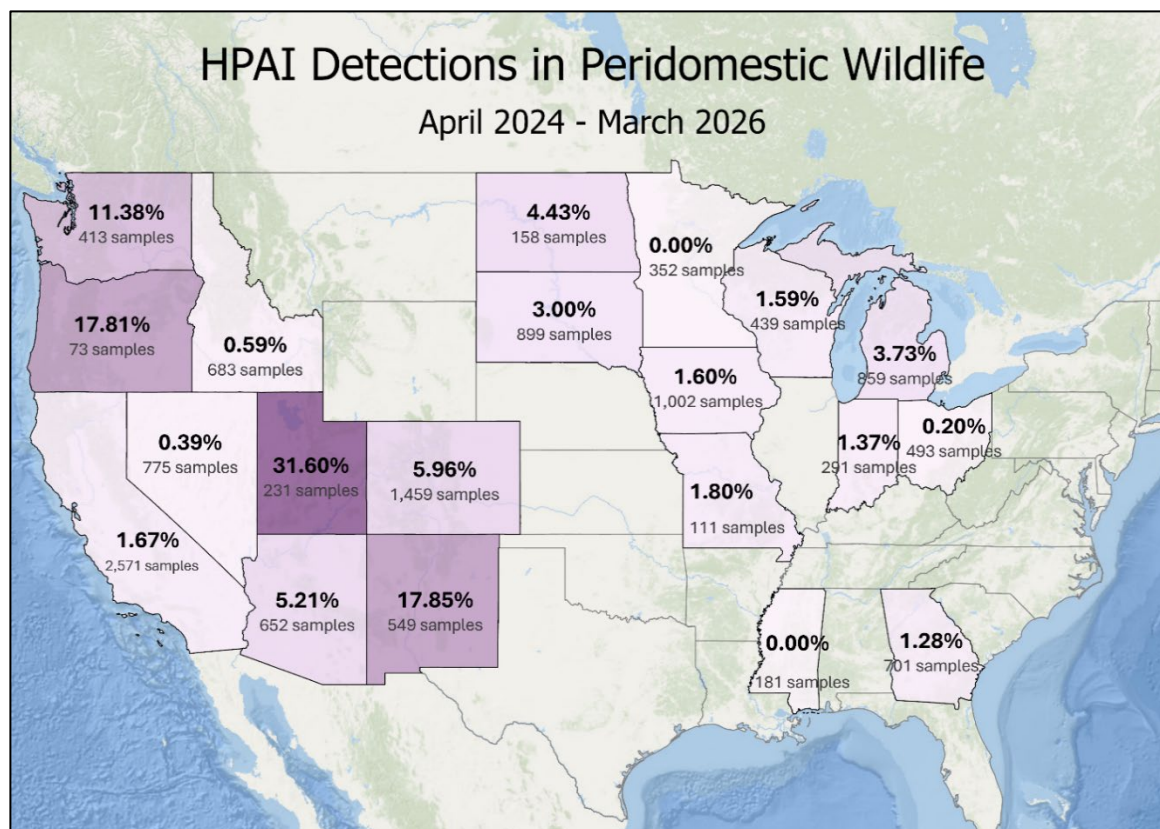


Figure 8. Peridomestic wildlife surveillance efforts for HPAI from April 1, 2024, to March 31, 2026. Sampling of both wild birds and mammals occurred on HPAI-affected dairy and poultry farms in the States colored purple. Darker colored States indicate higher apparent prevalence of HPAI in the wildlife 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 March 31, 2026, there have been 800 HPAI detections in at least 49 wild or captive wild mammal species in 42 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 peridomestic wildlife found in and around HPAI-positive farms has resulted in detections of HPAI in apparently healthy wild mammals.

