



United States Department of Agriculture

Animal and Plant  
Health Inspection  
Service

Veterinary  
Services

December 2025

# Influenza A Virus in Swine Surveillance

## Fiscal Year 2025 Quarterly Report

Surveillance Summary for Fourth Quarter Fiscal Year 2025: July 1 to September 30, 2025

### Report Summary

- This report covers the fourth quarter (Q4) of fiscal year (FY) 2025, from July 1 to September 30, 2025.
  - 977 samples were tested from 668 submitted accessions for a total of 4,158 samples from 3,352 accessions submitted in FY 2025.
  - H1N2 was the predominant subtype reported in USDA data for the quarter.
  - Over the last 8 quarters, H1N1 was the predominant subtype in Regions 1, 3, and 5 and H1N2 was the predominant subtype in Regions 2 and 4.
  - The Agricultural Research Service (ARS) characterized 68 isolates with published sequences in GenBank by phylogenetic analysis.
  - The National Veterinary Services Laboratory's (NVSL) Diagnostic Virology Laboratory (DVL) provided 28 isolates to two pharmaceutical and two government entities. NVSL received 165 isolates into the repository.

### Key Points

- All IAV-S submissions are voluntary and based on clinical case submissions to veterinary diagnostic labs. These data are not a statistically representative sampling of the U.S. swine population.
- Due to the voluntary nature of this surveillance, the information in this report cannot be used to determine regional and/or national incidence, prevalence, or other epidemiological measures, but it may help identify IAV-S trends.
- The report provides data from both national and regional levels.
- Limited accessions from a region can skew data and lead to misinterpretation. Therefore, less inference can be applied to results from Regions 3, 4, and especially 5.
- Where relevant, this report includes previous years' data for historical perspective.

### Introduction

This report, based on data received into the database as of December 17, 2025, provides a brief update on the status of national surveillance for influenza A virus in swine (IAV-S) for producers, swine practitioners, diagnosticians and the public. Summaries in this report may differ from those provided in past reports due to the regular addition of data from participating laboratories. The IAV-S surveillance program is voluntary and, as a result, the accessions and samples submitted represent a subset of the swine population. The surveillance system is not representative of the total U.S. domestic swine population; therefore, the data cannot be used to determine IAV-S prevalence or other epidemiologic measures in the swine population; however, the data may help identify influenza trends in swine. Program guidance indicates samples should only be collected from animals displaying influenza-like illness. Reporting months are based on the month the sample was collected. When the submitter does not report relevant information, data are recorded as "unknown."

A laboratory accession generally represents a set of samples collected at a single premises on a single day and subsequently received at the laboratory. While a nasal swab or lung tissue sample represents a single animal within the herd, a single oral fluid sample may represent one to two pens of animals in a herd. A positive sample status is based on the screening real-time reverse transcriptase polymerase chain reaction (rRT-PCR) on one or more samples within the accession. The subtype result is based on rRT-PCR-based subtyping assays. Virus isolation (VI) and sequencing in the National Animal Health Laboratory Network (NAHLN) labs are only attempted on rRT-PCR positives meeting criteria, with sequences deposited into [GenBank](#), the public sequence database. On a monthly basis, USDA NVSL also performs whole genome sequencing (WGS) on a selected subset of virus isolates received into the repository through the surveillance program and deposits those sequences into [Genbank](#). On a quarterly basis, a phylogenetic analysis is performed by USDA's Agricultural Research Service (ARS) National Animal Disease Center (NADC) influenza researchers; phylogenetic analyses are based on all successful USDA surveillance sequencing results deposited into [GenBank](#).

## Program Updates

Information on IAV-S and the IAV-S surveillance program, as well as previous IAV-S quarterly reports, can be found at:

<https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/animal-disease-information/swine-disease-information/influenza-a-virus>

The focus of IAV-S surveillance remains on acquiring and analyzing contemporary viruses from sick swine for ongoing genetic studies. The NAHLN has several submission options to ensure that unusual viruses identified by methods other than standardized NAHLN testing processes can be submitted into the program. An updated version of the IAV-S NAHLN testing guidelines and instruction sheet can be found at:

- Algorithm:  
[https://www.aphis.usda.gov/animal\\_health/animal\\_dis\\_spec/swine/downloads/appendix\\_c\\_testing\\_guidelines.pdf](https://www.aphis.usda.gov/animal_health/animal_dis_spec/swine/downloads/appendix_c_testing_guidelines.pdf)
- Instructions:  
[https://www-author.aphis.usda.gov/animal\\_health/animal\\_dis\\_spec/swine/downloads/iaav-s-algorithm-instructions.pdf](https://www-author.aphis.usda.gov/animal_health/animal_dis_spec/swine/downloads/iaav-s-algorithm-instructions.pdf)

IAV-S isolates can be requested from the NVSL repository by following the instructions found at:

- Isolate request:  
[https://www.aphis.usda.gov/animal\\_health/lab\\_info\\_services/downloads/OrderingIAV-SRepositoryIsolates.pdf](https://www.aphis.usda.gov/animal_health/lab_info_services/downloads/OrderingIAV-SRepositoryIsolates.pdf)

## IAV-S Surveillance Objectives

[USDA's National Surveillance Plan for Swine Influenza Virus in Pigs \(July 2010\)](#) describes the current surveillance system for IAV in swine in detail. The surveillance objectives are to:

1. Monitor genetic evolution of endemic IAV in swine to better understand endemic and emerging influenza virus ecology;
2. Make influenza isolates from swine available for research and establish a data management system to facilitate genetic analysis of these isolates and related information; and
3. Select proper isolates for the development of relevant diagnostic reagents, updated diagnostic assays, and vaccine seed stock products.

## Objective 1. Monitoring Genetic Evolution of Endemic IAV in Swine to Better Understand Endemic and Emerging Influenza Virus Ecology

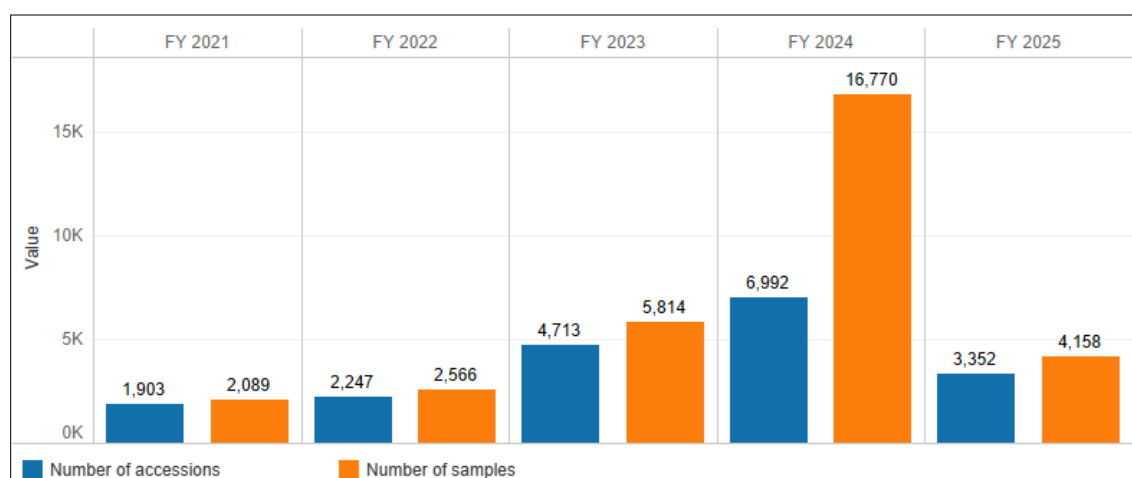
Objective 1 is met through the submission of diagnostic laboratory samples to the surveillance system, collection of the viruses that are isolated from the samples, and analysis of the hemagglutinin (HA) and neuraminidase (NA) sequences that are generated at the NAHLN laboratories. Each month, selected viruses undergo whole genome sequencing by the NVSL. Phylogenetic analysis of the genetic sequences submitted

through the surveillance program is provided through an interagency agreement with the USDA's Agricultural Research Service (ARS) National Animal Disease Center (NADC).

## National Surveillance Data Summary

The Cycle threshold (Ct) maximum value differs depending on the sample type. If lung/nasal samples have a Ct value of 25 or less and oral fluid samples have a Ct value of 20 or less, virus isolation and sequencing will be attempted. If there is something unique related to the virus, like it is causing high mortality, but the samples have higher than the established maximum Ct values, they will still enter the surveillance stream.

In Q4 FY2025, 977 samples were tested from 668 submitted accessions for a total of 4,158 samples from 3,352 accessions submitted in FY2025 (Figure 1). Figure 2 shows the overall trends in number of accessions submitted, rRT-PCR and VI positive accessions and subtyped accessions with a notable increase in accessions submitted and positive accessions beginning in August 2022 and continuing through Q2 FY2025 with a large spike from January 2024 through May 2024. The positivity rate, calculated by the number of positive accessions divided by the total number of accessions submitted for each month, shows seasonal fluctuations but has otherwise remained relatively consistent since 2022.



**Figure 1. Number of IAV-S laboratory accessions and samples tested in swine FY2021 through Q4 FY2025**

Figure 3 shows the number and distribution of subtype detections in Q4 FY2025. A total of 224 samples were subtyped, including H1N1 (n=71), H1N2 (n=79), H3N2 (n=69), and mixed subtype (n=5).

Figure 4 breaks down accessions by rRT-PCR subtype for FY2021 through Q4 FY2025. H1N1 was the predominant subtype detected in that time period with the exception of FY2025, where H1N2 was predominant. It is important to note that there is wide genetic diversity within each subtype.

Figure 5 displays the number of VI attempts in purple, successful VI attempts in orange, and the number of sequenced viral isolates submitted to [GenBank](#) in blue.

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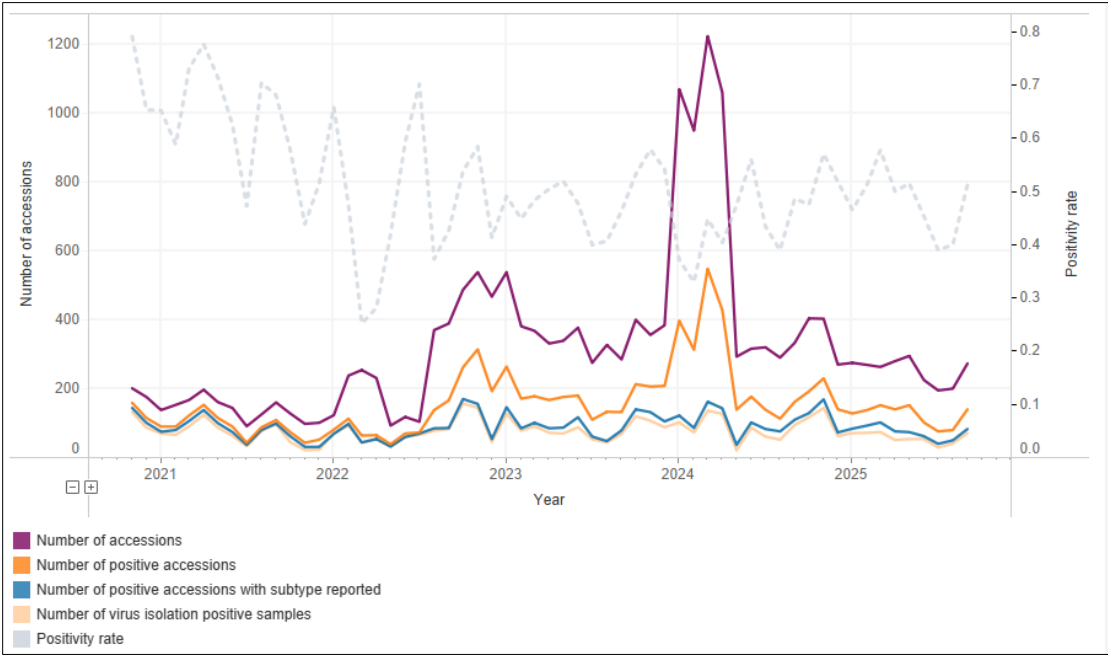


Figure 2. IAV-S number of accessions submitted, subtyped accessions, rRT-PCR positive accessions, virus isolation positive accessions, and positivity rate over time (monthly), FY2021 through Q4 FY2025