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

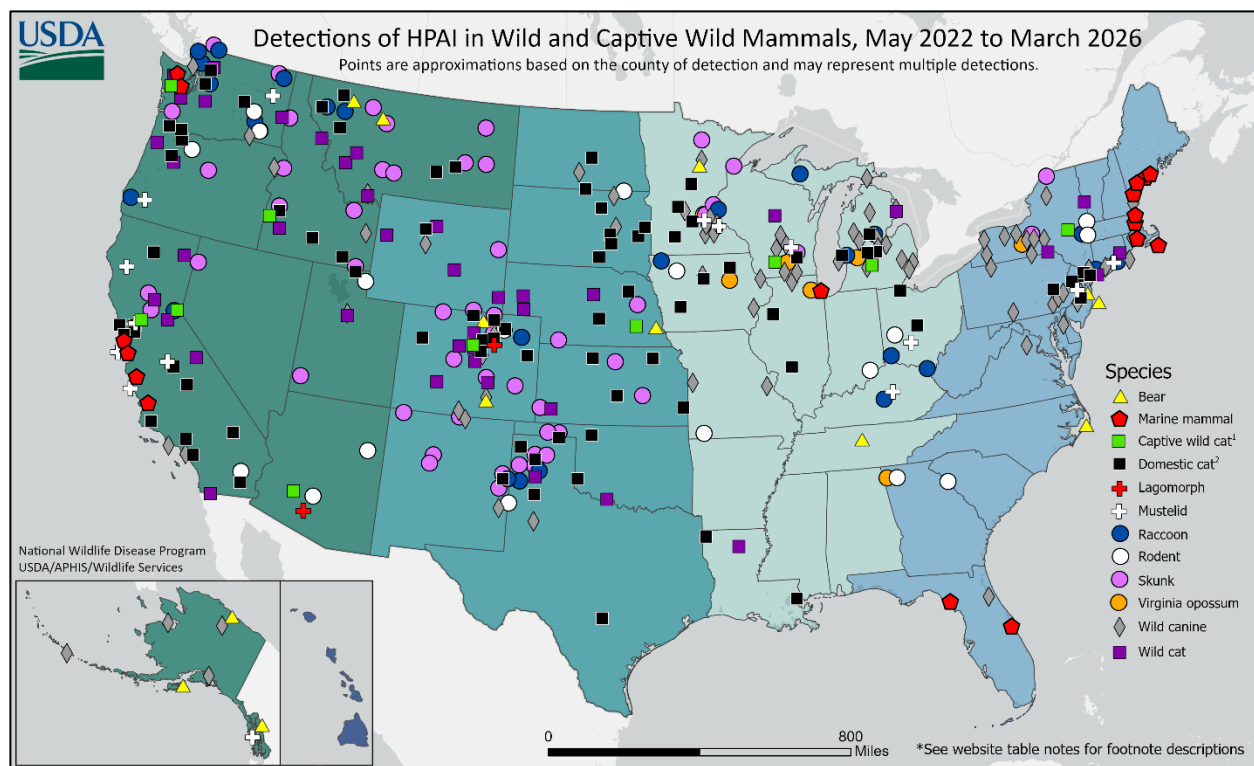


Figure 9. Detections of HPAI virus in wild mammals and captive wild mammals in the United States as of March 31, 2026. The map shows detections in both sick/dead mammals as well as apparently healthy mammals collected on HPAI-infected farms as part of peridomestic wildlife surveillance efforts.

PHYLOGENETICS

A. Background

The NVSL is the national confirmatory laboratory for influenza A virus in animals and conducts genomic sequencing on suspect and positive 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 150 genotypes have been described, as of March 31, 2026.

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**). There have been three independent spillover events of genotype D1.1 into dairy cattle, 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. The relative proportion of genotype detections in domestic poultry by State are depicted in **Figure 11**. 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 several new genotypes (D1.7 to D1.13) identified during this reporting period.