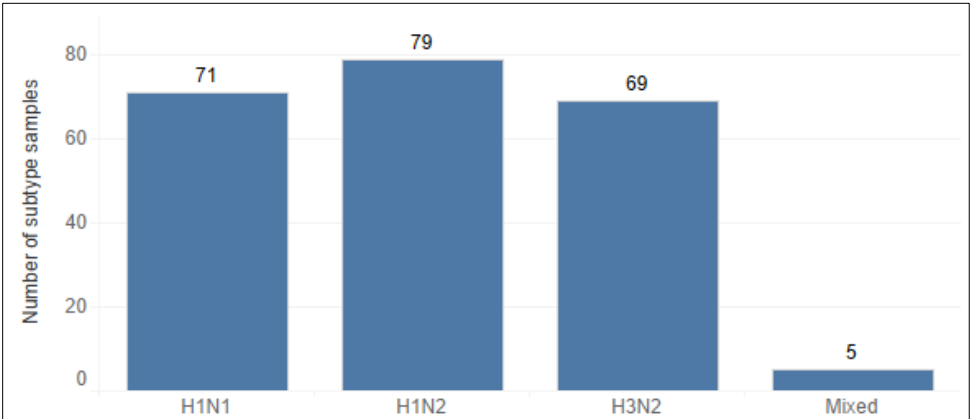


Figure 3. Number of IAV-S subtype detections in Q4 FY2025

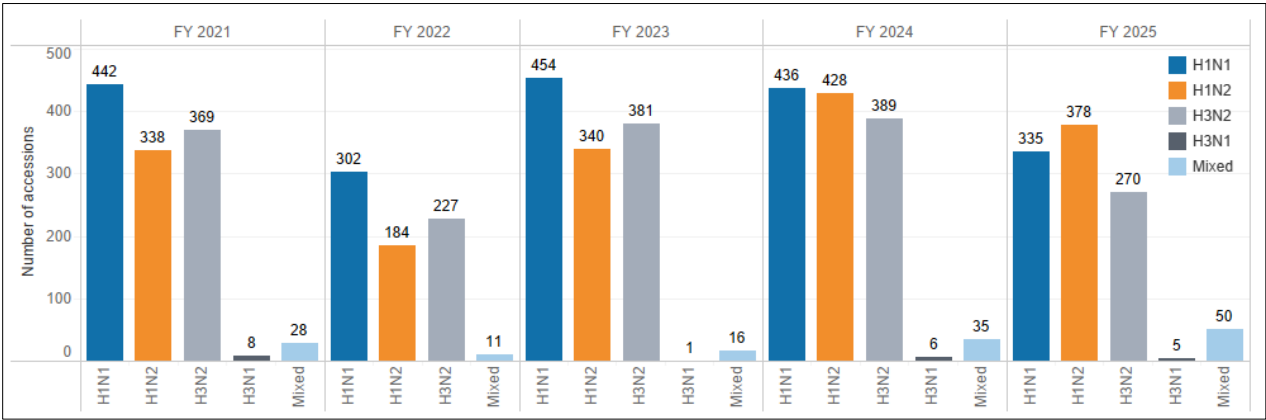
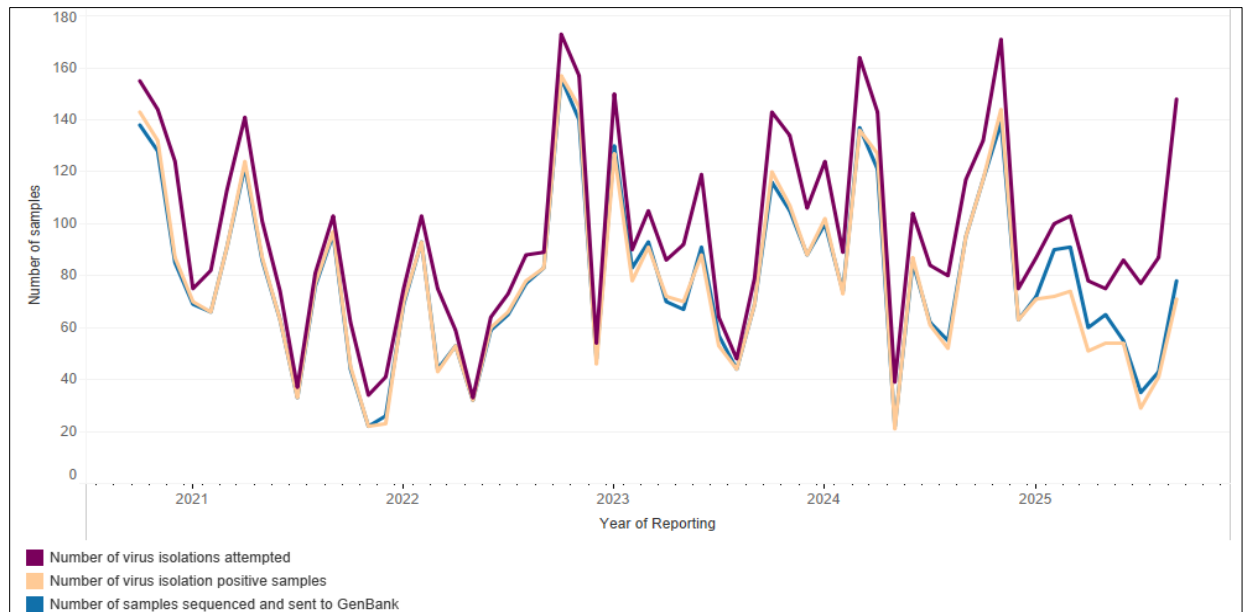


Figure 4. Breakdown of IAV-S accessions by subtype rRT-PCR from FY2021 through Q4 FY2025

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**Figure 5. Number of IAV-S virus isolations attempted, positive virus isolations, and GenBank submissions from FY2021 through Q4 FY2025**

Lab accessions were evaluated by age-class for the fourth quarter in FY2025. The most common subtype isolated in all of the classes was H1N2 (please note the overall low positive accessions from the sow/boar class) with the exception of the unknown/not recorded class where H1N1 was most predominant (Table 1). Table 2 displays the number of IAV-S positive accessions by specimen and viral subtype. All sample types yielded at least 56% or above in successful virus isolation (VI) attempts, peaking at 100% for oral fluid and other specimen types, followed by lung specimens at 83% with 126 successful attempts out of 151 accessions and nasal swab/wipe samples being the least fruitful with 56% success rate with 10 out of 18 accessions having successful VI. However, please note the very low number of accessions with subtypes reported for all sample types besides lung samples.

**Table 1. Number of positive accessions tested for IAV-S by age class and viral subtype, Q4 FY2025**

| Age Class (group)    | Number of H1N1 | Number of H1N2 | Number of H3N1 | Number of H3N2 | Number of Mixed |
|----------------------|----------------|----------------|----------------|----------------|-----------------|
| Suckling             | 13             | 14             | 0              | 12             | 1               |
| Nursery              | 23             | 27             | 0              | 19             | 4               |
| Grow/Finish          | 14             | 18             | 0              | 15             | 0               |
| Sow/Boar             | 0              | 3              | 0              | 0              | 0               |
| Not Recorded/Unknown | 5              | 4              | 0              | 1              | 0               |

**Table 2. Number of positive accessions\* tested for IAV-S by specimen type and by viral subtype, Q4 FY2025**

| Specimen Type (group) | Number of accessions with subtype reported | Percent of subtyped accessions with positive virus isolation | Number of H1N1 | Number of H1N2 | Number of H3N1 | Number of H3N2 | Number of Mixed | Number of samples sequenced and sent to GenBank |
|-----------------------|--------------------------------------------|--------------------------------------------------------------|----------------|----------------|----------------|----------------|-----------------|-------------------------------------------------|
| Lung                  | 151                                        | 83%                                                          | 47             | 52             | 0              | 42             | 0               | 141                                             |
| Nasal Swab or Wipe    | 10                                         | 56%                                                          | 3              | 4              | 0              | 3              | 0               | 10                                              |
| Oral Fluids           | 3                                          | 100%                                                         | 3              | 0              | 0              | 0              | 0               | 3                                               |
| Other Specimens       | 2                                          | 100%                                                         | 0              | 2              | 0              | 0              | 0               | 2                                               |

\*Accessions may include samples with multiple specimen types. In these cases, individual accessions are counted in more than one

specimen type category.

## Regional surveillance data

In this section, we present IAV-S surveillance data across five different regions of the United States (Figure 6). These regions are based on former USDA administrative districts only and do not represent specific industry distributions. Submissions are voluntary, as is providing any identifying information beyond State of animal origin with the submission. Therefore, regional and/or national incidence, prevalence, or other epidemiological measures cannot be determined from this data.



Figure 6. A map of the regions for national IAV-S surveillance

## Summary of Regional Data from ARS

Table 3 lists the predominant HA/NA phylo-type pairs by region from October 2024 through September 2025, with predominant being defined as comprising at least 10% of a region's HA/NA pairs. The total number column displays the total number of isolates that were phylo-typed for each region during that time. Historically, region 5 submits substantially fewer accessions than the other regions. Region 2 contains the most diversity of all the regions.

Figure 7 shows the distribution of rRT-PCR subtyped accessions across the five regions for Q4 FY2023 through Q4 FY2025. Over the last 8 quarters, H1N1 was the predominant subtype in Regions 1,3, and 5 (please note the overall low accessions for Region 5 (n=14) and H1N2 was the predominant subtype in Regions 2 and 4.

Table 3. Summary of predominant IAV-S HA/NA\* phylo-types by US region for the 1-year window from October 2024 through September 2025

| Region          | Total Number | Predominant HA/NA subtypes                                                                                             |
|-----------------|--------------|------------------------------------------------------------------------------------------------------------------------|
| 1               | 80           | H3N2 (H3-2010.1 / N2-2002B) (n=22)<br>H1N2 (H1-1B.2.1 / N2-1998B) (n=17)<br>H1N1 (H1-1A.1.1.3 / N1-C.3.2) (n=9)        |
| 2 <sup>+</sup>  | 610          | H1N1 (H1-1A.3.3.3-c3 / N1-C.3.2) (n=132)<br>H3N2 (H3-2010.1 / N2-2002B) (n=102)<br>H1N2 (H1-1B.2.1 / N2-1998B) (n=100) |
| 3               | 79           | H1N1 (H1-1A.1.1.3 / N1-C.2.1) (n=11)<br>H3N2 (H3-2010.1 / N2-2002B) (n=11)<br>H1N1 (H1-1A.1.1.3 / N1-P) (n=8)          |
| 4               | 44           | H1N2 (H1-1B.2.1 / N2-1998B) (n=15)<br>H3N2 (H3-2010.1 / N2-2002B) (n=12)<br>H1N1 (H1-1A.3.3.2 / N1-P) (n=3)            |
| 5 <sup>++</sup> | 4            | H1N1 (H1-1A.1.1.3 / N1-C.2.1) (n=1)<br>H1N1 (H1-1A.3.3.2 / N1-P) (n=1)<br>H1N2 (H1-1A.1.1.3 / N2-2002B) (n=1)          |
| All             | 817          | H3N2 (H3-2010.1 / N2-2002B) (n=148)<br>H1N1 (H1-1A.3.3.3-c3 / N1-C.3.2) (n=146)<br>H1N2 (H1-1B.2.1 / N2-1998B) (n=138) |

\*HA/NA pairs included if they comprise over 10% from a region

<sup>+</sup> Most diversity of all regions

<sup>++</sup> Low participation

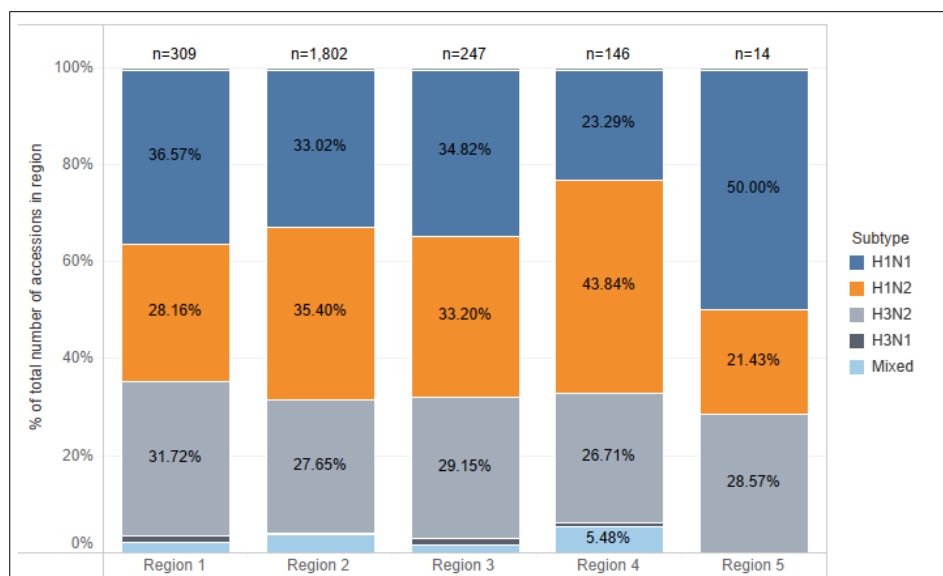


Figure 7. Distribution of IAV-S rRT-PCR subtyped accessions across five US regions for Q4 FY2023 through Q4 FY2025

### Phylogenetic analysis of sequences from the IAV-S surveillance system

Phylogenetic analysis of gene sequences of IAV in swine is conducted by ARS to further examine the genetic changes that occur in HA and NA genes of this rapidly changing virus. Through collaboration with ARS, a dataset of 68 isolates with published sequences in [GenBank](#) was characterized by phylogenetic analysis for the Q4 FY2025 report. This analysis provides information on the genetic diversity and evolutionary patterns of IAV in swine and allows for inferences about population and/or vaccine immunity.<sup>1</sup>

The following series of bar charts parse the data into an approximately 2-year window by quarters and region, describing virus subtypes (Figure 8) and phylogenetic clades of H1, H3, N1 and N2 subtypes (Figures 9-12). Regional charts depicting various combinations of HA and NA are available in Appendix 1.

Figure 8 demonstrates the four subtypes H1N1, H1N2, H3N1 and H3N2 across the five regions. Region 2 reported the most submissions with Regions 1, 3, and 4 all reporting a similar number of submissions. All were a mixture of mostly H1N1, H1N2, and H3N2 subtypes. Limited accessions from a region can skew data and lead to misinterpretation, therefore less inference can be applied to results from region 5.

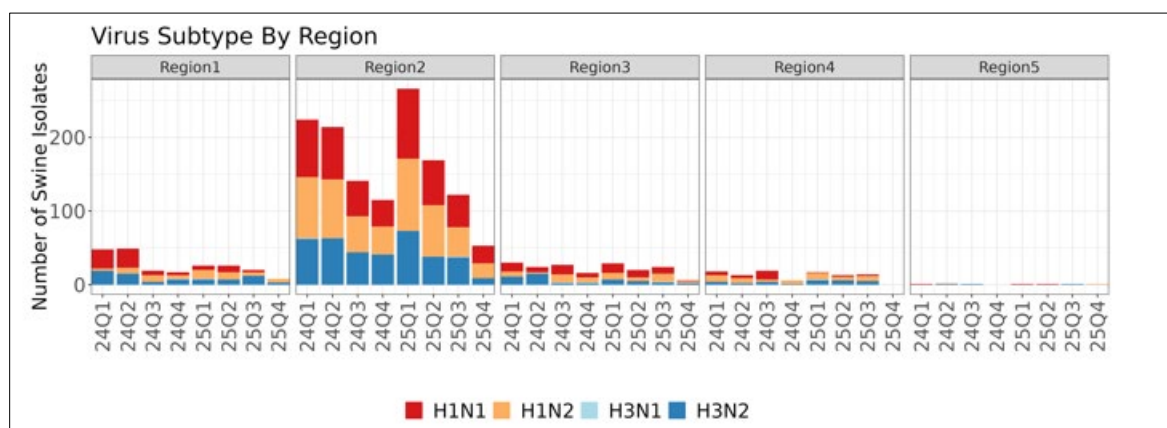


Figure 8. Temporal distribution of Influenza A virus of swine subtype by region for Q1 FY2024 to Q4 FY2025

<sup>1</sup> The ARS dataset is comprised of IAV-S surveillance isolate sequences from Genbank. This represents only a subset of the complete IAV-S surveillance dataset that includes PCR diagnostic test-based results as well as sequencing results. Therefore, ARS dataset results, such as subtype percentages, differ from the complete IAV-S dataset results provided in other sections of this report.