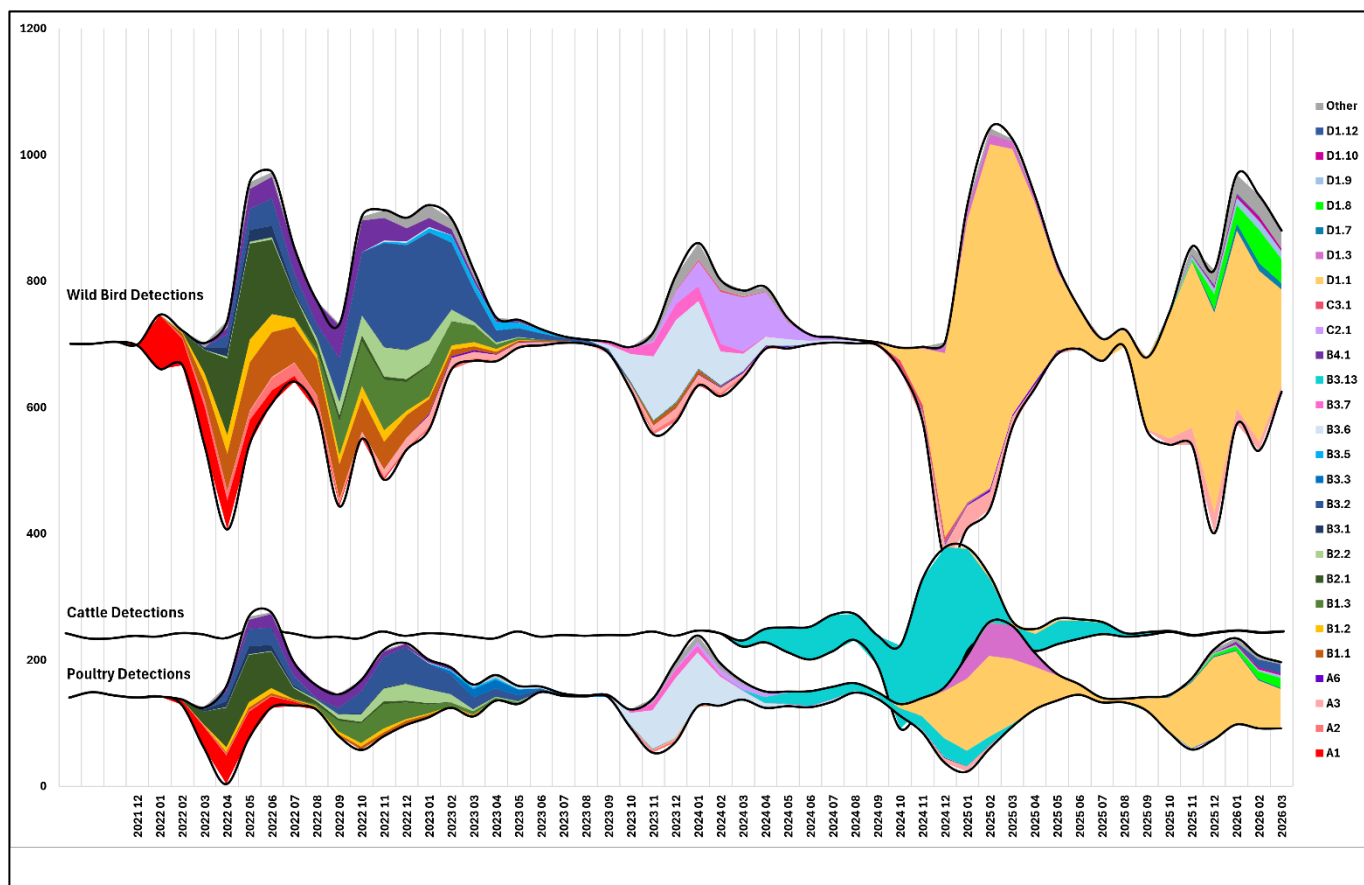


Figure 10. Genotype distribution over time of wild bird (top; n=9392), dairy cattle (middle; n=934), and poultry detections (bottom; n=1980), represented as moving quarterly averages, as of March 31, 2026. Data for poultry and dairy represent a single sequence for each affected premises and where high-quality sequence was obtained.