### National phylogenetic HA gene information

Due to the US clade classification being too coarse and no longer informative, starting in Q1 of FY2024, the HA genes from H1 subtype viruses are no longer classified using the US phylogenetic clades alpha, beta, gamma, delta1, delta2, or pandemic H1N1 2009 (H1N1pdm09). Similarly, for H3 subtype viruses, US phylogenetic clades Cluster IV, Cluster IV-A, Cluster IV-B, Cluster IV-C, Cluster IV-D, Cluster IV-E, Cluster IV-F, 2010.1, 2010.2, or human-like are no longer used. Instead, they are classified using global clades as described in these two published nomenclature systems: [A Phylogeny-Based Global Nomenclature System \(2016\)](#) and [Swine Influenza A Viruses and the Tangled Relationship with Humans \(2021\)](#). In Q4 FY2025, there were 6 H1 and 4 H3 clades detected. The predominant H1 HA clades were H1-1A.1.1.3, H1-1A.3.3.3-c3, and H1-1B.2.1, representing 83.3% of the H1 collection (n=54) (Figure 9). The predominant H3 HA clade was H3-2010.1, representing 64.3% of the H3 collection (n=14) (Figure 10). There was an increase of: 2.1% in clade H1-1B.2.2.2, 1.4% in clade H1-1A.3.3.3-c3, and 1.1% in clade H3-1990.4.i over the last year. There was a decrease of: 2.9% in clade H3-1990.4.a, 1.3% in clade H3-2010.1, and 0.6% in clade H1-1A.1.1.3 over the last year.

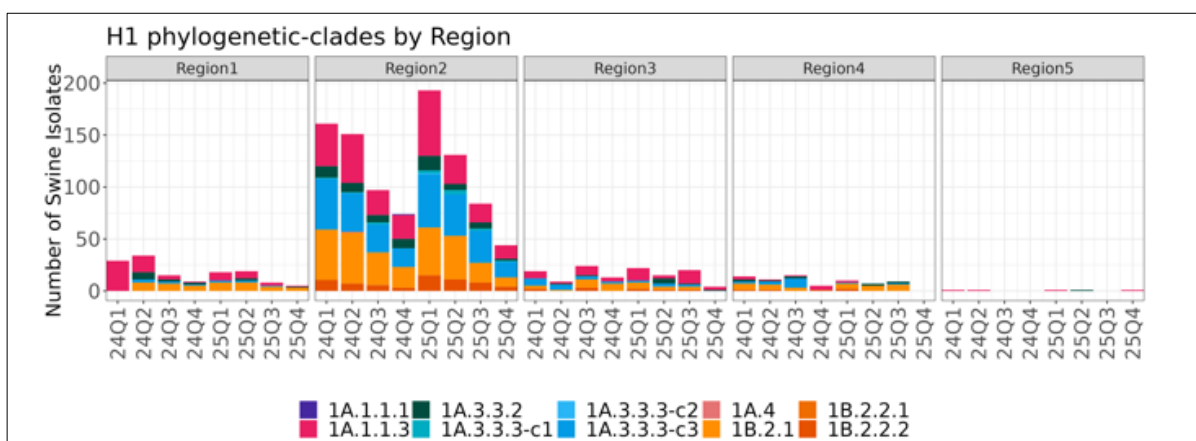


Figure 9. Temporal distribution of IAV-S H1 phylogenetic clades by region for Q1 FY2024 to Q4 FY2025

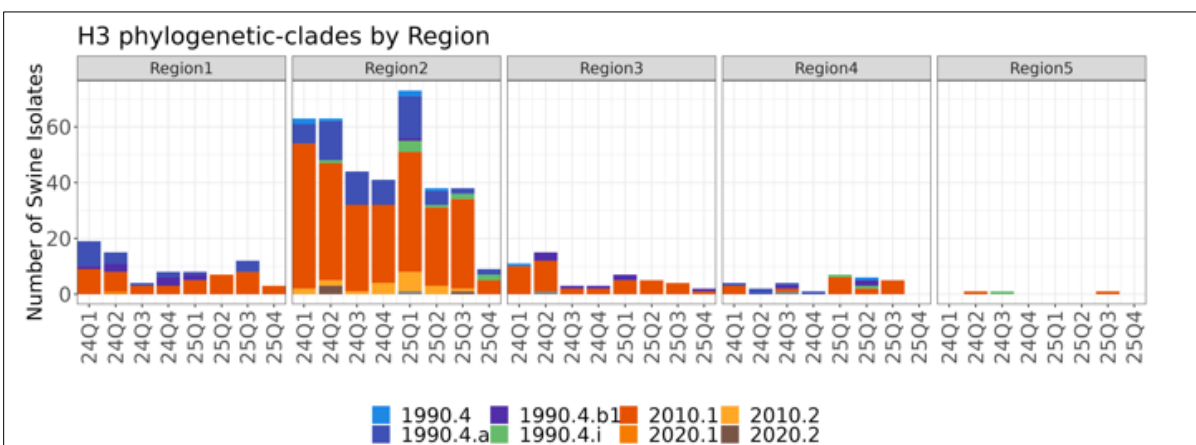


Figure 10. Temporal distribution of IAV-S H3 phylogenetic clades by region Q1 FY2024 to Q4 FY2025

### National phylogenetic NA gene information

In Q4 FY2025, N1-C.3.2 and N1-P, were the predominant N1 phylogenetic-clades, representing approximately 96.0% of the N1 collection (n=25). In Q4 FY2025, the predominant N2 phylogenetic-clades were N2-2002B and N2-1998B, representing approximately 88.4% of the N2 collection (n=43). Figures 11 and 12 show the temporal distribution of IAV-S N1 and N2 phylogenetic-clades by region for Q1 FY2024 through Q4 FY2025.

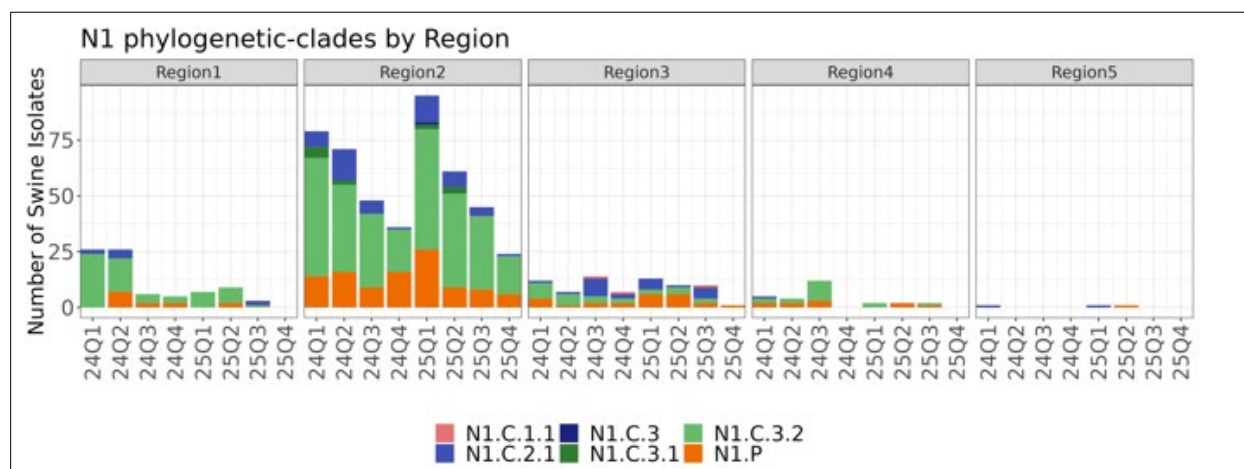


Figure 11. Temporal distribution of IAV-S N1 phylogenetic-clades by region for Q1 FY2024 to Q4 FY2025