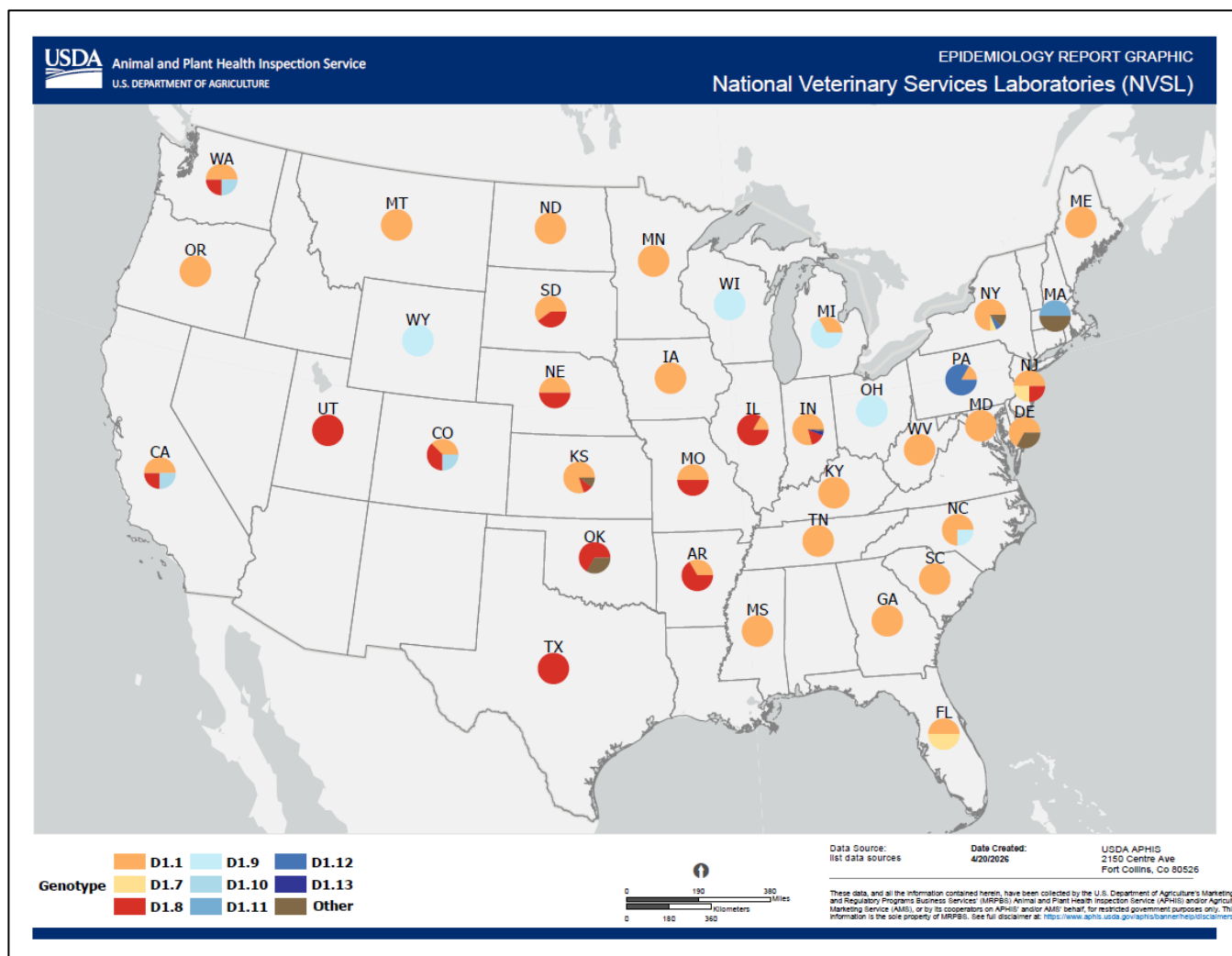


Figure 11. Genotype distribution in domestic poultry by State, from January 1, 2026, to March 31, 2026.

SPILLOVER AND TRANSMISSION EVENTS

A. Reporting Period: January 1, 2026, to March 31, 2026

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 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 196 out of 200 detections. A table of introduction type (IND versus CSLT) by month and year is available in **Appendix Table 2**.

Between January and March 2026, there were 108 independent wild bird introductions. This is above average for the number of IND introductions for the same period (January to March) in previous years: 95 in 2022, 66 in 2023, 36 in 2024, and 121 in 2025. In contrast, the 87 detections attributed to CSLT from January and March 2026 were considerably greater than the 6 detections between January and March in 2022 (partially due to the start of the HPAI 2022 event occurring in February 2022), the 26 detections in 2023, and the 19 detections in 2024. However, the number of detections attributed to CSLT was less than the 169 detections in 2025.

Of the 87 cases of CSLT between January and March 2026, 59 were commercial poultry, 17 backyard poultry, 3 backyard non-poultry, and 8 LBM. The 59 commercial poultry can be further divided into 9 turkey, 11 table egg, 6 broiler, and all 33 duck premises. The predominant production types impacted by CSLT during the reporting period were ducks and backyard poultry, which accounted for 37.9 percent (33 out of 87) and 19.5 percent (17 out of 87) of confirmed detections, respectively (**Figure 12**). All confirmed detections in commercial duck premises were attributed to CSLT. No production type has consistently been the predominant production type impacted by CSLT during January to March in previous years of this event. Backyard poultry predominated in 2023 (16 out of 25), and table egg and turkey predominated in 2025 (41 out of 168 and 69 out of 168, respectively).

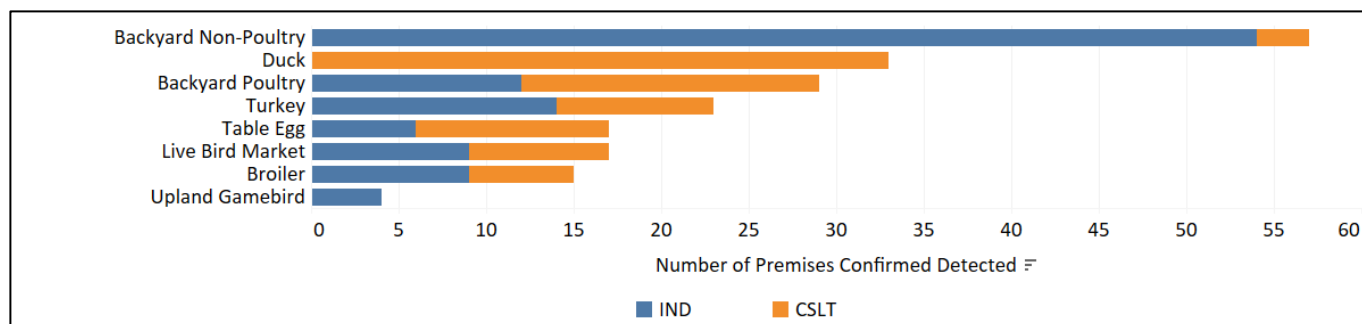


Figure 12. Number of premises confirmed detected between January 2026 and March 2026, by production type and potential route of introduction. IND, independent introduction; CSLT, common source or lateral transmission.

B. Entire Event to Date: February 2022 to March 2026

Over the course of the entire event to date, phylogenetic analysis was available for 2,144 out of 2,185 detections. Overall, 67.0 percent (1,437 out of 2,144) of detections are attributed to independent wild bird introductions. The percentage of IND detections by migratory flyway were as follows: 18.6 percent (267 out of 1,437) in the Atlantic flyway, 31.5 percent (452 out of 1,437) in the Mississippi flyway, 27.3 percent (392 out of 1,437) in the Central flyway, and 22.7 percent (326 out of 1,437) in the Pacific flyway.

The occurrence and frequency of independent wild bird introductions increase the risk for subsequent transmission to additional poultry premises (e.g., common source or lateral transmission). Overall, 32.8 percent (704 out of 2,144) of detections have been attributed to common source or lateral transmission; however, it is important to note 15.8 percent (111 out of 704) 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 that predominately occurred in 2024.

Although CSLT reflects a smaller subset of detections in the 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, 51.3 percent (304 out of 592) in 2025, and 44.4 percent (87 out of 196) in the first three months of 2026 (**Figure 13; Appendix Table 2**). 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. Of the CSLT detections in 2025, 36.6 percent (112 out of 304), occurred within the October through December 2025 reporting period, predominately in Indiana. CSLT spread in Indiana has continued into the current reporting period, with Indiana accounting for 46 percent (40 out of 87) of CSLT detections between January and March of 2026 and Pennsylvania contributing 33.3 percent (29 out of 87).

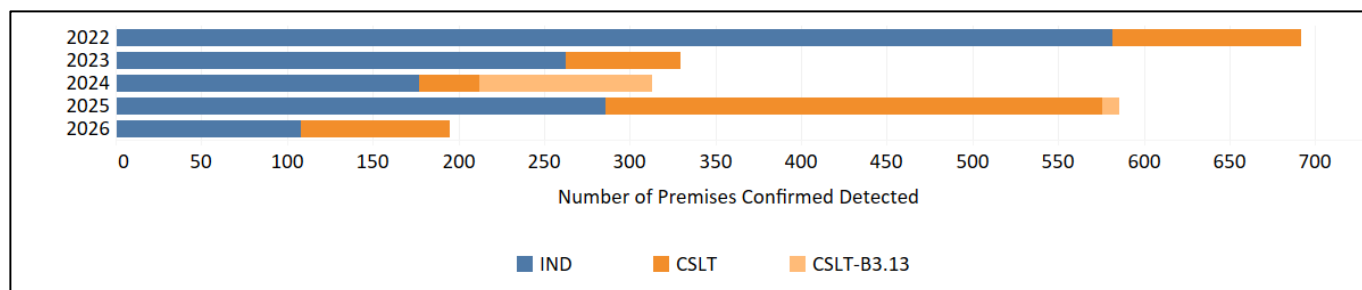


Figure 13. Number of premises confirmed detected over the entire HPAI event, by year and potential route of introduction. IND, independent introduction; CSLT, common source or lateral transmission.

STATE-SPECIFIC HPAI DETECTIONS: JANUARY 1, 2026, TO MARCH 31, 2026

During the reporting period, there were 200 confirmed detections. Phylogenetic evidence suggests that CSLT events occurred in 13 States: 40 in Indiana, 29 in Pennsylvania, 4 in New York, 2 each in Wisconsin, Minnesota, Illinois, and Colorado, and 1 each in North Carolina, Michigan, Maryland, Kansas, Iowa, and Georgia.

Indiana

Nearly one-quarter (48 of 200) of confirmed HPAI detections for the reporting period occurred in Indiana. Detections in the State were a continuation of sustained transmission that started in October of 2025; the longest period without a detection (18 days) took place in late January. Over the course of the previous reporting period (October 1, 2025, to December 31, 2025) and the current reporting period, a total of 131 (83 and 48, respectively) detections occurred in Indiana. There have been 176 detections in that State since the national HPAI event started in February 2022.

During the reporting period, the NVSL confirmed HPAI on 36 commercial poultry (4 turkey, 32 duck), 11 backyard poultry, and 1 backyard non-poultry premises in Indiana. Phylogenetic evidence attributed 83.3 percent (40 out of 48) of detections to CSLT, with 77.5 percent (31 out of 40) of those CSLT detections occurring in ducks. Compared to the overall event, a greater percentage of ducks were detected and a greater percentage of CSLT occurred in ducks during the reporting period.

Throughout the overall event, flock types affected included 113 commercial poultry, 49 backyard poultry, and 14 backyard non-poultry. Among the 113 commercial poultry premises affected, there were 19 turkey, 8 table egg, 2 broiler, and 84 duck operations. Phylogenetic evidence suggests that 79.0 percent (139 out of 176) of detections occurred by CSLT, with 56.1 percent (78 out of 139) in duck and 28.8 percent (40 out of 139) in backyard poultry premises.

LaGrange and Elkhart counties accounted for the majority of detections: 81.3 percent (39 out of 48) during the reporting period and 71.0 percent (125 out of 176) for the entire event. Of the detections in these two counties during the entire event, 94.4 percent (118 out of 125) occurred in fall of 2025 or spring of 2026, with only a few detections in 2022.