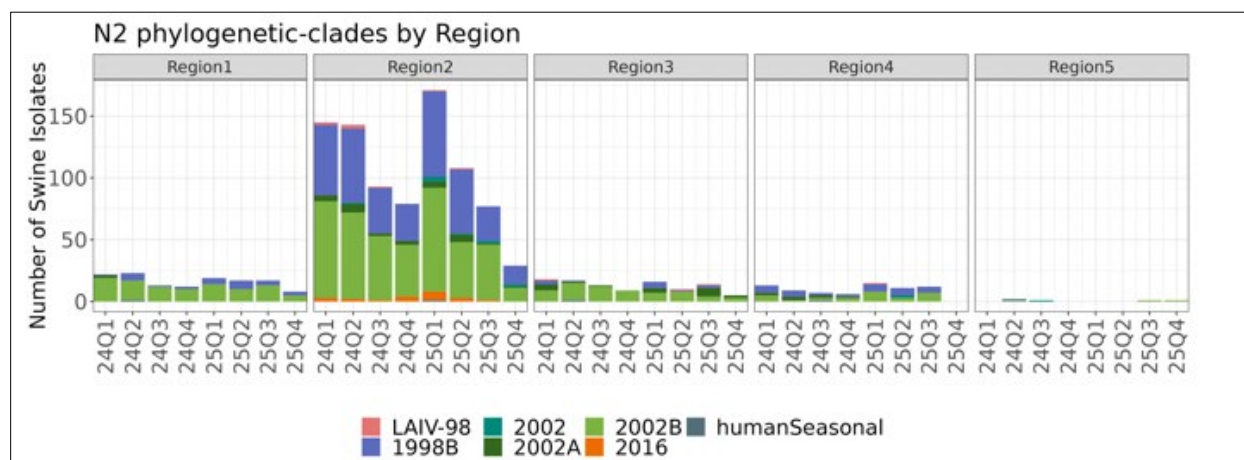


Figure 12. Temporal distribution of IAV-S N2 phylogenetic-clades by region for Q1 FY2024 to Q4 FY2025

### Representative HA genes

Six months of IAV-S data, April 2025–September 2025, were used by the NADC to identify circulating HA clades. An objective algorithm was used to identify the best-matched field strain housed in the USDA IAV-S virus repository (Table 4).

**Table 4. IAV-S Surveillance NADC Representative HA genes\***

| Strain                           | GenBank  | Global Clade   |
|----------------------------------|----------|----------------|
| A/swine/Missouri/A02858562/2025  | PV642386 | H1-1A.1.1.3    |
| A/swine/Iowa/A02858616/2025      | PV768573 | H1-1A.3.3.2    |
| A/swine/Minnesota/A02858524/2025 | PV579117 | H1-1A.3.3.3-c3 |
| A/swine/Illinois/A02858525/2025  | PV579119 | H1-1B.2.1      |
| A/swine/Iowa/A02858509/2025      | PV579093 | H1-1B.2.2.2    |
| A/swine/Michigan/A02858722/2025  | PX068532 | H3-1990.4.a    |
| A/swine/Indiana/A02858566/2025   | PV667545 | H3-2010.1      |
| A/swine/Kansas/A02858535/2025    | PV602059 | H3-2010.1      |

\*6-month HA1 objective algorithm and best-matched field strain in the repository was identified.

- April 2025 to September 2025 USDA HA data downloaded ( $n = 235$  H1,  $n = 103$  H3) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (<https://github.com/flu-crew/parnas>).
- The 5 H1 selections cover 86% of observed diversity; 3 H3 selections cover 48% of observed diversity.
- Clades were required to have a detection rate of at least 2% to be considered for selection ( $n \geq 7$ ).
  - Omitted H1-1A.3.3.3-c1 ( $n=3$ ), H3-1990.4.b1 ( $n=1$ ), H3-1990.4.i ( $n=6$ ), H3-2010.2 ( $n=1$ ), and H3-2020.2 ( $n=2$ )
- Note that 2 selections were made within H3-2010.1, which represents 89% of all H3 detections.

### Representative NA genes

Six months of IAV-S data, April 2025–September 2025, were used by the NADC to identify circulating NA clades. An objective algorithm was used to identify the best-matched field strain housed in the USDA IAV-S virus repository (Table 5).

**Table 5. IAV-S Surveillance NADC Representative NA genes\***

| Strain                           | GenBank  | Global Clade |
|----------------------------------|----------|--------------|
| A/swine/Texas/A02858512/2025     | PV579100 | N1-C.2.1     |
| A/swine/Minnesota/A02978932/2025 | PX060486 | N1-C.3.2     |
| A/swine/Minnesota/A02858557/2025 | PV642379 | N1-P         |
| A/swine/Iowa/A02858689/2025      | PV901737 | N2-1998B     |
| A/swine/Missouri/A02858549/2025  | PV642365 | N2-2002A     |
| A/swine/Iowa/A02858555/2025      | PV642375 | N2-2002B     |

\*6-month NA1 objective algorithm and best-matched field strain in the repository was identified.

- April 2025 to September 2025 USDA NA data downloaded ( $n = 115$  N1,  $n = 223$  N2) and a phylogenetic tree was inferred. For each HA clade, an objective representative selection was made using PARNAS (<https://github.com/flu-crew/parnas>).
- The 3 N1 selections cover 81% of observed diversity; the 3 N2 selections cover 60% of observed diversity.
- Clades were required to have a detection rate of at least 2% to be considered for selection ( $n \geq 7$ ).
  - Omitted N1-C.1.1 ( $n=1$ ), N2-2002 ( $n=6$ ), N2-2016 ( $n=1$ ), N2-LAIV-98 ( $n=2$ ).

### **Gene constellations**

Please note that complete WGS data and associated figures for Q4 FY2025 are not included in this report. This is due to a recent change in data processing timelines which impacted the availability of the most recent data needed for our comprehensive analysis. The comprehensive WGS analysis covering this time period will be provided in subsequent reports.

## Objective 2. Make Influenza Isolates from Swine Available for Research and Establish a Data Management System to Facilitate Genetic Analysis of these Isolates and Related Information

A primary goal of the IAV swine surveillance program is to share selected virus isolates obtained through the surveillance system with public health, animal health, and academic researchers to facilitate genetic analysis and research on viruses of interest. The NVSL Diagnostic Virology Laboratory maintains a repository of the viruses submitted into the surveillance system and provides these viruses upon request.