During the reporting period, 10 previously affected and depopulated premises experienced repeat detections. Eight of these, all commercial duck operations, were again attributed to CSLT, while one was IND, and another was a potential reinfection with the same viral strain. The median time between these repeat detections was 121 days (range: 63–269 days). Generally, repeat infections have shown some degree of seasonality, occurring no sooner than annually. With less than six months median time between repeat detections and most repeat detections attributed to CSLT, Indiana premises appeared to experience increased disease pressure and transmission risk.

Pennsylvania

During the reporting period, 18 commercial poultry, 7 backyard poultry, 1 backyard non-poultry, and 4 LBM premises were affected in Pennsylvania. The 18 commercial poultry premises included 3 turkey, 9 table egg, 4 broiler, and 2 duck operations. Phylogenetic evidence suggests that 96.7 percent (29 out of 30) of these detections were attributed to CSLT, compared to 65.9 percent (87 out of 132) for the overall event.

For the overall event, Pennsylvania accounted for 132 detections, making it the most impacted State in the Atlantic flyway and ranking it among the top five affected States (**Appendix Figure 2**). Over the entire event, 60 commercial poultry, 45 backyard poultry, 20 backyard non-poultry, and 7 LBM premises were affected. The 60 commercial poultry premises included 15 turkey, 18 table egg, 10 broiler, 15 duck, and 2 upland gamebird operations. Phylogenetic evidence suggests that 65.9 percent (87 out of 132) of detections were attributed to CSLT, with 36.8 percent (32 out of 87) occurring among backyard poultry and 18.4 percent (16 out of 87) among table egg operations.

In addition to having a relatively higher number of detections both during the reporting period and overall outbreak, Pennsylvania accounted for 42.2 percent (8,746,531 out of 20,724,974) of the birds affected with HPAI during the reporting period, and 7.8 percent (15,952,544 out of 205,743,954) of the U.S. flock inventory affected over the entire event. Additionally, detections during the reporting period accounted for 54.8 percent (8,746,531 out of 15,952,544) of all birds affected in Pennsylvania over the course of the entire event, due to more than 7.5 million egg layers being impacted.

In Pennsylvania, most detections occur in January, February, and March (64.4 percent; 85 out of 132) compared to the remaining months. Over the course of the entire HPAI outbreak, the first three months of each year in Pennsylvania have been characterized by 30 or more detections, with the exception of 2024. There have been 35 detections in 2022, 33 in 2023, 3 in 2024, 31 in 2025, and 30 in the first three months of 2026.

During the reporting period, 80.0 percent (24 out of 30) of confirmed detections occurred in Lancaster County. For the entire event, Lancaster County accounts for 53.8 percent (71 out of 132) of confirmed detections in Pennsylvania. Among U.S. counties, Lancaster County, Pennsylvania ranks among the top counties for the number of poultry operations and the number of egg layers.⁶ The confirmed detections were geographically close to one another and frequently had direct and indirect affiliations.

The detections during the reporting period included four premises (2 table egg and 2 LBM) previously affected and depopulated; phylogenetic evidence suggests that all four detections were attributed to CSLT. All premises only had one previous introduction, three of which were attributed to CSLT and one attributed to IND. Only one other premises in Pennsylvania has had a reintroduction, and it was not affected during this reporting period.

New York

During the reporting period, the flock types affected in New York included 13 LBMs and 3 backyard non-poultry. Phylogenetic evidence attributed 31.2 percent (5 out of 16) of detections to CSLT, and 68.8 percent (11 out of 16) of detections attributed to IND.

For the overall event, New York accounted for 80 detections. The flock types affected in New York over the entire outbreak included 2 commercial poultry, 8 backyard poultry, 24 backyard non-poultry, and 46 LBM. The 2 commercial poultry premises included one duck and one upland gamebird premises. Phylogenetic evidence suggests that 43.8 percent (35 out of 80) of detections were attributed to CSLT. Of the 35 CSLT detections, 94.3 percent (33 out of 35) were live bird markets and 5.7 percent (2 out of 35) were backyard poultry.

⁶ https://www.lancasteragcouncil.com/wp-content/uploads/2021/03/Lancaster-Ag-Snapshot_March-2021.pdf

Nationally, New York accounted for 65.7 percent (46 out of 77) of LBM detections over the course of the entire HPAI event, where 71.7 percent (33 out of 46) of LBM detections were attributed to CSLT. Live bird markets are at a higher risk for HPAI spread, due to the frequent introduction of new birds and dissemination of birds through marketing channels. As a result, they are more susceptible to reintroductions from multiple external sources.

Detections during the reporting period included six premises previously affected and depopulated; one detection was attributed to CSLT, while the remaining five were attributed to IND. One of the six premises was detected twice during the reporting period, with one detection attributed to IND. No sequence was obtained from the second detection. Of the six premises previously affected, four have been affected once during the HPAI event, while the other two have been detected four times each. Four of the LBMs had previous detections attributed to CSLT but were attributed to IND during the reporting period. The remaining two markets have been attributed exclusively to either CSLT or IND.

Other States

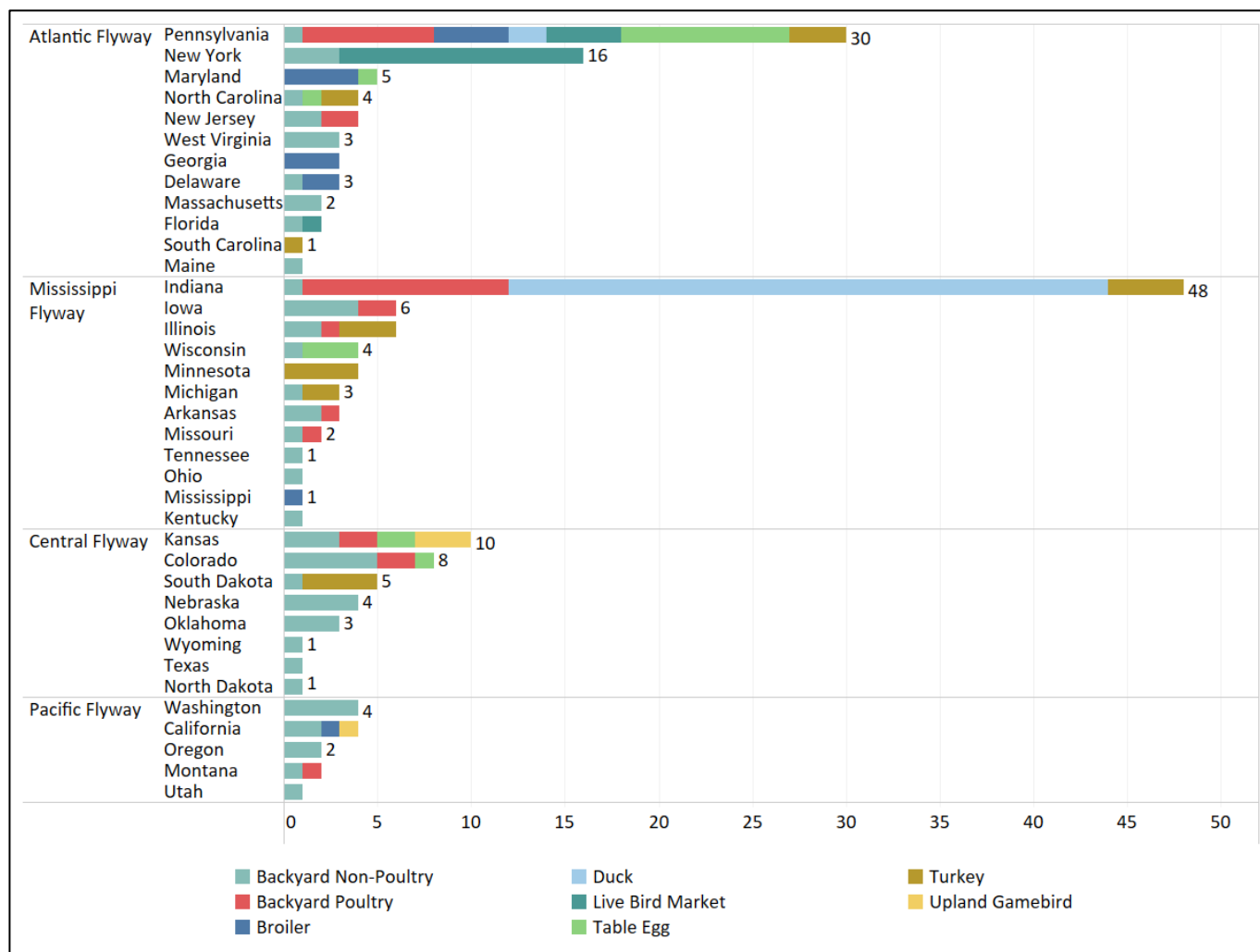
During the reporting period, premises that were suspected instances of CSLT had detailed epidemiological investigations conducted for genomically linked HPAI clusters in Colorado, Florida, Georgia, Iowa, Illinois, Kansas, Maryland, Michigan, Minnesota, North Carolina, and Wisconsin. These genomically linked events are characterized by closely related H5N1 virus sequences across premises that share SNP patterns that may indicate directionality of transmission.

Although definitive links for transmission across premises were not identified, common patterns among these clusters included common ownership across clustered premises, external visitors or equipment entering the premises during the 28-day reference period prior to the outbreak, use of staff that visit other livestock/poultry premises, introduction of new animals to the farm, presence of an open body of water within 350 yards of the farm, barn proximity to wild birds, and access of farmed birds to the outdoors.