In Q4 FY2025, the NVSL Diagnostic Virology Laboratory provided a total of 28 isolates to two pharmaceutical and two government entities. NVSL received 165 isolates into the repository. Table 6 reports the total number of virus isolates received into the repository each year from FY2014 through FY2025. Table 7 reports the total number of isolates by subtype available in the repository for sharing.

IAV-S isolates can be requested from the NVSL repository by following the instructions found at:

[https://www.aphis.usda.gov/animal\\_health/lab\\_info\\_services/downloads/OrderingIAV-SRepositoryIsolates.pdf](https://www.aphis.usda.gov/animal_health/lab_info_services/downloads/OrderingIAV-SRepositoryIsolates.pdf)

**Table 6. IAV-S isolates received in NVSL repository by fiscal year**

| Fiscal Year  | Number of Isolates |
|--------------|--------------------|
| FY2025       | 1,091              |
| FY2024       | 1,083              |
| FY2023       | 1,035              |
| FY2022       | 641                |
| FY2021       | 1,108              |
| FY2020       | 1,074              |
| FY2019       | 1,055              |
| FY2018       | 994                |
| FY2017       | 844                |
| FY2016       | 1,046              |
| FY2015       | 883                |
| FY2014       | 765                |
| <b>TOTAL</b> | <b>11,619</b>      |

**Table 7. Total number of subtyped IAV-S isolates collected from 2009- Q4 FY2025 and available through the NVSL repository**

| Subtype      | Number of Isolates Received in Q4 FY2025 | Total Number of Isolates in Repository |
|--------------|------------------------------------------|----------------------------------------|
| H3N2         | 53                                       | 3,740                                  |
| H3N1         | 2                                        | 33                                     |
| H1N1         | 58                                       | 4,339                                  |
| H1N2         | 52                                       | 4,235                                  |
| Mixed        | 0                                        | 304                                    |
| <b>TOTAL</b> | <b>165</b>                               | <b>12,651</b>                          |

## Objective 3. Select Proper Isolates for Development of Relevant Diagnostic Reagents, Updating Diagnostic Assays, and Vaccine Seed Stock Products

USDA makes IAV-S isolates available in the public domain for further research. ARS-NADC conducts research on isolates obtained from the repository and sequences generated from the surveillance system. Genetic sequencing from the USDA program that is reported to [GenBank](https://www.ncbi.nlm.nih.gov/genbank/) is available for private corporations, government entities, academia, and other scientific community partners for research and vaccine strain selection and efficacy testing. NVSL and ARS staff are consulted as subject matter experts when necessary.

## **Conclusion**

The IAV-S voluntary surveillance system in swine continues to provide insight into the genetic makeup of circulating influenza A virus in limited populations of commercial pigs. Genetic information and virus isolates are made publicly available for further research and possible vaccine strain selection and efficacy testing. Influenza A virus in swine remains a dynamic virus with high levels of genetic variability in the hemagglutinin and neuraminidase genes.

## **Appendix 1. Regional Charts of IAV-S HA and NA Combinations by Percentage**

The following charts present the percentages of combinations of IAV-S HA and NA by region based on ARS-NADC phylogenetic analyses. The results are reported from October 2024 through September 2025 for regions 1-3, October 2024 through June 2025 for region 4, and November 2024 through July 2025 for region 5. These “heat maps” represent the percentage of combinations by using a color gradient where a deeper gradient color represents a greater percentage occurrence for a particular HA-NA combination. HA clusters are listed on the left vertical axis of the chart and NA clusters are listed on the bottom horizontal axis. Line up the HA cluster with the corresponding NA cluster to determine the occurrence of that particular combination.



# Region 1

Percentage of HA and NA combinations - Oct 2024 to Sep 2025

| HA Clade       | N1.C.2.1 | N1.C.3.2 | N1.P | N2.1998B | N2.2002B | HA.Total |
|----------------|----------|----------|------|----------|----------|----------|
| H1.1A.1.1.3    | 2.5      | 11.2     |      | 2.5      | 7.5      | 23.7     |
| H1.1A.3.3.2    |          |          | 2.5  |          | 1.2      | 3.7      |
| H1.1A.3.3.3-c3 |          | 6.2      |      |          |          | 6.2      |
| H1.1B.2.1      |          |          |      | 21.2     | 7.5      | 28.7     |
| H3.1990.4.a    |          |          |      |          | 6.2      | 6.2      |
| H3.1990.4.b1   |          |          |      |          | 2.5      | 2.5      |
| H3.2010.1      |          | 1.2      |      |          | 27.5     | 28.7     |
| NA.Total       | 2.5      | 18.6     | 2.5  | 23.7     | 52.4     |          |
|                | N1.C.2.1 | N1.C.3.2 | N1.P | N2.1998B | N2.2002B | HA.Total |
|                | NA Clade |          |      |          |          |          |

Total HA & NA combinations – 80



## Region 2

Percentage of HA and NA combinations - Oct 2024 to Sep 2025

| HA Clade       | N1.C.2.1 | N1.C.3 | N1.C.3.1 | N1.C.3.2 | N1.P | N2.1998B | N2.2002 | N2.2002A | N2.2002B | N2.2016 | N2.humanSeasonal | N2.LAIV-98 | HA.Total |
|----------------|----------|--------|----------|----------|------|----------|---------|----------|----------|---------|------------------|------------|----------|
| H1.1A.1.1.3    | 2.6      |        |          | 2.1      | 3.6  | 9.7      |         | 0.2      | 1.8      |         |                  |            | 20       |
| H1.1A.3.3.2    |          |        |          |          | 4.4  |          |         |          | 0.2      |         |                  |            | 4.6      |
| H1.1A.3.3.3-c1 | 1.3      |        |          |          |      |          |         |          | 0.3      |         |                  |            | 1.6      |
| H1.1A.3.3.3-c2 |          | 0.2    |          |          |      |          |         |          |          |         |                  |            | 0.2      |
| H1.1A.3.3.3-c3 |          |        | 0.8      | 21.6     |      |          |         |          |          |         |                  |            | 22.4     |
| H1.1B.2.1      |          |        |          |          |      | 16.4     |         |          | 2.6      |         |                  |            | 19       |
| H1.1B.2.2.2    |          |        |          |          |      | 0.8      |         | 1        | 4.1      |         |                  | 0.3        | 6.2      |
| H3.1990.4      |          |        |          |          |      |          |         |          | 0.5      |         |                  |            | 0.5      |
| H3.1990.4.a    |          |        |          |          |      |          |         | 0.2      | 3.8      |         |                  |            | 4        |
| H3.1990.4.b1   |          |        |          |          |      |          |         |          | 0.2      |         |                  |            | 0.2      |
| H3.1990.4.i    |          |        |          |          |      |          | 1.5     |          |          |         |                  |            | 1.5      |
| H3.2010.1      |          |        |          | 0.2      |      |          |         | 0.8      | 16.7     |         |                  |            | 17.7     |
| H3.2010.2      |          |        |          |          |      |          |         |          |          | 1.8     |                  |            | 1.8      |
| H3.2020.2      |          |        |          |          |      |          |         |          | 0.2      |         |                  |            | 0.2      |
| H3.other-human |          |        |          |          |      |          |         |          |          |         | 0.2              |            | 0.2      |
| NA.Total       | 3.9      | 0.2    | 0.8      | 23.9     | 8    | 26.9     | 1.5     | 2.2      | 30.4     | 1.8     | 0.2              | 0.3        |          |

NA Clade

Total HA & NA combinations – 610



# Region 3

Percentage of HA and NA combinations - Oct 2024 to Sep 2025

| HA Clade       | N1.C.1.1 | N1.C.2.1 | N1.C.3.2 | N1.P | N2.1998B | N2.2002A | N2.2002B | N2.LAIV-98 | HA.Total |
|----------------|----------|----------|----------|------|----------|----------|----------|------------|----------|
| H1.1A.1.1.3    |          | 13.9     |          | 10.1 | 2.5      | 8.9      | 1.3      | 2.5        | 39.2     |
| H1.1A.3.3.2    |          |          |          | 8.9  |          |          |          |            | 8.9      |
| H1.1A.3.3.3-c3 |          |          | 8.9      |      |          |          |          |            | 8.9      |
| H1.1B.2.1      |          |          |          |      | 7.6      |          | 7.6      |            | 15.2     |
| H1.1B.2.2.2    |          |          |          |      |          | 3.8      | 1.3      |            | 5.1      |
| H3.1990.4.b1   |          |          |          |      |          |          | 3.8      |            | 3.8      |
| H3.2010.1      | 1.3      |          |          |      |          | 3.8      | 13.9     |            | 19       |
| NA.Total       | 1.3      | 13.9     | 8.9      | 19   | 10.1     | 16.5     | 27.9     | 2.5        |          |
|                | N1.C.1.1 | N1.C.2.1 | N1.C.3.2 | N1.P | N2.1998B | N2.2002A | N2.2002B | N2.LAIV-98 | HA.Total |
|                | NA Clade |          |          |      |          |          |          |            |          |

Total HA & NA combinations – 79



# Region 4

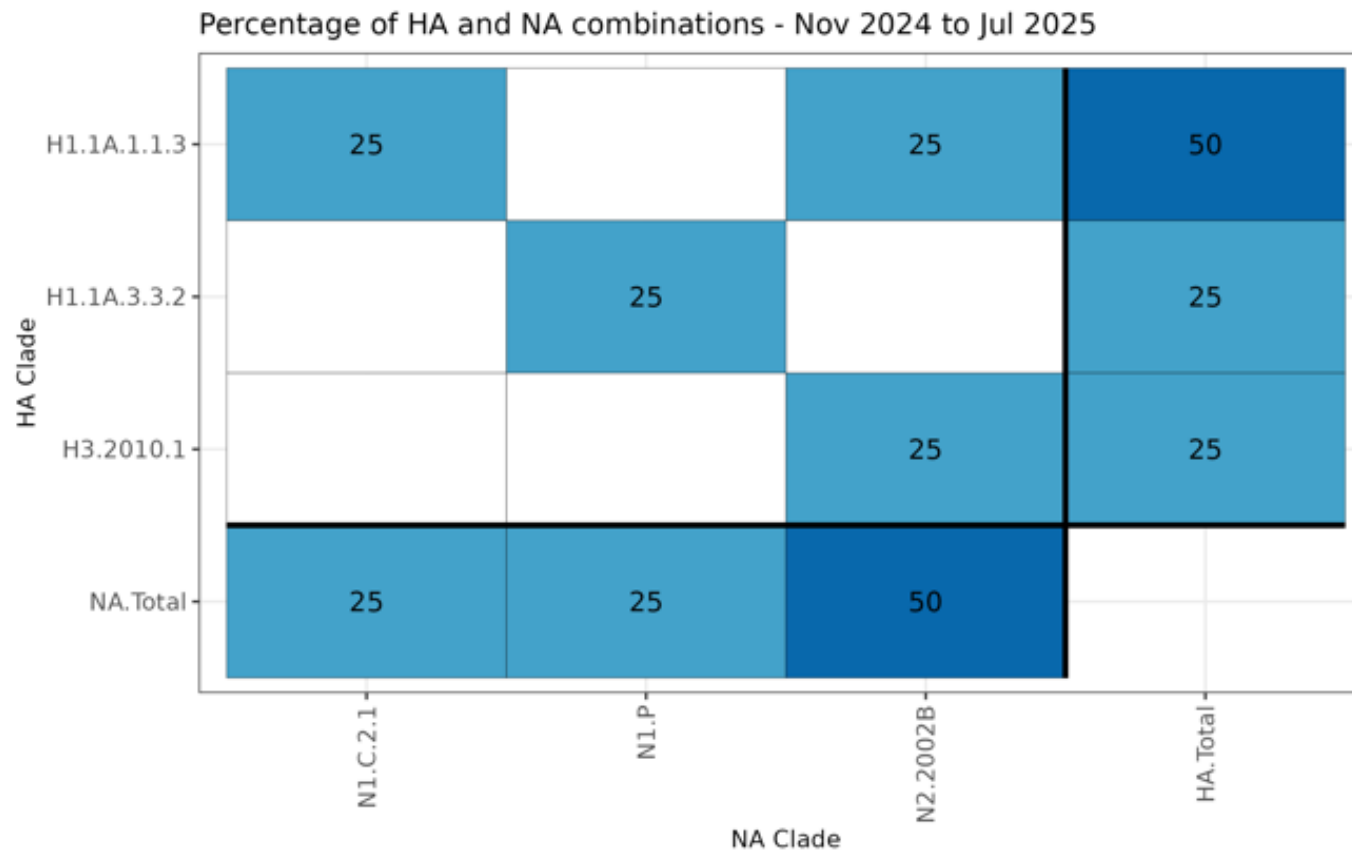
Percentage of HA and NA combinations - Oct 2024 to Jun 2025

| HA Clade       | N1.C.3.2 | N1.P | N2.1998B | N2.2002 | N2.2002B | N2.LAIV-98 | HA.Total |
|----------------|----------|------|----------|---------|----------|------------|----------|
| H1.1A.1.1.3    |          |      | 2.3      |         | 2.3      |            | 4.6      |
| H1.1A.3.3.2    |          | 6.8  |          |         | 2.3      |            | 9.1      |
| H1.1A.3.3.3-c3 | 4.5      |      |          |         |          |            | 4.5      |
| H1.1B.2.1      |          |      | 34.1     |         | 2.3      |            | 36.4     |
| H1.1B.2.2.2    |          |      |          |         | 2.3      | 2.3        | 4.6      |
| H3.1990.4      |          |      |          | 2.3     |          |            | 2.3      |
| H3.1990.4.b1   |          |      |          |         | 4.5      |            | 4.5      |
| H3.1990.4.i    | 2.3      |      |          | 2.3     |          |            | 4.6      |
| H3.2010.1      |          |      | 2.3      |         | 27.3     |            | 29.6     |
| NA.Total       | 6.8      | 6.8  | 38.7     | 4.6     | 41       | 2.3        |          |
|                | N1.C.3.2 | N1.P | N2.1998B | N2.2002 | N2.2002B | N2.LAIV-98 | HA.Total |
|                | NA Clade |      |          |         |          |            |          |

Total HA & NA combinations – 44



## Region 5



Total HA & NA combinations – 4