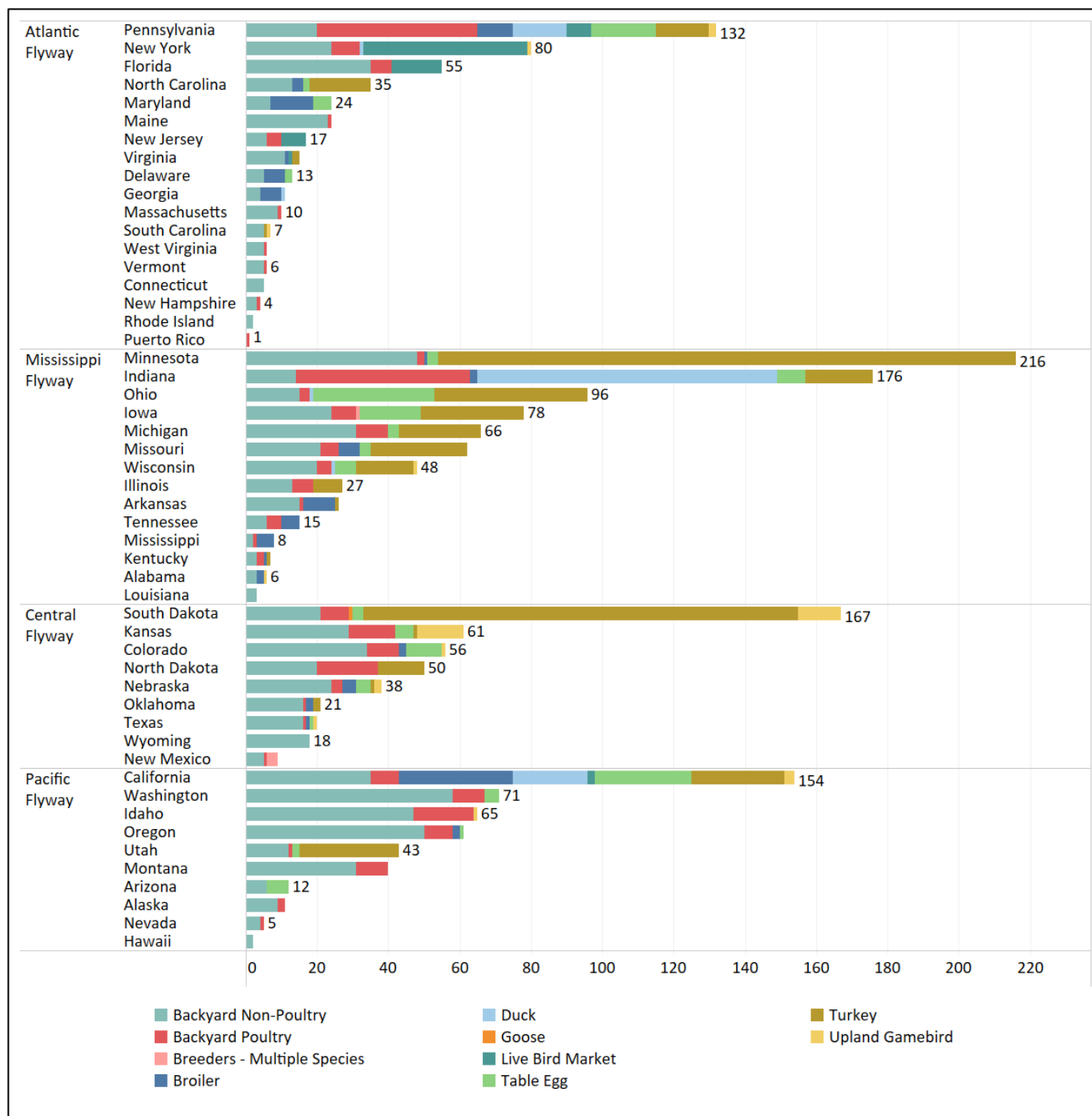
APPENDIX A

Appendix Table 1. Number of confirmed detections between January 1, 2026, and March 31, 2026, by flock type, commercial species, and production type.

Flock Type	Species	Production Type	Confirmed Detections
Backyard Non-Poultry		WOAH Non-Poultry	59
Backyard Poultry		WOAH Poultry	30
Commercial Poultry	Chicken	Broiler Breeder	3
		Broiler Production	12
	Duck	Duck Breeder	5
		Duck Meat Bird	29
	Chicken	Table Egg Breeder	1
		Table Egg Layer	12
		Table Egg Pullets	4
	Turkey	Turkey Breeder Hens	4
		Turkey Meat Bird	19
	Pheasant	Raised for Release Upland Game Bird	4
Other		Live Bird Market	18



Appendix Figure 1. Numbers of confirmed detections between January 1, 2026, and March 31, 2026, by flyway, State, and production type.



Appendix Figure 2. Numbers of confirmed detections by migratory flyway, State, and production type between February 8, 2022, and March 31, 2026.

Appendix Table 2. 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	24
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	80
CSLT	14	30	44									
2026 IND	47	32	29									
Total	61	62	73									

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